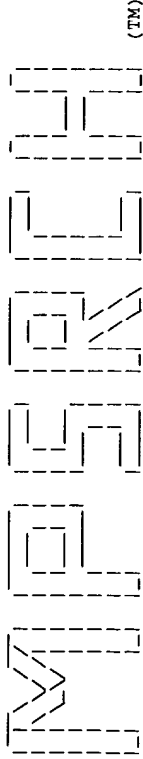


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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu May 22 08:50:36 1997; MasPar time 1.92 Seconds  
Tabular output not generated. 67.949 Million cell updates/sec

Title: >US-08-653-294-36  
Description: {1-12} from US08653294.pep  
Perfect Score: 98  
Sequence: 1 YRLAIRRIALRY 12

Scoring table: PAM 150  
Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Maximum DB seq length 60

Database: a-geneseq26  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19

Statistics: Mean 19.057; Variance 63.971; scale 0.298

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	98	100.0	12	18	R95429	2.34e-03
2	61	62.2	18	13	R71429	Human MHC 1 alpha 1 d 1.74e-01
3	52	53.1	20	16	R92911	HLA-B2702 CTL modul 1.27e+02
4	52	53.1	25	18	R95422	HLA-B2702 CTL modul 1.27e+02
5	52	53.1	25	8	R48286	Peptide fragment of H 1.27e+02
6	52	53.1	25	16	R83093	HLA-B2702 CTL modul 1.27e+02
7	50	51.0	20	18	R95415	HLA-B7.84-75-84 Palin 1.94e+02
8	50	51.0	20	16	R92913	HLA-B7.84-75-84 Palin 1.94e+02
9	49	50.0	10	18	R95423	HLA-B2702.75-84(D) 2.40e+02
10	49	50.0	10	18	R95413	Alpha1-helix of HLA-B 2.40e+02
11	49	50.0	10	8	R41208	Peptide fragment of C 2.40e+02
12	49	50.0	20	18	R95430	HLA-B2702 84-75T/75-8 2.40e+02
13	49	50.0	20	18	R95428	HLA-B2702 84-75-84 pa 2.40e+02
14	49	50.0	20	1	R05012	Papilloma virus type 2.40e+02
15	49	50.0	25	18	R95416	HLA-B2702.60-84. 2.40e+02
16	49	50.0	25	8	R41205	Peptide fragment of C 2.40e+02
17	49	50.0	25	16	R83090	HLA-B2702 CTL modul 2.40e+02

Note: Post-processor removed 28 summaries from list due to search parameters chosen.

ALIGNMENTS

RESULT 1  
ID R95429 standard; peptide; 12 AA.  
AC R95429;  
DT 12-NOV-1996 (first entry)  
DE HLA-B2702 84-79-84 palindrome.  
KW HLA: p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
KW cytolysis; antigen presenting cell.  
OS Synthetic.  
PN WO9513288-A1.  
PD 18-MAY-1995.  
PF 10-NOV-1994; U12985.  
PR 10-NOV-1993; US-150493.  
PA (STRD) UNIV LELAND STANFORD JUNIOR.  
PI Clayberger C, Krensky AM;  
DR WPI; 95-194027/25.  
PT Compsns. comprising lymphoid surface membrane proteins - which may  
inhibit cytolytic activity and differentiation of CTLs.  
PS Example; Page 12; 29pp; English.  
CC R95413, and R95415-R95431 represent palindromes and fragments of  
human-leucocyte-associated antigens. This sequence represents the  
HLA-B2702 84-79-84 palindrome. These sequences can be used to isolate  
the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
protein associated with T-cell activation in mammalian T-cells, and is  
also immunologically cross reactive with the heat shock protein Hsc70.  
p74 is found in a limited number of cell types, but is particularly  
expressed on B and T cells. p74 can be isolated by lysis of a suitable  
cell with an amphoteric detergent, and then passed through an affinity  
column containing a covalently bound HLA-B2702 palindromic peptide.  
Compositions comprising the extracellular fragment of p74 combined with  
HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate  
compounds can be screened for their effect on the cytolytic activity of  
T-cells, by combining them with the extracellular portion of p74 and  
determining the amount of binding between the candidate compound and p74.  
Modulation of CTL activity can be inhibited in a cellular composition  
containing T-cells and antigen presenting cells (APCs), by adding to the  
mix the extracellular portion of p74, in an amount sufficient to compete  
with p74 for the binding of the p74 ligand.  
SQ Sequence 12 AA;  
Query Match 100.0%; Score 98; DB 18; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.34e-03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 YRLAIRRIALRY 12  
QY 1 YRLAIRRIALRY 12  
RESULT 2  
ID R71429 standard; peptide; 18 AA.  
AC R71429;  
DT 12-OCT-1995 (first entry)  
DE Human MHC 1 alpha 1 domain peptide [Ala81]-Dk-(69-85).  
KW Major histocompatibility complex class 1; MHC 1; cell receptor;  
KW alpha 1 domain; peptide [Ala81]-Dk-(69-85); interaction modulation;  
KW arthritis; neoplasias; lupus erythematosus.  
OS Homo sapiens.  
PN WO9505189-A.  
PD 23-FEB-1995.  
PF 12-AUG-1994; U09189.  
PR 12-AUG-1993; US-105416.  
PA (REGC) UNIV CALIFORNIA.  
PI Goldstein A, Goodenow RS, Olsson L;  
DR WPI; 95-098577/13.  
PT Regulating cell surface receptor response - by modulating  
interaction between MHC class I antigen and the cell surface

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PT receptor
PS Example 4; Page 45; 103pp; English.
CC R71424-R71438 are human major histocompatibility complex class 1
CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they
CC were used to modulate interactions between MHC 1 and cell surface
CC receptors. Via competitive inhibition the peptides diminish the
CC receptors response, this feature may be useful for the treatment
CC of neoplasias, lupus erythematosus and arthritis.
SQ Sequence 18 AA;

Query Match 62.2%; Score 61; DB 13; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.74e+01;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 6 frvdlrtlalry 17
   ||: ||: |||||
QY 1 YRLAIRRIALRY 12

RESULT 3
ID R92911 standard; peptide; 20 AA.
AC R92911;
DT 16-MAY-1996 (first entry)
DE HLA-B*702 CTL modulating peptide (B*702.84-75/84-75).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B*702.
OS Synthetic.
PN W09526975-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B*7-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
CC Class I major histocompatibility complex (MHC) antigens. This sequence
CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC
CC HLA-B*702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;

Query Match 53.1%; Score 52; DB 16; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.27e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Db 1 yrlair-lnery 11
   |||||: ||
QY 1 YRLAIRRIALRY 12

RESULT 4
ID R95422 standard; peptide; 25 AA.
AC R95422;
DT 12-NOV-1996 (first entry)
DE HLAB38.6084.
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
PN W09513288-A1.
PD 18-MAY-1995.

PT receptor
PS Example 4; Page 45; 103pp; English.
CC R71424-R71438 are human major histocompatibility complex class 1
CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they
CC were used to modulate interactions between MHC 1 and cell surface
CC receptors. Via competitive inhibition the peptides diminish the
CC receptors response, this feature may be useful for the treatment
CC of neoplasias, lupus erythematosus and arthritis.
SQ Sequence 18 AA;

Query Match 62.2%; Score 61; DB 13; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.74e+01;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 6 frvdlrtlalry 17
   ||: ||: |||||
QY 1 YRLAIRRIALRY 12

RESULT 3
ID R92911 standard; peptide; 20 AA.
AC R92911;
DT 16-MAY-1996 (first entry)
DE HLA-B*702 CTL modulating peptide (B*702.84-75/84-75).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B*702.
OS Synthetic.
PN W09526975-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B*7-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
CC Class I major histocompatibility complex (MHC) antigens. This sequence
CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC
CC HLA-B*702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;

Query Match 53.1%; Score 52; DB 16; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.27e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Db 1 yrlair-lnery 11
   |||||: ||
QY 1 YRLAIRRIALRY 12

RESULT 4
ID R95422 standard; peptide; 25 AA.
AC R95422;
DT 12-NOV-1996 (first entry)
DE HLAB38.6084.
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
PN W09513288-A1.
PD 18-MAY-1995.

PF 10-NOV-1994; U12985.
PR 10-NOV-1993; US-150493.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI; 95-194027/25.
PT Compens. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 9; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLAB38.6084. These sequences can be used to isolate the protein p74 from
CC a T-cell lysate. p74 is a T-cell surface membrane protein associated
CC with T-cell activation in mammalian T-cells, and is also immunologically
CC cross reactive with the heat shock protein Hsc70. p74 is found in a
CC limited number of cell types, but is particularly expressed on B and T
CC cells. p74 can be isolated by lysis of a suitable cell with an
CC amphoteric detergent, and then passed through an affinity column
CC containing a covalently bound HLA-B*2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B*2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
CC compounds can be screened for their effect on the cytolytic activity of
CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition
CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.
SQ Sequence 25 AA;

Query Match 53.1%; Score 52; DB 18; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.27e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Db 15 yrenlr-ialry 25
   ||: || |||||
QY 1 YRLAIRRIALRY 12

RESULT 5
ID R48286 standard; peptide; 25 AA.
AC R48286;
DT 15-MAR-1994 (first entry)
DE Peptide fragment of HLA-B*38 antigen.
KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW parasitic disease; cytotoxic T lymphocyte; modulation.
OS Synthetic.
PN W09317699-A.
PD 16-SEP-1993.
PF 25-FEB-1993; U01758.
PR 02-MAR-1992; US-844716.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger CA, Krensky AM;
DR WPI; 93-303134/38.
PT New peptide(s) based on Class I HLA antigen domains - used for
PT modulating cytotoxic T-lymphocyte activity towards targets
PS Example 13; Page 39; 61pp; English.
CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
CC activity, either by inhibition or stimulation. It can be used for
CC inhibiting CTL toxicity in transplantations, for inducing CTL
CC activity in parasitic diseases and neoplasia and in studies on viral
CC infection. The peptide can also be used for identifying CTLs which
CC bind to it and removing subsets of CTLs from a T-cell composition.
CC This peptide is derived from the HLA-B*38 antigen and corresponds
CC to the amino acid positions 60-84 of that antigen.
SQ Sequence 25 AA;

Query Match 53.1%; Score 52; DB 8; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.27e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Db 15 yrenlr-ialry 25
   ||: || |||||

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OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Misc difference 3  
 FT /note- "NSD mutation"  
 PN WO9513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI: 95-194027/25.  
 PT Compens. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 11: 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the HLA-B2702.75-84(D). These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.  
 CC Sequence 10 AA;  
 SQ

Query Match 50.0%; Score 49; DB 18; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.40e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 r1alry 10  
 |||||  
 QY 7 R1ALRY 12

RESULT 10  
 ID R95413 standard; peptide; 10 AA.  
 AC R95413;  
 DT 12-NOV-1996 (first entry)  
 DE Alpha1-helix of HLA-B2702.  
 KW HLA: p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytotoxicity; antigen presenting cell.  
 OS Synthetic.  
 PN WO9513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI: 95-194027/25.  
 PT Compens. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 11: 29pp; English.  
 CC This sequence represents the alpha1-helix of the human-leucocyte-associated antigen B2702 (HLA-B2702). This sequence, epitopes, and palindromes of it (such as R95428) can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable

CC cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.  
 CC Sequence 10 AA;  
 SQ

Query Match 50.0%; Score 49; DB 18; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.40e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 r1alry 10  
 |||||  
 QY 7 R1ALRY 12

RESULT 11  
 ID R41208 standard; peptide; 10 AA.  
 AC R41208;  
 DT 15-MAR-1994 (first entry)  
 DE Peptide fragment of Class I HLA peptide.  
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;  
 KW parasitic disease; cytotoxic T lymphocyte; modulation.  
 OS Synthetic.  
 PN WO9317699-A.  
 PD 16-SEP-1993.  
 PF 25-FEB-1993; U01758.  
 PR 02-MAR-1992; US-844716.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger CA, Krensky AM;  
 DR WPI: 93-303134/38.  
 PT New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets  
 PS Claim 11; Page 54; 61pp; English.  
 CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition. This peptide sequence is more commonly found within larger peptide compounds of not more than 30 amino acids in length.  
 CC Sequence 10 AA;  
 SQ

Query Match 50.0%; Score 49; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.40e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 r1alry 10  
 |||||  
 QY 7 R1ALRY 12

RESULT 12  
 ID R95430 standard; peptide; 20 AA.  
 AC R95430;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B2702 84-75T/75-84T palindromic.  
 KW HLA: p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytotoxicity; antigen presenting cell.  
 OS Synthetic.  
 PN WO9513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.



PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI: 95-194027/25.  
 PT Compns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 12; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B2702 84-75/75-84 palindromic. These sequences can be used to  
 CC isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface  
 CC membrane protein associated with T-cell activation in mammalian T-cells,  
 CC and is also immunologically cross reactive with the heat shock protein  
 CC Hsc70. p74 is found in a limited number of cell types, but is  
 CC particularly expressed on B and T cells. p74 can be isolated by lysis of  
 CC a suitable cell with an amphoteric detergent, and then passed through an  
 CC affinity column containing a covalently bound HLA-B2702 palindromic  
 CC peptide. Compositions comprising the extracellular fragment of p74  
 CC combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and  
 CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity.  
 CC Candidate compounds can be screened for their effect on the cytolytic  
 CC activity of T-cells, by combining them with the extracellular portion of  
 CC p74 and determining the amount of binding between the candidate compound  
 CC and p74. Modulation of CTL activity can be inhibited in a cellular  
 CC composition containing T-cells and antigen presenting cells (APCs), by  
 CC adding to the mix the extracellular portion of p74, in an amount  
 CC sufficient to compete with p74 for the binding of the p74 ligand.  
 CC Sequence 20 AA;

Query Match 50.0%; Score 49; DB 18; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.40e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6  
 | | | | |  
 QY 1 YRLAIR 6

RESULT 13  
 ID R95428 standard; peptide; 20 AA.  
 AC R95428;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B2702 84-75-84 palindromic.  
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytotoxicity; antigen presenting cell.  
 OS Synthetic.  
 PN WO9513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI: 95-194027/25.  
 PT Compns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 12; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B2702 84-75-84 palindromic. These sequences can be used to isolate  
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
 CC protein associated with T-cell activation in mammalian T-cells, and is  
 CC also immunologically cross reactive with the heat shock protein Hsc70.  
 CC p74 is found in a limited number of cell types, but is particularly  
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
 CC cell with an amphoteric detergent, and then passed through an affinity  
 CC column containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and

CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 CC Sequence 20 AA;

Query Match 50.0%; Score 49; DB 18; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.40e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6  
 | | | | |  
 QY 1 YRLAIR 6

RESULT 14  
 ID R05012 standard; protein; 20 AA.  
 AC R05012;  
 DT 03-OCT-1990 (first entry)  
 DE Papilloma virus type 16 L2 peptide no. 55.  
 KW Papilloma virus; PV type 16; immunoglobulin; L2; ELISA; cervical cancer.  
 OS Synthetic.  
 PN WO9004790-A.  
 PD 03-MAY-1990.  
 PF 30-OCT-1989; SE0612.  
 PR 28-OCT-1989; SE-003870.  
 PA (MEDS-) Medscand AB.  
 PI Dillner J, Dillner L;  
 DR WPI: 90-164122/21.  
 PT Detecting papilloma virus infections - by identifying specific  
 PT antibodies against partic. viral proteins or fragments, esp. for  
 PT rapid diagnosis of cervical cancer.  
 PS Disclosure; 7pp; English.  
 CC The peptide is one of 66 overlapping peptides which together cover  
 CC the entire sequences of the L1 and L2 proteins of human PV type 16.  
 CC The peptide was found to be unreactive with Ig Abs in the sera of  
 CC patients with type 16 cervical cancer.  
 CC See also R04958-R05023.  
 CC Sequence 20 AA;

Query Match 50.0%; Score 49; DB 1; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 2.40e+02;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 8 ltsrrtgirly 17  
 | : | | : | |  
 QY 3 LAIRRIALRY 12

RESULT 15  
 ID R95416 standard; peptide; 25 AA.  
 AC R95416;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B2702.60-84.  
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytotoxicity; antigen presenting cell.  
 OS Synthetic.  
 PN WO9513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI: 95-194027/25.  
 PT Compns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 9; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents  
 CC HLA-B2702.60-84. These sequences can be used to isolate the protein p74.

CC from a T-cell lysate. p74 is a T-cell surface membrane protein  
 CC associated with T-cell activation in mammalian T-cells, and is also  
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is  
 CC found in a limited number of cell types, but is particularly expressed on  
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an  
 CC amphoteric detergent, and then passed through an affinity column  
 CC containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC this sequence, induces calcium influx, and inhibits cytotoxic T  
 CC lymphocyte (CTL) differentiation or cytotoxicity. Candidate compounds can  
 CC be screened for their effect on the cytotoxic activity of T-cells, by  
 CC combining them with the extracellular portion of p74 and determining the  
 CC amount of binding between the candidate compound and p74. Modulation of  
 CC CTL activity can be inhibited in a cellular composition containing  
 CC T-cells and antigen presenting cells (APCs), by adding to the mix the  
 CC extracellular portion of p74, in an amount sufficient to compete with p74  
 CC for the binding of the p74 ligand.  
 SQ Sequence 25 AA;

Query Match 50.0%; Score 49; DB 18; Length 25;  
 Best Local Similarity 100.0%; Pred.No. 2.40e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 20 rialry 25  
 QY 7 RIALRY 12  
 |||||

Search completed: Thu May 22 08:50:42 1997  
 Job time : 6 secs.

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MPSEARCH

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MPsearch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu May 22 08:36:18 1997; MasPar time 2.92 Seconds  
Tabular output not generated. 116.962 Million cell updates/sec

Title: >US-08-653-294-36  
Description: (1-12) from US08653294.pep  
Perfect Score: 98  
Sequence: 1 YRLAIRRLRY 12

Scoring table: PAM 150  
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir50  
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3  
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8  
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 26.905; Variance 45.950; scale 0.586

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	63	64.3	128	11	hypothetical protein	2.74e+00
2	58	59.2	388	16	hypothetical protein	1.59e+01
3	57	58.2	281	10	stf protein - Strep	2.23e+01
4	57	58.2	348	6	histocompatibility a	2.23e+01
5	56	57.1	78	10	DNA-directed RNA pol	3.13e+01
6	56	57.1	416	3	nicotinic acetylchol	3.13e+01
7	56	57.1	495	16	acetylcholine recept	3.13e+01
8	56	57.1	499	7	nicotinic acetylchol	3.13e+01
9	56	57.1	503	7	nicotinic acetylchol	3.13e+01
10	56	57.1	788	12	COI intron alpha-sen	3.13e+01
11	56	57.1	1151	11	GRR1 protein - yeast	3.13e+01
12	55	56.1	176	14	gene RXRbeta1 protei	4.36e+01
13	55	56.1	212	11	hypothetical protein	4.36e+01
14	55	56.1	281	10	stf protein - Strep	4.36e+01
15	55	56.1	491	3	ACBOE	4.36e+01
16	55	56.1	493	7	nicotinic acetylchol	4.36e+01
17	55	56.1	511	10	hypothetical protein	4.36e+01
18	55	56.1	583	8	chaperonin-60 alpha	4.36e+01
19	55	56.1	1420	5	apolipoprotein(a) (E	4.36e+01
20	55	56.1	2242	12	pyrimidine synthesis	4.36e+01
21	54	55.1	267	16	stf protein - Strep	6.05e+01

22	54	55.1	267	10	S44228	stf protein - Strep	6.05e+01
23	54	55.1	298	12	S53849	ribosomal protein S3	6.05e+01
24	54	55.1	462	11	S53114	hypothetical protein	6.05e+01
25	54	55.1	493	3	ACMSE	nicotinic acetylchol	6.05e+01
26	54	55.1	493	3	ACRTE	nicotinic acetylchol	6.05e+01
27	54	55.1	500	7	S12899	hypothetical protein	6.05e+01
28	54	55.1	551	9	S47750	phosphotransferase s	6.05e+01
29	54	55.1	699	1	WQBSGS	RNA12 protein - yeast	6.05e+01
30	54	55.1	850	12	S20462	DNA-directed RNA pol	6.05e+01
31	54	55.1	880	5	B33926	DNA-directed RNA pol	6.05e+01
32	54	55.1	880	5	S04717	DNA-directed RNA pol	6.05e+01
33	54	55.1	1748	1	JQ1555	RNA-directed RNA pol	6.05e+01
34	53	54.1	203	11	S05980	NHP10 protein - yeast	8.37e+01
35	53	54.1	252	16	I48120	p-glycoprotein - ham	8.37e+01
36	53	54.1	259	16	I48119	p-glycoprotein - ham	8.37e+01
37	53	54.1	324	13	S43424	zipper containing pr	8.37e+01
38	53	54.1	334	10	I40338	biotin synthetase -	8.37e+01
39	53	54.1	454	7	B39218	nicotinic acetylchol	8.37e+01
40	53	54.1	508	1	TVUT4B	phosphoglycerate kin	8.37e+01
41	53	54.1	622	3	ACCH4N	nicotinic acetylchol	8.37e+01
42	53	54.1	1281	14	I48123	p-glycoprotein isofo	8.37e+01
43	53	54.1	1858	4	A44214	genome polyprotein 1	8.37e+01
44	53	54.1	3391	4	GNWV16	genome polyprotein -	8.37e+01
45	53	54.1	3391	4	GNWV26	genome polyprotein -	8.37e+01

ALIGNMENTS

RESULT 1  
ENTRY #type complete  
TITLE hypothetical protein YDR360w - yeast (Saccharomyces cerevisiae)  
ORGANISM #formal\_name Saccharomyces cerevisiae  
DATE 23-Aug-1996 #sequence\_revision 06-Sep-1996 #text\_change 06-Sep-1996  
ACCESSIONS S69745  
REFERENCE S69745  
#authors Du, Z.  
#submission submitted to the EMBL Data Library, June 1995  
#description The sequence of S. cerevisiae cosmid 9476.  
#accession S69745  
#molecule\_type DNA  
#residues 1-128 #label DUZ  
#cross-references EMBL:U28372  
GENETICS  
#map\_position 4R  
SUMMARY #length 128 #molecular-weight 14014 #checksum 3949

Query Match 64.3%; Score 63; DB 11; Length 128;  
Best Local Similarity 54.5%; Pred. No. 2.74e+00;  
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 113 yilsrvr1tlr 123  
QY 1 YRLAIRRLRY 11

RESULT 2  
ENTRY #type complete  
TITLE hypothetical protein (insertion sequence ISH27-3) - Halobacterium halobium  
ORGANISM #formal\_name Halobacterium halobium  
DATE 21-Nov-1993 #sequence\_revision 21-Nov-1993 #text\_change 21-Nov-1993  
ACCESSIONS S15593  
REFERENCE S15593  
#authors Pfeiffer, F.; Blaselo, U.  
#journal Nucleic Acids Res. (1990) 18:6921-6925  
#title Transposition burst of the ISH27 insertion element family in Halobacterium halobium.  
#cross-references MUID:91088266  
#accession S15593  
#status preliminary

```

5
RESULT
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#accession
##status
##molecule_type
##residues
##cross-references
GENETICS
#map_position
KEYWORDS
SUMMARY
Db
Qy
RESULT
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#accession
##status
##molecule_type
##residues
##cross-references
GENETICS
#introns
CLASSIFICATION
KEYWORDS
FEATURE

```

```

70-84,134-135 #disulfide_bonds #status predicted\
83,295,329 #binding_site carbohydrate (Asn) (covalent) #status
predicted
SUMMARY #length 416 #checksum 3404

Query Match 57.1%; Score 56; DB 3; Length 416;
Best Local Similarity 58.3%; Pred. No. 3.13e+01;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 144 yslvirrlply 155
| | | | | | |
| | | | | | |
QY 1 YRLAIRRLRY 12

RESULT 7
ENTRY #type complete
TITLE acetylcholine receptor alpha chain precursor - bovine
ORGANISM #formal_name Bos primigenius taurus #common_name cattle
DATE 27-Apr-1996 #sequence_revision 27-Apr-1996 #text_change
27-Apr-1996
ACCESSIONS S60589
REFERENCE Criado, M.; Alamo, L.; Navarro, A.
#authors Neurochem. Res. (1992) 17:281-287
#journal Primary structure of an agonist binding subunit of the
#title nicotinic acetylcholine receptor from bovine adrenal
chromaffin cells.
#accession S60589
#status preliminary
#residues 1-495 #label CRI
#cross-references EMBL:X57032
SUMMARY #length 495 #molecular-weight 56914 #checksum 5081

Query Match 57.1%; Score 56; DB 15; Length 495;
Best Local Similarity 58.3%; Pred. No. 3.13e+01;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 223 yslvirrlply 234
| | | | | | |
| | | | | | |
QY 1 YRLAIRRLRY 12

RESULT 8
ENTRY #type complete
TITLE nicotinic acetylcholine receptor alpha-3 chain precursor -
rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change
15-Jun-1996
ACCESSIONS A24572
REFERENCE Boulter, J.; Evans, K.; Goldman, D.; Martin, G.; Treco, D.;
#authors Heinemann, S.; Patrick, J.
#journal Nature (1986) 319:368-374
#title Isolation of a cDNA clone coding for a possible neural
nicotinic acetylcholine receptor alpha-subunit.
#cross-references MUID:86118671
#accession A24572
#molecule_type mRNA
#residues 1-499 #label BOU
CLASSIFICATION #superfamily acetylcholine receptor
KEYWORDS glycoprotein; ion channel; neurotransmitter receptor;
postsynaptic membrane; transmembrane protein
FEATURE
1-25 #domain signal sequence #label SIG\
26-499 #product nicotinic acetylcholine receptor alpha chain
#label NAT
SUMMARY #length 499 #molecular-weight 57347 #checksum 1936

Query Match 57.1%; Score 56; DB 7; Length 499;
Best Local Similarity 58.3%; Pred. No. 3.13e+01;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

Db 227 yslvirrlply 238
| | | | | | |
| | | | | | |
QY 1 YRLAIRRLRY 12

RESULT 9
ENTRY #type complete
TITLE nicotinic acetylcholine receptor alpha-3 chain precursor,
neuronal - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change
08-Sep-1996
ACCESSIONS A53956
REFERENCE Mihovilovic, M.; Roses, A.D.
#authors Exp. Neurol. (1991) 111:175-180
#journal Expression of mRNAs in human thymus coding for the alpha3
#title subunit of a neuronal acetylcholine receptor.
#accession A53956
#status preliminary
#molecule_type mRNA
#residues 1-503 #label MIH
#cross-references GB:M37981
REFERENCE S21338
#authors Anand, R.; Lindstrom, J.
#submission submitted to the EMBL Data Library, June 1990
#description Nucleotide sequence of the mature human nicotinic
acetylcholine receptor beta-3 subunit gene.
#accession S21338
#status preliminary
#molecule_type mRNA
#residues 30-503 #label ANA
#cross-references EMBL:X53559
GENETICS GDB:CHRNA3
#gene
#cross-references GDB:125219
#map_position 15q24-15q24
CLASSIFICATION #superfamily acetylcholine receptor
SUMMARY #length 503 #molecular-weight 57153 #checksum 8851

Query Match 57.1%; Score 56; DB 7; Length 503;
Best Local Similarity 58.3%; Pred. No. 3.13e+01;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 231 yslvirrlply 242
| | | | | | |
| | | | | | |
QY 1 YRLAIRRLRY 12

RESULT 10
ENTRY #type complete
TITLE COI intron alpha-sen DNA protein - Podospora anserina
mitochondrion (SGC3)
ORGANISM #formal_name mitochondrion Podospora anserina
DATE 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
17-Feb-1994
ACCESSIONS B48327
REFERENCE Cummings, D.J.; Michel, F.; McNally, K.L.
#authors Curr. Genet. (1989) 16:381-406
#journal DNA sequence analysis of the 24.5 kilobase pair cytochrome
#title oxidase subunit I mitochondrial gene from Podospora
anserina: a gene with sixteen introns.
#accession B48327
#status preliminary
#molecule_type DNA
#residues 1-788 #label CUM
#cross-references GB:X55026; GB:M30937; GB:M61734
GENETICS mitochondrion
#genome
#genetic_code SGC3
KEYWORDS mitochondrion
SUMMARY #length 788 #molecular-weight 89463 #checksum 3000

```

```

Query Match          57.1%; Score 56; DB 12; Length 788;
Best Local Similarity 70.0%; Pred. No. 3.13e+01;
Matches              7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 598 lpirdilrly 607
      ||| |||
QY 3 LAIRRIALRY 12

RESULT 11
ENTRY GRRI protein - yeast (Saccharomyces cerevisiae)
TITLE protein J1885; protein YJR090c
ALTERNATE_NAMES #formal name Saccharomyces cerevisiae
ORGANISM 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
DATE 13-Sep-1995
ACCESSIONS A41529; S57109; S57111; S17487
REFERENCE A41529
#authors Flick, J.S.; Johnston, M.
#journal Mol. Cell. Biol. (1991) 11:5101-5112
#title GRRI of Saccharomyces cerevisiae is required for glucose
#cross-references MUID:92017785
#accession A41529
#molecule_type DNA
#residues 1-1151 #label FLI
#cross-references GB:M59247
REFERENCE S57085
#authors Manus, V.; Huang, M.E.; Galibert, F.
#submission submitted to the Protein Sequence Database, September 1995
#accession S57109
#molecule_type DNA
#residues 1-1151 #label MAN
#cross-references EMBL:249590
REFERENCE S57111
#authors Ramezani Rad, M.; Kirchrath, L.; Hollenberg, C.P.
#submission submitted to the Protein Sequence Database, September 1995
#accession S57111
#molecule_type DNA
#residues 1-2 #label RAM
#cross-references EMBL:249590
GENETICS
#gene LISTA:GRR1
#map_position 10R
KEYWORDS tandem repeat
FEATURE
409-725
SUMMARY #region 26-residue repeats
#length 1151 #molecular-weight 132733 #checksum 1173

Query Match          57.1%; Score 56; DB 11; Length 1151;
Best Local Similarity 41.7%; Pred. No. 3.13e+01;
Matches              5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 386 yrimikrlnfsf 397
      ||| ||| :
QY 1 YRLAIRRIALRY 12

RESULT 12
ENTRY gene RXRBeta1 protein - mouse (fragment)
TITLE #formal name Mus musculus #common name house mouse
ORGANISM 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
DATE 02-Jul-1996
ACCESSIONS I48752
REFERENCE I48752
#authors Nagata, T.; Kanno, Y.; Ozato, K.; Taketo, M.
#journal Gene (1994) 142:183-189
#title The mouse Rxrb gene encoding RXR beta: genomic organization
#cross-references MUID:94252565
and two mRNA isoforms generated by alternative splicing of
transcripts initiated from CpG island promoters.

```

```

#accession I48752
#status preliminary; translated from GB/EMBL/DBAJ
#molecule_type DNA
#residues 1-176 #label RES
#cross-references EMBL:X72017; NID:g510152; CDS-PID:g510153
GENETICS
#introns 76/1; 137/2
#note gene name RXRBeta1
SUMMARY #length 176 #checksum 8478

Query Match          56.1%; Score 55; DB 14; Length 176;
Best Local Similarity 66.7%; Pred. No. 4.36e+01;
Matches              6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 125 lqirrlslr 133
      ||| ||| :
QY 3 LAIRRIALR 11

RESULT 13
ENTRY S17476 #type complete
TITLE hypothetical protein YCL034w - yeast (Saccharomyces
ALTERNATE_NAMES cerevisiae)
ORGANISM #hypothetical protein YCL186
DATE 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change
ACCESSIONS S17476; S19362
REFERENCE S17471
#authors Ramezani Rad, M.; Luetzenkirchen, K.; Xu, G.; Kleinhans, U.;
#journal Hollenberg, C.P.
#title Yeast (1991) 7:533-538
#accession S17476
#cross-references EMBL:X59720
REFERENCE S19350
#authors Hollenberg, C.P.; Kleinhans, U.; Lutzenkirchen, K.; Ramezani
#submission submitted to the Protein Sequence Database, March 1992
#accession S19362
#molecule_type DNA
#residues 1-212 #label HOL
#cross-references EMBL:X59720
GENETICS
#map_position 3L
SUMMARY #length 212 #molecular-weight 23590 #checksum 526

Query Match          56.1%; Score 55; DB 11; Length 212;
Best Local Similarity 77.8%; Pred. No. 4.36e+01;
Matches              7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 115 airrkvlry 123
      ||| |||
QY 4 AIRRIALRY 12

RESULT 14
ENTRY S44230 #type complete
TITLE strf protein - Streptomyces glaucescens
ORGANISM #formal name Streptomyces glaucescens
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
ACCESSIONS S44230
REFERENCE S44224
#authors Mayer, G.; Piepersberg, W.
#submission submitted to the EMBL Data Library, April 1994
#accession S44230
#status preliminary
#molecule_type DNA

```

```
##residues      1-281 ##label MAY
##cross-references EMBL:X78974
GENETICS
#start_codon   GTG
SUMMARY      #length 281 #molecular-weight 31427 #checksum 4100
Query Match      56.1%; Score 55; DB 10; Length 281;
Best Local Similarity 70.0%; Pred. No. 4.36e+01;
Matches      7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db      234 riaarlr 243
      1 1 1 1 1 1 1
QY      2 RLAIIRIALR 11

RESULT 15
ENTRY   ACBOE      #type complete
TITLE   nicotinic acetylcholine receptor epsilon chain precursor -
        bovine
ORGANISM #formal_name Bos primigenius taurus #common_name cattle
DATE     28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change
        08-Dec-1994
ACCESSION A031174
REFERENCE A031174
#authors  Takai, T.; Noda, M.; Mishina, M.; Shimizu, S.; Furutani, Y.;
        Kayano, T.; Ikeda, T.; Kubo, T.; Takahashi, H.; Takahashi,
        T.; Kuno, M.; Numa, S.
#journal  Nature (1985) 315:761-764
#title    Cloning, sequencing and expression of cDNA for a novel
        subunit of acetylcholine receptor from calf muscle.
#cross-references MUID:85240565
#accession A031174
#molecule_type mRNA
#residues 1-491 ##label TAK
COMMENT   The epsilon chain can replace the gamma chain to form a functional
        receptor molecule.
CLASSIFICATION #superfamily acetylcholine receptor
KEYWORDS  glycoprotein; ion channel; neurotransmitter receptor;
        postsynaptic membrane; transmembrane protein
FEATURE
1-20      #domain signal sequence #status predicted #label SIG\
21-491    #product acetylcholine receptor epsilon chain #status
        predicted #label MAT\
240-266   #domain transmembrane #status predicted #label TM1\
273-291   #domain transmembrane #status predicted #label TM2\
307-328   #domain transmembrane #status predicted #label TM3\
420-436   #domain transmembrane amphipathic helix #status
        predicted #label TMH\
457-480   #domain transmembrane #status predicted #label TM4\
86,161,327 #binding_site carbohydrate (Asn) (covalent) #status
        predicted\
148-162   #disulfide_bonds #status predicted
SUMMARY   #length 491 #molecular-weight 54565 #checksum 7419
Query Match      56.1%; Score 55; DB 3; Length 491;
Best Local Similarity 58.3%; Pred. No. 4.36e+01;
Matches      7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Db      232 yslirrkplfy 243
      1 1 1 1 1 1 1
QY      1 YRLAIRIALRY 12
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Search completed: Thu May 22 08:36:46 1997  
Job time : 28 secs.

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:34:07 1997; Maspar time 2.32 Seconds  
Tabular output not generated. 182.533 Million cell updates/sec

Title: >US-08-653-294-31  
Description: (1-20) from US08653294.pep  
Perfect Score: 154  
Sequence: 1 YRLAIRLNERYLAIRLNER 20

Scoring table: PAM 150  
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot34  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 30.299; Variance 54.375; scale 0.557

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	71	46.1	361	3	FDEH_PSEPU 5-EXO-ALCOHOL DEHYDRO	9.83e+01
2	70	45.5	279	5	LEP3_ERWCA TYPE 4 PREPILIN-LIKE	1.38e+00
3	70	45.5	782	3	DPO2_ECOLI DNA POLYMERASE II (EC	1.38e+00
4	68	44.2	252	8	PYG4_ANASP PHYCOBILISOME ROD-COR	2.71e+00
5	68	44.2	253	8	PYG3_MASLA PHYCOBILISOME ROD-COR	2.71e+00
6	68	44.2	349	6	NTRB_ECOLI NITROGEN REGULATION P	2.71e+00
7	68	44.2	1051	5	ITR3_CRISP INTEGRIN ALPHA-3 PREC	2.71e+00
8	68	44.2	1051	5	ITR3_HUMAN INTEGRIN ALPHA-3 PREC	2.71e+00
9	67	43.5	346	8	RFAE_HAEIN ADP-HEPTOSE--LPS HEPT	3.77e+00
10	67	43.5	424	11	YQ05_CAEEL HYPOTHETICAL 48.0 KD	3.77e+00
11	65	42.2	349	6	NTRB_SALTY NITROGEN REGULATION P	7.24e+00
12	65	42.2	643	2	CR72_BACTI 72 KD CRYSTAL PROTEIN	7.24e+00
13	64	41.6	648	1	BGR_RAT BETA-GLUCURONIDASE PR	9.99e+00
14	64	41.6	1104	6	NIR_EMENT NITRATE REDUCTASE (NA	9.99e+00
15	64	41.6	3224	6	N358_HUMAN NUCLEAR PORE COMPLEX	9.99e+00
16	63	40.9	115	10	VG52_HSVSA HYPOTHETICAL GENE 52	1.37e+01
17	63	40.9	485	10	VGLC_HSV4 GLYCOPROTEIN C PRECUR	1.37e+01
18	63	40.9	580	4	GPC3_HUMAN GLYPICAN-3 PRECURSOR	1.37e+01
19	63	40.9	597	4	GPC3_RAT GLYPICAN-3 PRECURSOR	1.37e+01
20	63	40.9	648	1	AMT_PYRFU ALPHA-AMYLASE (EC 3.2	1.37e+01
21	62	40.3	253	7	PKNA_MYCLE PROTEIN KINASE PKNA.	1.88e+01
22	62	40.3	293	8	RL5_SCHPO 60S RIBOSOMAL PROTEIN	1.88e+01

23	62	40.3	558	10	VP10_RBSDV PROTEIN S10.	1.88e+01
24	62	40.3	818	9	SAP4_YEAST S1T4-ASSOCIATING PROT	1.88e+01
25	62	40.3	1176	6	NIR_NEUCR NITRATE REDUCTASE (NA	1.88e+01
26	61	38.6	239	3	CYSH_THIRO 3'-PHOSPHOADENOSINE 5	2.57e+01
27	61	39.6	354	4	FUT2_RABIT GALACTOSIDE 2-L-FUCOS	2.57e+01
28	61	39.6	358	11	YV29_MYCTU HYPOTHETICAL 39.3 KD	2.57e+01
29	61	39.6	587	7	PH84_YEAST INORGANIC PHOSPHATE T	2.57e+01
30	61	39.6	635	9	TPOR_HUMAN THROMBOPOIETIN RECEPT	2.57e+01
31	61	39.6	685	9	TGLC_MOUSE PROTEIN-GLUTAMINE GAM	2.57e+01
32	61	39.6	687	9	TGLC_BOVIN PROTEIN-GLUTAMINE GAM	2.57e+01
33	61	39.6	881	4	GALA_YEAST REGULATORY PROTEIN GA	2.57e+01
34	61	39.6	907	1	AVRA_PSESG AVIRULENCE A PROTEIN.	2.57e+01
35	61	39.6	928	8	RE_HUMAN RETINOBLASTOMA-ASSOCI	2.57e+01
36	61	39.6	1483	3	CYPL1_YEAST CYPL1 ACTIVATORY PROTE	2.57e+01
37	61	39.6	3712	1	ACVS_CEPAC DELTA-(L-ALPHA-AMINO	2.57e+01
38	60	38.0	114	10	UR96_HSVU PROTEIN U58.	3.49e+01
39	60	39.0	314	9	TRUB_ECOLI TRNA PSEUDOURIDINE 55	3.49e+01
40	60	39.0	337	3	DFRA_VITVI DIHYDROFLAVONOL-4-RED	3.49e+01
41	60	39.0	367	11	YV29_MYCLE HYPOTHETICAL 40.5 KD	3.49e+01
42	60	39.0	396	7	P53_SALIR CELLULAR TUMOR ANTIGE	3.49e+01
43	60	39.0	622	5	KUP_ECOLI KUP SYSTEM POTASSIUM	3.49e+01
44	60	39.0	693	8	RECG_HAEIN ATP-DEPENDENT DNA HEL	3.49e+01
45	60	39.0	921	8	RE_HUMAN RETINOBLASTOMA-ASSOCI	3.49e+01

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	361 AA.
ID	FDEH_PSEPU			
AC	P09347;			
DT	01-MAR-1989 (REL. 10, CREATED)			
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	5-EXO-ALCOHOL DEHYDROGENASE (EC 1.1.1.-) (FDEH).			
GN	CAND.			
OS	PSEUDOMONAS PUTIDA.			
OC	PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;			
ON	PSEUDOMONADACEAE.			
RC	[1]			
RP	SEQUENCE FROM N.A., AND REVISIONS TO 97-100.			
RC	STRAIN-ATCC 17453;			
RX	MEDLINE; 93326643.			
RA	ARAMAKI H., KOGA H., SAGARA Y., HOSOI M., HORIUCHI T.;			
RA	BIOCHIM. BIOPHYS. ACTA 1174:91-94(1993).			
RN	[2]			
RP	SEQUENCE OF 1-100 FROM N.A., AND SEQUENCE OF 1-45.			
RC	STRAIN-ATCC 17453;			
RX	MEDLINE; 86223770.			
RA	KOGA H., ARAMAKI H., YAMAGUCHI E., TAKEUCHI K., HORIUCHI T.;			
RA	GUNSALUS I.C.;			
RL	J. BACTERIOL. 166:1089-1095(1986).			
CC	-1- CATALYTIC ACTIVITY: 5-EXO-HYDROXYCAMPHOR + NAD(+) =			
CC	2,5-DIKETOCAMPHOR + NADH.			
CC	-1- COFACTOR: THIS IS A ZINC-CONTAINING DEHYDROGENASE.			
CC	-1- PATHWAY: SECOND STEP FOR CATABOLISM OF CAMPHOR.			
CC	-1- INDUCTION: BY CAMPHOR.			
CC	-1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE			
CC	FAMILY.			
DR	EMBL; D14680; G473746; ..			
DR	EMBL; M13471; G551925; ALT_SEQ.			
DR	PIR; A29844; A29844.			
DR	HSSP; P00327; 1ADF.			
DR	PROSITE; PS00059; ADH_ZINC.			
DR	OXIDOREDUCTASE; ZINC; NAD.			
KW	METAL 40 40			
FT	FT METAL 62 62			
FT	FT METAL 98 98			
FT	FT METAL 101 101			
FT	FT METAL 104 104			
FT	FT METAL 170 170			
SQ	SEQUENCE 361 AA; 38460 MW; E46D28F7 CRC32;			
Query Match	46.1%;	Score 71;	DB 3;	Length 361;

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RL MOL. GEN. GENET. 226:24-33(1991).
[2]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE; 91083835.
RA CHEN H., SUN Y., STARK T., BEATTIE W., MOSES R.E.;
RL DNA CELL BIOL. 9:631-635(1990).
[3]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE; 92334977.
RA YURA T., MORI H., NAGAI H., NAGATA T., ISIHAMA A., FUJITA N.,
RA ISONO K., MIZOBUCHI K., NAKATA A.;
RL NUCLEIC ACIDS RES. 20:3305-3308(1992).
[4]
RN RN
RP SEQUENCE OF 1-457 FROM N.A., AND SEQUENCE OF 1-27.
RC STRAIN-K12;
RX MEDLINE; 91017565.
RA BONNER C.A., HAYS S., MCENTEE K., GOODMAN M.F.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:7663-7667(1990).
CC -1- FUNCTION: THOUGHT TO BE INVOLVED IN DNA REPAIR AND/OR MUTAGENESIS.
CC -1- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE -
CC N PYROPHOSPHATE + DNA(N).
CC -1- ENZYME REGULATION: DNA POLYMERASE II ACTIVITY IS REGULATED BY
CC THE LEXA GENE DURING THE SOS RESPONSE.
CC -1- SIMILARITY: BELONGS TO FAMILY B OF DNA POLYMERASES.
DR EMBL; X54847; G581193; -
DR EMBL; M37727; G145746; -
DR EMBL; M62646; G147318; -
DR EMBL; M35371; E27155; ALT_SEQ.
DR EMBL; M38283; G705349; -
DR EMBL; D10483; G285766; -
DR PIR; S15943; JDEC22.
DR PIR; B36236; B36236.
DR PIR; JQ0780; JQ0780.
DR PIR; S19263; S19263.
DR ECOGENE; EG10747; POLB.
DR PROSITE; PS00116; DNA_POLYMERASE_B.
KW DNA-DIRECTED DNA POLYMERASE; SOS RESPONSE; DNA REPAIR; DNA-BINDING.
FT INIT_MET 0 0 G -> A (IN REF. 2).
FT CONFLICT 171 171 EH -> DD (IN REF. 4).
FT CONFLICT 256 257 R -> G (IN REF. 4).
FT CONFLICT 271 271 N -> T (IN REF. 2).
FT CONFLICT 734 734 LQVQSPLDYHYVLTQLQVVAEGILPFIEDNFATL
FT CONFLICT 739 782 MTQGLGIF -> PGLPTFTGLTSLDPPATRRGG
FT NTPFY (IN REF. 2).
SQ SEQUENCE 782 AA; 89921 MW; 0762928E CRC32;

Query Match 45.5%; Score 70; DB 3; Length 782;
Best Local Similarity 50.0%; Pred. No. 1.38e+00;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 230 rmlqkhaeryrlplrl 245
| : | | | | | |
QY 2 RLAIRLNERYRLAIRL 17

RESULT 4
ID PYG4_ANASP STANDARD; PRT; 252 AA.
AC P29899;
AD 01-APR-1993 (REL. 25, CREATED)
DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE PHYCOBILISOME ROD-CORE LINKER POLYPEPTIDE CPCG4 (L-RC 29.2).
GN CPCG4.
OS ANABAENA SP. (STRAIN PCC 7120).
OC PROKARYOTA; GRACILICUTES; OXYPHOTOBACTERIA;
OC CYANOBACTERIA (BLUE-GREEN ALGAE); NOSTOCALES.
[1]
RN RN
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-22.
RX MEDLINE; 92077441.
RA RYANT D.A., STIREWALT V.L., GLAUSER M., FRANK G., SIDLER W.,

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RA ZUBER H.;
RL GENE 107:91-99(1991).
CC -1- FUNCTION: ROD-CORE LINKER PROTEIN REQUIRED FOR ATTACHMENT OF
CC PHYCOCYANIN TO ALLOPHYCOCYANIN IN CORES OF PHYCOBILISOMES.
CC -1- FUNCTION: LINKER POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION
CC AND THE LOCATION OF THE DISC-SHAPED PHYCOBILIPROTEIN UNITS WITHIN
CC THE PHYCOBILISOME AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN
CC ORDER TO MEDATE A DIRECTED AND OPTIMAL ENERGY TRANSFER.
CC -1- SUBUNIT: THE PHYCOBILISOME IS A HEMIDISCOIDAL STRUCTURE THAT IS
CC COMPOSED OF TWO DISTINCT SUBSTRUCTURES: A CORE COMPLEX (THAT
CC CONTAINS PHYCOBILIPROTEINS) AND A NUMBER OF RODS RADIATING FROM
CC THE CORE.
CC -1- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
DR EMBL; M80435; G142102; -.
DR PIR; JS0595; JS0595.
KW PHYCOBILISOME; PHOTOSYNTHESIS; MULTIGENE FAMILY.
FT INIT_MET 0
SQ SEQUENCE 252 AA; 29191 MW; 0C1A6468 CRC32;

Query Match 44.2%; Score 68; DB 8; Length 252;
Best Local Similarity 53.8%; Pred. No. 2.71e+00;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 94 yrlvsvnnnyrl 106
QY 1 YRLAIRLNERYRL 13

RESULT 5
ID PYG3_MASLA STANDARD; PRT; 253 AA.
AC P29733;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PHYCOBILISOME ROD-CORE LINKER POLYPEPTIDE CPCG3 (L-RC 29.6).
GN CPCG3.
OS MASTIGOCILADUS LAMINOSUS (FISCHERELLA SP.).
OC PROKARYOTA; GRACILICUTES; OXYPHOTOBACTERIA;
OC CYANOBACTERIA (BLUE-GREEN ALGAE); STIGONEMATALES.
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-PCC 7603;
RX MEDLINE; 92249337.
RA GLAUSER M., STIREWALT V.L., BRYANT D.A., SIDLER W., ZUBER H.;
RL EUR. J. BIOCHEM. 205:97-937(1992).
CC -1- FUNCTION: ROD-CORE LINKER PROTEIN REQUIRED FOR ATTACHMENT OF
CC PHYCOCYANIN TO ALLOPHYCOCYANIN IN CORES OF PHYCOBILISOMES.
CC -1- FUNCTION: LINKER POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION
CC AND THE LOCATION OF THE DISC-SHAPED PHYCOBILIPROTEIN UNITS WITHIN
CC THE PHYCOBILISOME AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN
CC ORDER TO MEDATE A DIRECTED AND OPTIMAL ENERGY TRANSFER.
CC -1- SUBUNIT: THE PHYCOBILISOME IS A HEMIDISCOIDAL STRUCTURE THAT IS
CC COMPOSED OF TWO DISTINCT SUBSTRUCTURES: A CORE COMPLEX (THAT
CC CONTAINS PHYCOBILIPROTEINS) AND A NUMBER OF RODS RADIATING FROM
CC THE CORE.
CC -1- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
DR EMBL; X59763; G44401; -.
DR PIR; S16060; S16060.
DR PIR; S23475; S23475.
KW PHYCOBILISOME; PHOTOSYNTHESIS; MULTIGENE FAMILY.
FT INIT_MET 0
SQ SEQUENCE 253 AA; 29493 MW; 820A835D CRC32;

Query Match 44.2%; Score 68; DB 8; Length 253;
Best Local Similarity 53.8%; Pred. No. 2.71e+00;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 94 yrlvsvnnnyrl 106
QY 1 YRLAIRLNERYRL 13

RESULT 6

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ID NTRB_ECOLI STANDARD; PRT; 349 AA.
AC P06712;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE NITROGEN REGULATION PROTEIN NR(II) (EC 2.7.3.-).
GN GLN OR NTRB OR GLNR.
OS ESCHERICHIA COLI.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC ENTEROBACTERIACEAE.
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE; 87174797.
RA MIRANDA-RIOS J., SANCHEZ-PESCADOR R., URDEA M., COVARRUBIAS A.A.;
RL NUCLEIC ACIDS RES. 15:2757-2770(1987).
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE; 93347969.
RA PLUNKETT G. III, BURLAND V.D., DANIELS D.L., BLATTNER F.R.;
RL NUCLEIC ACIDS RES. 21:3391-3398(1993).
RN 13
RP SEQUENCE OF 1-22 FROM N.A.
RX MEDLINE; 85006814.
RA UENO-NISHIO S., MANGO S., REITZER L.J., MAGASANIK B.;
RL J. BACTERIOL. 160:379-384(1984).
RN 14
RP SEQUENCE OF 1-24 FROM N.A.
RX MEDLINE; 86013370.
RA ROCHA M., VAZQUEZ M., GARCIAARRUBIO A., COVARRUBIAS A.A.;
RL GENE 37:91-99(1985).
RN 15
RP PHOSPHORYLATION SITE.
RX MEDLINE; 91201336.
RA NINFA A.J., BENNETT R.L.;
RL J. BIOL. CHEM. 266:6888-6893(1991).
CC -1- FUNCTION: NTRB ACTS AS A SIGNAL TRANSDUCER WHICH RESPONDS TO THE
CC NITROGEN LEVEL OF CELL AND MODULATES THE ACTIVITY OF NTRC. IN
CC NITROGEN LIMITATION NTRB ACTIVATES NTRC BY PHOSPHORYLATING IT,
CC WHILE IN NITROGEN EXCESS NTRC IS DEPHOSPHORYLATED AND CONSEQUENTLY
CC INACTIVATED BY NTRB.
CC -1- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
CC KINASES.
DR EMBL; X05173; G41564; -.
DR EMBL; K02176; G146162; -.
DR EMBL; L19201; G304974; -.
DR PIR; Q00553; RGECEG.
DR PIR; B23970; B23970.
DR PIR; S40814; S40814.
DR ECOGENE; EG10387; GLNL.
KW SENSORY TRANSDUCTION; TRANSFERASE; KINASE; PHOSPHORYLATION;
KW NITROGEN FIXATION; ATP-BINDING.
FT DOMAIN 116 349 TRANSMITTER DOMAIN (POTENTIAL).
FT MOD_RES 139 139 PHOSPHORYLATION (AUTO-).
FT BINDING 329 329 ATP (BY SIMILARITY).
SQ SEQUENCE 349 AA; 38556 MW; 6A017919 CRC32;

Query Match 44.2%; Score 68; DB 6; Length 349;
Best Local Similarity 44.4%; Pred. No. 2.71e+00;
Matches 8; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

Db 268 fqtlh-geryrlaaid 284
QY 1 YRLAIRLNERYRLAIRLN 18

RESULT 7
ID ITA3_CRISP STANDARD; PRT; 1051 AA.
AC P17852;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

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DE INTEGRIN ALPHA-3 PRECURSOR (GALACTOPROTEIN B3) (GAPB3) (VLA-3 ALPHA  
 DE CHAIN) (CD49C).  
 GN ITGA3.  
 OS CRICETIDAE SP. (HAMSTER).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=FIBROBLAST;  
 RX MEDLINE: 90216739.  
 RA TSUJI T., YAMAMOTO F.-I., MIURA Y., TAKIO K., TITANI K., PAWAR S.,  
 RA OSAWA T., HAKOMORI S.-I.;  
 RL J. BIOL. CHEM. 265:7016-7021(1990).  
 CC -!- SUBUNIT: DIMER OF AN ALPHA AND BETA CHAINS. THE ALPHA CHAIN IS  
 CC COMPOSED OF AN HEAVY AND LIGHT CHAINS LINKED BY A DISULFIDE BOND.  
 CC ALPHA-3 ASSOCIATES WITH BETA-1.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: WITH OTHER ALPHA CHAINS FROM THE INTEGRIN FAMILY OF  
 CC CELL-SURFACE RECEPTOR.  
 DR EMBL: J05281; G304508; -.  
 DR PIR: A35761; A35761.  
 DR PROSITE: PS00242; INTEGRIN\_ALPHA.  
 KW CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; SIGNAL; INTEGRIN;  
 KW EXTRACELLULAR MATRIX; CYTOSKELETON; REPEAT.  
 FT SIGNAL 1 32  
 FT CHAIN 33 1051 INTEGRIN ALPHA-3.  
 FT CHAIN 33 872 HEAVY CHAIN (POTENTIAL).  
 FT CHAIN 876 1051 LIGHT CHAIN (POTENTIAL).  
 FT DOMAIN 33 991 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 992 1019 POTENTIAL.  
 FT DOMAIN 1020 1051 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 49 461 7 X APPROXIMATE REPEATS.  
 FT REPEAT 49 94 I.  
 FT REPEAT 120 165 II.  
 FT REPEAT 195 227 III.  
 FT REPEAT 246 279 IV.  
 FT REPEAT 304 345 V.  
 FT REPEAT 366 402 VI.  
 FT REPEAT 426 461 VII.  
 FT CARBOHYD 86 86 POTENTIAL.  
 FT CARBOHYD 500 500 POTENTIAL.  
 FT CARBOHYD 511 511 POTENTIAL.  
 FT CARBOHYD 573 573 POTENTIAL.  
 FT CARBOHYD 605 605 POTENTIAL.  
 FT CARBOHYD 656 656 POTENTIAL.  
 FT CARBOHYD 697 697 POTENTIAL.  
 FT CARBOHYD 841 841 POTENTIAL.  
 FT CARBOHYD 923 923 POTENTIAL.  
 FT CARBOHYD 926 926 POTENTIAL.  
 FT CARBOHYD 935 935 POTENTIAL.  
 FT CARBOHYD 969 969 POTENTIAL.  
 SQ SEQUENCE 1051 AA; 116455 MW; 336B3FE0 CRC32;  
 Query Match 44.2%; Score 68; DB 5; Length 1051;  
 Best Local Similarity 37.5%; Pred. No. 2.71e+00;  
 Matches 6; Conservative 7; Mismatches 3; Indels 0; Gaps 0;  
 Db 574 yslplmpdrklgm 589  
 QY 1 YRLAIRLNERYLRAIR 16  
 RESULT 8  
 ID ITA3\_HUMAN STANDARD; PRT: 1051 AA.  
 AC F26006;  
 DT 01-MAY-1992 (REL. 22, CREATED)  
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE INTEGRIN ALPHA-3 PRECURSOR (GALACTOPROTEIN B3) (GAPB3) (VLA-3 ALPHA  
 DE CHAIN) (CD49C).  
 GN ITGA3.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 92011866.  
 RA TAKADA Y., MURPHY E., PIL P., CHEN C., GINSBERG M.H., HEMLER M.E.;  
 RL J. CELL BIOL. 115:257-266(1991).  
 RN [2]  
 RP SEQUENCE OF 33-1051 FROM N.A.  
 RC TISSUE=FIBROBLAST;  
 RX MEDLINE: 91331981.  
 RA TSUJI T., HAKOMORI S.-I., OSAWA T.;  
 RL J. BIOCHEM. 109:659-665(1991).  
 RN [3]  
 RP SEQUENCE OF 33-46.  
 RX MEDLINE: 87204112.  
 RA TAKADA Y., STROMINGER J.L., HEMLER M.E.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 84:3239-3243(1987).  
 CC -!- FUNCTION: VLA-3 ACTS A RECEPTOR FOR FIBRONECTIN, LAMININ AND  
 CC COLLAGEN.  
 CC -!- SUBUNIT: DIMER OF AN ALPHA AND BETA CHAINS. THE ALPHA CHAIN IS  
 CC COMPOSED OF AN HEAVY AND LIGHT CHAINS LINKED BY A DISULFIDE BOND.  
 CC ALPHA-3 ASSOCIATES WITH BETA-1.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: WITH OTHER ALPHA CHAINS FROM THE INTEGRIN FAMILY OF  
 CC CELL-SURFACE RECEPTOR.  
 DR EMBL: M59911; G186497; -.  
 DR PIR: JX0161; JX0161.  
 DR PROSITE: PS00242; INTEGRIN\_ALPHA.  
 KW CELL ADHESION; GLYCOPROTEIN; TRANSMEMBRANE; SIGNAL; INTEGRIN;  
 KW EXTRACELLULAR MATRIX; CYTOSKELETON; REPEAT.  
 FT SIGNAL 1 32  
 FT CHAIN 33 1051 INTEGRIN ALPHA-3.  
 FT CHAIN 33 872 HEAVY CHAIN (POTENTIAL).  
 FT CHAIN 876 1051 LIGHT CHAIN (POTENTIAL).  
 FT DOMAIN 33 991 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 992 1019 POTENTIAL.  
 FT DOMAIN 1020 1051 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 49 461 7 X APPROXIMATE REPEATS.  
 FT REPEAT 49 94 I.  
 FT REPEAT 120 165 II.  
 FT REPEAT 195 227 III.  
 FT REPEAT 246 279 IV.  
 FT REPEAT 304 345 V.  
 FT REPEAT 366 402 VI.  
 FT REPEAT 426 461 VII.  
 FT CARBOHYD 86 86 POTENTIAL.  
 FT CARBOHYD 107 107 POTENTIAL.  
 FT CARBOHYD 265 265 POTENTIAL.  
 FT CARBOHYD 500 500 POTENTIAL.  
 FT CARBOHYD 511 511 POTENTIAL.  
 FT CARBOHYD 573 573 POTENTIAL.  
 FT CARBOHYD 605 605 POTENTIAL.  
 FT CARBOHYD 656 656 POTENTIAL.  
 FT CARBOHYD 697 697 POTENTIAL.  
 FT CARBOHYD 841 841 POTENTIAL.  
 FT CARBOHYD 857 857 POTENTIAL.  
 FT CARBOHYD 926 926 POTENTIAL.  
 FT CARBOHYD 935 935 POTENTIAL.  
 FT CARBOHYD 969 969 POTENTIAL.  
 SQ SEQUENCE 1051 AA; 116612 MW; 1D8A7B0F CRC32;  
 Query Match 44.2%; Score 68; DB 5; Length 1051;  
 Best Local Similarity 43.8%; Pred. No. 2.71e+00;  
 Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
 Db 574 yslplmpdrklgm 589  
 QY 1 YRLAIRLNERYLRAIR 16  
 RESULT 9  
 ID REAF\_HAELIN STANDARD; PRT: 346 AA.

```

AC P45042;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE ADP-HEPTOSE-LPS HEPTOSYLTRANSFERASE II.
GN REAF OR H11105
OS HAEMOPHILUS INFLUENZAE.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTEURELLACEAE.
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN-RD / KW20;
RX MEDLINE; 95350630.
RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
RA KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
RA MCKENNEY K., SHUTLEY G., FITZHUGH W., FIELDS C.A., GOCCAYNE J.D.,
RA SCOTT J.D., SUTTON R., LIU L.-I., GLODEX A., KELLEY J.M.,
RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLUM E., COTTON M.D.,
RA UTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
RA FINE L.B., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
RA GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
RA VENTER J.C.;
RL SCIENCE 269;496-512(1995).
RC -1- PATHWAY; LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS.
DR ENBL; L45741; G1006405; -.
DR ENBL; U32790; G926169; -.
KW LIPOPOLYSACCHARIDE BIOSYNTHESIS; TRANSFERASE.
SQ SEQUENCE 346 AA; 38847 MW; 1B4C2E89 CRC32;

Query Match 43.5%; Score 67; DB 8; Length 346;
Best Local Similarity 52.9%; Pred. No. 3.77e+00;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps

Db 70 yrlgslrccydmav1 86
QY 1 YRLAIRNERYLAIRL 17
|||: | | : || |
||||: | | : || |

RESULT. 10
ID YQO5_CAEEL STANDARD; PRT; 424 AA.
AC QO9535;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 48.0 KD PROTEIN FI0B5.5 IN CHROMOSOME III.
GN FI0B5.5.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; ACCELLOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN-BRISTOL N2.
RA SIMMS M.;
RL SUBMITTED (FEB-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC -1- SIMILARITY: DISTANTLY RELATED TO THE AAA FAMILY OF ATPASES.
DR ENBL; Z48334; G671827; -.
DR WORMPEP; FI0B5.5; CE01547.
FW HYPOTHETICAL PROTEIN; ATP-BINDING.
KT NP_BIND 179 186 ATP (POTENTIAL).
SQ SEQUENCE 424 AA; 48022 MW; 8C8A7686 CRC32;

Query Match 43.5%; Score 67; DB 11; Length 424;
Best Local Similarity 35.3%; Pred. No. 3.77e+00;
Matches 6; Conservative 8; Mismatches 3; Indels 0; Gaps

Db 195 hlsirmodysksvmie 211
QY 2 RLAIRLNERYLAIRLN 18
:|||:|||:| ::|:

RESULT 11
ID NTRB_SALTU STANDARD; PRT; 349 AA.
AC P41788;
DT 01-NOV-1995 (REL. 32, CREATED)

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RP SEQUENCE FROM N.A.  
RA JOHNSONE, I.O.L., MCCABE P.C., GREAVES P., GURR S.J., COLE G.E.,  
RX J. J. BIOL. CHEM. 270:14209-14213(1995).  
RL BROW M.A.D., UNKLES S.E., CLUTTERBUCK A.J., KINGHORN J.R., INNIS M.A.;  
RL GENE 90:181-192(1990).  
CC -1- PATHWAY: SECOND STEP IN NITRATE ASSIMILATION (DENITRIFICATION).  
CC -1- CATALYTIC ACTIVITY: 3 NAD(P)H + NITRITE = 3 NAD(P)(+ ) + NH(4)OH +  
CC H(2)O.  
CC -1- SUBUNIT: HOMODIMER.  
CC -1- COFACTOR: THIS ENZYME IS A FAD FLAVOPROTEIN THAT ALSO CONTAINS  
CC A SIROHEME AND ONE 2FE-2S IRON-SULFUR CENTER.  
CC -1- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN  
CC FOUND IN NITRITE REDUCTASES (EC 1.6.6.4 AND EC 1.7.7.1) AND  
CC SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).  
DR EMBL: M58289; GI68064; -  
DR PIR: JH0181; JH0181  
DR PROSITE: PS00365; NIR\_STR.  
DR OXIDOREDUCTASE; FAD; FLAVOPROTEIN; IRON-SULFUR; NITRATE ASSIMILATION;  
KW HEME; NADP.  
KW FT ME\_BIND 44 79 FAD (POTENTIAL).  
FT FT NP\_BIND 146 176 NAD(P)H (POTENTIAL).  
FT FT METAL 720 720 IRON-SULFUR (2FE-2S) (POTENTIAL).  
FT FT METAL 726 726 IRON-SULFUR (2FE-2S) (POTENTIAL).  
FT FT METAL 760 760 IRON-SULFUR (2FE-2S) (POTENTIAL).  
FT FT METAL 764 764 IRON-SULFUR (2FE-2S) AND SIROHEME  
FT (BY SIMILARITY).  
SQ SEQUENCE 1104 AA; 122731 MW; 7A485174 CRC32;  
  
Query Match 41.6%; Score 64; DB 6; Length 1104;  
Best Local Similarity 57.1%; Pred. No. 9.99e+00;  
Matches 8; Conservative 5; Mismatches 0; Indels 1; Gaps  
  
Db 736 mairleqvryk-slr 748  
:||||:||||:||||  
QY 3 LAIRLNERFLAIR 16  
  
RESULT 15  
ID N358\_HUMAN STANDARD; PRT: 3224 AA.  
AC A49792;  
DT 01-OCT-1996 (REL. 34, CREATED)  
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
DE 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
DE NUCLEAR PORE COMPLEX PROTEIN NUP358 (NUCLEOPORIN NUP358) (358 KD  
DE NUCLEOPORIN) (P270).  
GN NUP358.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 95294031.  
RX WU J., MATUNIS M.J., KRAEMER D., BLOBEL G., COUTAVAS E.;  
RL J. BIOL. CHEM. 270:14209-14213(1995).  
CC -1- FUNCTION: INVOLVED IN TRANSPORT FACTOR (RAN-GTP, KARYOPHERIN)-  
CC MEDIATED PROTEIN IMPORT VIA THE F-G REPEAT-CONTAINING DOMAIN  
CC WHICH ACTS AS A DOCKING SITE FOR SUBSTRATES. COULD ALSO HAVE  
CC ISOMERASE OR CHAPERONE ACTIVITY AND MAY BIND RNA OR DNA.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR PORE COMPLEX. CYTOPLASMIC FILAMENTS.  
CC -1- DOMAIN: CONTAINS MANY X-X-F-G AND X-F-X-F-G REPEATS.  
CC -1- SIMILARITY: CONTAINS 4 RANBP1-LIKE DOMAINS.  
CC -1- SIMILARITY: CONTAINS A CYCLOPHILIN-LIKE PPIASE DOMAIN.  
DR EMBL: L41840; G857368; -  
DR NUCLEAR PROTEIN; TRANSPORT; REPEAT; ZINC-FINGER; ISOMERASE; ROTAMASE.  
KW DOMAIN 1172 1301 RANBP1-LIKE.  
FT FT NP\_BIND 1356 1375 C4-TYPE.  
FT FT ZN\_FING 1419 1439 C4-TYPE.  
FT FT ZN\_FING 1483 1503 C4-TYPE.  
FT ZN\_FING 1547 1567 C4-TYPE.  
FT ZN\_FING 1610 1630 C4-TYPE.  
FT ZN\_FING 1669 1689 C4-TYPE.  
FT ZN\_FING 1728 1748 C4-TYPE.  
FT ZN\_FING 1785 1805 C4-TYPE.

FT DOMAIN 2013 2142 RANBP1-LIKE.  
FT DOMAIN 2310 2439 RANBP1-LIKE.  
FT DOMAIN 2912 3040 RANBP1-LIKE.  
FT DOMAIN 3063 3224 PPIASE, CYCLOPHILIN-TYPE.  
SQ SEQUENCE 3224 AA; 358214 MW; 113D9513 CRC32;

Query Match 41.6%; Score 64; DB 6; Length 3224;  
Best Local Similarity 44.4%; Pred. No. 9.99e+00;  
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db 166 hvnrlrlevyrstkrld 183  
QY 2 RLAINERYRLAIRUNE 19  
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Search completed: Thu May 22 08:34:19 1997  
Job time : 12 secs.

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W P S R E H

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:37:03 1997; MasPar time 2.04 Seconds

Tabular output not generated. 64.216 Million cell updates/sec

Title: >US-08-653-294-36  
Description: (1-12) from US08653294.pep  
Perfect Score: 98  
Sequence: 1 YRLAIRRIALRY 12

Scoring table: PAM 150  
Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq26  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19

Statistics: Mean 19.057; Variance 63.971; scale 0.298

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	98	100.0	12 18	R95429	HLA-B2702 84-79-84 pa	2.34e+03
2	61	62.2	18 13	R71429	Human MHC 1 alpha 1 d	1.74e+01
3	55	56.1	911 18	R95634	DNA-ligase-III.	6.61e+01
4	53	54.1	334 5	R28073	Brevibacterium flavum	1.02e+02
5	53	54.1	772 15	R79949	Enzyme M-11.	1.02e+02
6	53	54.1	959 14	R78066	Yeast MSH1 protein.	1.02e+02
7	53	54.1	971 14	R78070	Yeast MSH1 protein w1	1.02e+02
8	52	53.1	20 16	R92911	HLA-B2702 CTL modul	1.27e+02
9	52	53.1	25 18	R95422	HLA-B2702 CTL modul	1.27e+02
10	52	53.1	25 18	R48286	Peptide fragment of H	1.27e+02
11	52	53.1	25 16	R83093	HLA-B2702 CTL modul	1.27e+02
12	52	53.1	362 2	R03144	Sequence of HLA-B51 a	1.27e+02
13	52	53.1	362 3	R12463	HLA-Bw53 exon.	1.27e+02
14	52	53.1	362 2	R03142	Sequence of HLA-Bw52	1.27e+02
15	52	53.1	529 14	R73966	Alpha 2 subunit of a	1.27e+02
16	52	53.1	640 15	R82249	Chloroperoxidase	1.27e+02
17	51	52.0	263 14	R74182	Type I ribosome-inact	1.57e+02
18	51	52.0	939 1	R04104	pJH1 gene product - b	1.57e+02
19	51	52.0	3567 8	R44431	eryA region polypepti	1.57e+02
20	50	51.0	20 18	R95415	HLA-B7.84-75-84 Palin	1.94e+02

21	50	51.0	20 16	R92913	HLA-B7 CTL modulating	1.94e+02
22	50	51.0	224 9	R46556	fbp2, for reverse gen	1.94e+02
23	50	51.0	387 9	R49828	3-acylating enzyme.	1.94e+02
24	50	51.0	4472 19	R37246	Virulence gene cluste	2.40e+02
25	49	50.0	10 18	R95425	HLA-B2702.75-84(D).	2.40e+02
26	49	50.0	10 18	R95413	Alphal-helix of HLA-B	2.40e+02
27	49	50.0	10 8	R41208	Peptide fragment of C	2.40e+02
28	49	50.0	20 18	R95430	HLA-B2702 84-75T/75-8	2.40e+02
29	49	50.0	20 18	R95428	HLA-B2702 84-75-84 pa	2.40e+02
30	49	50.0	20 1	R95012	Papilloma virus type	2.40e+02
31	49	50.0	25 18	R95416	HLA-B2702.60-84.	2.40e+02
32	49	50.0	25 8	R41205	Peptide fragment of C	2.40e+02
33	49	50.0	25 16	R83090	HLA-B2702 CTL modul	2.40e+02
34	49	50.0	248 2	R07518	Synthetic alpha-trich	2.40e+02
35	49	50.0	248 5	R25573	Mature alpha-Trichosa	2.40e+02
36	49	50.0	255 14	R74181	Type I ribosome-inact	2.40e+02
37	49	50.0	289 2	R07514	Trichosanthin from Tr	2.40e+02
38	49	50.0	289 5	R25572	Trichosanthin from Tr	2.40e+02
39	49	50.0	289 6	R29272	Trichosanthin protein	2.40e+02
40	49	50.0	289 6	R32986	Encodes chinese cucum	2.40e+02
41	49	50.0	289 10	R55129	Alpha-trichosanthin c	2.40e+02
42	49	50.0	428 7	R39284	Murine somatostatin r	2.40e+02
43	49	50.0	4302 19	W00870	Polycystic kidney dis	2.40e+02
44	49	50.0	4339 19	R87539	Polycystic kidney dis	2.40e+02
45	49	50.0	4339 15	R75916	Polycystic kidney dis	2.40e+02

#### ALIGNMENTS

RESULT 1  
ID R95429 standard; peptide; 12 AA.  
AC R95429;  
DE 12-NOV-1996 (first entry)  
KW HLA-B2702 84-79-84 palindrome.  
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
KW cytolysis; antigen presenting cell.  
OS Synthetic.  
PN W09513288-A1.  
PD 18-MAY-1995.  
PF 10-NOV-1994; U12985.  
PR 10-NOV-1993; US-150493.  
PS (STRD ) UNIV LELAND STANFORD JUNIOR.  
PI Clayberger C. Krensky AM;  
PT WPI: 95-194027/25.  
DR Compsns. comprising lymphoid surface membrane proteins - which may  
PT inhibit cytolytic activity and differentiation of CTLs.  
PS Example; Page 12: 29pp; English.  
CC R95413, and R95415-R95431 represent palindromes and fragments of  
CC human-leucocyte-associated antigens. This sequence represents the  
CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
CC protein associated with T-cell activation in mammalian T-cells, and is  
CC also immunologically cross reactive with the heat shock protein Hsc70.  
CC p74 is found in a limited number of cell types, but is particularly  
CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
CC cell with an amphoteric detergent, and then passed through an affinity  
CC column containing a covalently bound HLA-B2702 palindromic peptide.  
CC Compositions comprising the extracellular fragment of p74 combined with  
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate  
CC compounds can be screened for their effect on the cytolytic activity of  
CC T-cells, by combining them with the extracellular portion of p74 and  
CC determining the amount of binding between the candidate compound and p74.  
CC Modulation of CTL activity can be inhibited in a cellular composition  
CC containing T-cells and antigen presenting cells (APCs), by adding to the  
CC mix the extracellular portion of p74, in an amount sufficient to compete  
CC with p74 for the binding of the p74 ligand.  
SQ Sequence 12 AA;  
Query Match 100.0%; Score 98; DB 18; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.34e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 YRLAIRRLRY 12  
 |||||  
 QY 1 YRLAIRRLRY 12

## RESULT 2

ID R71429 standard; peptide; 18 AA.  
 AC R71429;  
 DT 12-OCT-1995 (first entry)  
 DE Human MHC I alpha 1 domain peptide [Ala81]-Dk-(69-85).  
 KW Major histocompatibility complex class I; MHC I; cell receptor;  
 KW alpha 1 domain; peptide [Ala81]-Dk-(69-85); interaction modulation;  
 KW arthritis; neoplasias; lupus erythematosus.  
 OS Homo sapiens.  
 PN W09505189-A.  
 PD 23-FEB-1995.  
 PF 12-AUG-1994; U09189.  
 PR 12-AUG-1993; US-105416.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Goldstein A, Goodenow RS, Olsson L;  
 DR WPI; 95-098577/13.  
 PT Regulating cell surface receptor response - by modulating  
 PT interaction between MHC class I antigen and the cell surface  
 PT receptor  
 PS Example 4; Page 45; 103pp; English.  
 CC R71424-R71438 are human major histocompatibility complex class I  
 CC (MHC I) alpha 1 domain derived peptides and peptide mutants, they  
 CC were used to modulate interactions between MHC I and cell surface  
 CC receptors. Via competitive inhibition the peptides diminish the  
 CC receptors response, this feature may be useful for the treatment  
 CC of neoplasias, lupus erythematosus and arthritis.  
 CC Sequence 18 AA;  
 SQ

Query Match 62.2%; Score 61; DB 13; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 1.74e+01;  
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 6 frvdlrlalry 17  
 :||:|  
 QY 1 YRLAIRRLRY 12

## RESULT 3

ID R95634 standard; Protein; 911 AA.  
 AC R95634;  
 DT 20-OCT-1996 (first entry)  
 DE DNA-ligase-III.  
 KW Human; DNA-ligase-III; activated T-lymphocyte; DNA repair;  
 KW diagnostic; antibody; immunoassay; antitumor; immunostimulant;  
 KW gene therapy; DNA-ligase-III-antagonist.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Peptide 1..67  
 FT /note= "Putative signal peptide"  
 PN W09614394-A1.  
 PD 17-MAY-1996.  
 PF 08-NOV-1994; U12922.  
 PR 08-NOV-1994; WO-U12922.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Haseltine WA, Wei Y;  
 DR WPI; 96-251747/25.  
 DR N-PSDB; T27092.  
 PT New isolated human DNA ligase III gene - used to develop prods. to  
 PT treat, prevent or diagnose DNA disorders such as abnormal cellular  
 PT proliferation.  
 PS Claim 1; Fig 1; 65pp; English.  
 CC This sequence represents human DNA-ligase-III from activated  
 CC T-lymphocytes, and includes a putative signal peptide sequence.  
 CC DNA-ligase-III is a new protein larger than DNA-ligase-II, and  
 CC differs from DNA-ligase-I in repairing single-strand breaks in DNA  
 CC efficiently, but not performing blunt-end joining or AMP-dependent

CC relaxation of supercoiled DNA. The DNA, protein and  
 CC ligase-specific antibodies against it may be used as diagnostic  
 CC agents for cancer, immunosuppression, hypersensitivity to DNA-  
 CC damaging agents, etc. A DNA-ligase-antagonist protein may be used  
 CC in therapy of these conditions, and DNA encoding the antagonist may  
 CC be used in gene therapy.  
 SQ Sequence 911 AA;

Query Match 56.1%; Score 55; DB 18; Length 911;  
 Best Local Similarity 54.5%; Pred. No. 6.61e+01;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 837 rlaikalelrf 847  
 ||||:|  
 QY 2 RLAIRRLRY 12

## RESULT 4

ID R28073 standard; Protein; 334 AA.  
 AC R28073;  
 DT 26-MAR-1993 (first entry)  
 DE Brevibacterium flavum MJ-233 biotin synthetase.  
 KW bioB; ss.  
 OS Brevibacterium flavum MJ-233.  
 PN J04278088-A.  
 PD 02-OCT-1992.  
 PF 04-MAR-1991; 062563.  
 PR 04-MAR-1991; JP-062563.  
 PA (MITP ) MITSUBISHI PETROCHEMICAL CO LTD.  
 DR WPI; 92-377571/46.  
 DR N-PSDB; Q30766.  
 PT DNA fragment contg. corynebacterium biotin synthetase gene -  
 PT used to produce biotin synthetase with high efficiency  
 PS Claim 6; Page 3; 20pp; Japanese.  
 CC The bioB gene from B.flavum MJ-233 can be inserted into a plasmid  
 CC and used to transform host microorganisms for increased production  
 CC of biotin synthetase.  
 SQ Sequence 334 AA;

Query Match 54.1%; Score 53; DB 5; Length 334;  
 Best Local Similarity 41.7%; Pred. No. 1.02e+02;  
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 265 frlaphmtlrf 276  
 :|||:|  
 QY 1 YRLAIRRLRY 12

## RESULT 5

ID R79949 standard; Protein; 772 AA.  
 AC R79949;  
 DT 24-APR-1996 (first entry)  
 DE Enzyme M-11.  
 KW Enzyme; M-11; Q36; rhizobium; arthrobacter; trehalose;  
 KW amylaceous saccharide.  
 OS Rhizobium sp. M11.  
 FH Key Location/Qualifiers  
 FT Misc\_difference 502..506  
 FT /note= "used for production of probe sequence (T04206)"  
 FT Misc\_difference 621..625  
 FT /note= "used for production of probe sequence (T04207)"  
 PN EP-674005-A2.  
 PD 27-SEP-1995.  
 PF 23-FEB-1995; 301176.  
 PR 23-FEB-1994; JP-047956.  
 PR 23-FEB-1994; JP-047940.  
 PR 06-APR-1994; JP-090728.  
 PR 06-APR-1994; JP-090705.  
 PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
 PI Kubota M, Maruta K, Sugimoto T, Tsusaki K;  
 DR WPI; 95-329870/43.  
 DR N-PSDB; T04155.  
 PT DNA encoding enzyme reduces amylaceous saccharide to produce

PT non-reducing sugar with trehalose end gp. - useful in foods,  
 PT cosmetics, pharmaceuticals, etc.  
 PS Claim 3; Page 21-22; 178pp; English.  
 CC This sequence represents an enzyme that forms a non-reducing sugar with a  
 CC trehalose end group, from a reducing anylaceous saccharide. The  
 CC anylaceous saccharides have a degree of glucose polymerisation of 3 or  
 CC higher. This sequence was extracted from a liquid culture of Rhizobium  
 CC species M-11. By using an oligonucleotide probe based on a fragment of  
 CC this sequence, the encoding sequence was obtained. The encoding sequence  
 CC was then ligated into a vector and used to produce M-11 in E.coli  
 CC transformants. This can also be performed for the DNA encoding enzyme  
 CC Q36 (see T04156), which was obtained from Arthrobacter sp. Q36. The  
 CC non-reducing sugars produced by the action of these enzymes can be used  
 CC in foods, cosmetics, pharmaceuticals and feeds. They are used as  
 CC sweeteners, taste and quality improvers, stabilisers, fillers, excipients  
 CC and adjuvants. The sugars can also be used as intermediates for  
 CC trehalose. The advantages with using these sugars, are that, they are  
 CC practically non-reducing (so no browning reaction occurs when they are  
 CC heated with proteins), have a mild but good quality sweetness, adequate  
 CC viscosity and moisture-retaining properties.  
 SQ Sequence 772 AA;

Query Match 54.1%; Score 53; DB 15; Length 772;  
 Best Local Similarity 85.7%; Pred. No. 1.02e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 8 yrlgrr 14  
 ||| |||  
 QY 1 YRLAIR 7

RESULT 6  
 ID R76066 standard; Protein; 959 AA.

AC R76066; (first entry)  
 DT 16-JAN-1996  
 DE Yeast MSH1 protein.  
 KW Mismatch repair; MSH2; primer; identification; defect; alteration;  
 KW cancer; tumour; vaccine.  
 OS Saccharomycetes cerevisiae.  
 PN W09514085-A2.  
 PD 26-MAY-1995.  
 PF 17-NOV-1994; U13385.  
 PR 17-NOV-1993; US-154792.  
 PR 07-DEC-1993; US-163449.  
 PR 13-JUN-1994; US-259310.  
 PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.  
 PA (DAND ) DANA FARMER CANCER INST.  
 PI Fishel R, Kolodner RD, Reenan RAG;  
 DR WPI; 95-200377/26.  
 DT Determining alteration in human mismatch repair pathways - used in  
 PT the diagnosis, prognosis and therapy of cancers and in screening  
 PT assays

PS Example 15; Page 149-153; 256pp; English.  
 CC R76066 is the S.cerevisiae mismatch repair pathway protein MSH1. It  
 CC is used in the analysis of possible mutations in the human mismatch  
 CC repair genes. Defects or alterations in such a gene result in the  
 CC accumulation of unstable repeated DNA sequences, a feature of a number  
 CC of different cancers. The identification of a defect in the mismatch  
 CC repair pathway can be diagnostic of a predisposition to cancer and  
 CC prognostic for a particular mammalian cancer e.g colorectal, ovarian,  
 CC endometrial (uterine), renal, bladder, skin, rectal and bowel. The  
 CC nucleotide sequences and polypeptides of the hMSH2 gene may also be  
 CC used for therapy and in vaccines.  
 SQ Sequence 959 AA;

Query Match 54.1%; Score 53; DB 14; Length 959;  
 Best Local Similarity 50.0%; Pred. No. 1.02e+02;  
 Matches 6; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Db 11 fr-plsrslry 21  
 :| :| :| :| :|  
 QY 1 YRLAIRIALRY 12

RESULT 7  
 ID R76070 standard; Protein; 971 AA.  
 AC R76070;  
 DT 16-JAN-1996 (first entry)  
 DE Yeast MSH1 protein with I2CA5 epitope tag.  
 KW Mismatch repair; MSH2; primer; identification; defect; alteration;  
 KW cancer; tumour; vaccine.  
 OS Saccharomycetes cerevisiae.  
 PN W09514085-A2.  
 PD 26-MAY-1995.  
 PF 17-NOV-1994; U13385.  
 PR 17-NOV-1993; US-154792.  
 PR 07-DEC-1993; US-163449.  
 PR 13-JUN-1994; US-259310.  
 PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.  
 PA (DAND ) DANA FARMER CANCER INST.  
 PI Fishel R, Kolodner RD, Reenan RAG;  
 DR WPI; 95-200377/26.  
 DT Determining alteration in human mismatch repair pathways - used in  
 PT the diagnosis, prognosis and therapy of cancers and in screening  
 PT assays

PS Disclosure; Page 167-171; 256pp; English.  
 CC R76070 is the S.cerevisiae mismatch repair pathway protein MSH1,  
 CC containing the I2CA5 epitope. It is used in the analysis of possible  
 CC mutations in the human mismatch repair genes. Defects or alterations  
 CC in such a gene result in the accumulation of unstable repeated DNA  
 CC sequences, a feature of a number of different cancers. The  
 CC identification of a defect in the mismatch repair pathway can be  
 CC diagnostic of a predisposition to cancer and prognostic for a  
 CC particular mammalian cancer e.g colorectal, ovarian, endometrial  
 CC (uterine), renal, bladder, skin, rectal and bowel. The nucleotide  
 CC sequences and polypeptides of the hMSH2 gene may also be used for  
 CC therapy and in vaccines.  
 SQ Sequence 971 AA;

Query Match 54.1%; Score 53; DB 14; Length 971;  
 Best Local Similarity 50.0%; Pred. No. 1.02e+02;  
 Matches 6; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Db 11 fr-plsrslry 21  
 :| :| :| :| :|  
 QY 1 YRLAIRIALRY 12

RESULT 8  
 ID R92911 standard; peptide; 20 AA.

AC R92911;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PF 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.  
 DT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B\*5-84 MHC antigen of the recipient  
 PT host

PS Example 15; Page 36; 80pp; English.  
 CC R83051-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC  
 CC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to

CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 53.1%; Score 52; DB 16; Length 20;  
 Best Local Similarity 66.7%; Pred. No. 1.27e+02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;  
 Db 1 yrlair-lney 11  
 ||||| : ||  
 QY 1 YRLAIRRALRY 12

RESULT 9  
 ID R95422 standard; peptide; 25 AA.  
 AC R95422;  
 DT 12-NOV-1996 (first entry)  
 DE HLAB38.6084.  
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN W09513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI; 95-194027/25.  
 PT Compsns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 9; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLAB38.6084. These sequences can be used to isolate the protein p74 from  
 CC a T-cell lysate. p74 is a T-cell surface membrane protein associated  
 CC with T-cell activation in mammalian T-cells, and is also immunologically  
 CC cross reactive with the heat shock protein Hsc70. p74 is found in a  
 CC limited number of cell types, but is particularly expressed on B and T  
 CC cells. p74 can be isolated by lysis of a suitable cell with an  
 CC amphoteric detergent, and then passed through an affinity column  
 CC containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B2702.60-84 (see R95415), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 25 AA;

Query Match 53.1%; Score 52; DB 18; Length 25;  
 Best Local Similarity 66.7%; Pred. No. 1.27e+02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;  
 Db 15 yrenlr-lalry 25  
 || : |||||  
 QY 1 YRLAIRRALRY 12

RESULT 10  
 ID R48286 standard; peptide; 25 AA.  
 AC R48286;  
 DT 15-MAR-1994 (first entry)  
 DE Peptide fragment of HLA-B38 antigen.  
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;  
 KW parasitic disease; cytotoxic T lymphocyte; modulation.

OS Synthetic.  
 PN W09317699-A.  
 PD 16-SEP-1993.  
 PF 25-FEB-1993; U01758.  
 PR 02-MAR-1992; US-844716.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger CA, Krensky AM;  
 DR WPI; 93-303134/38.  
 PT New peptide(s) based on Class I HLA antigen domains - used for  
 PT modulating cytotoxic T-lymphocyte activity towards targets  
 PS Example 13; Page 39; 61pp; English.  
 CC The peptide is used to modulate or stimulate. It can be used for  
 CC activity, either by inhibition or stimulation, for inducing CTL  
 CC inhibiting CTL toxicity in transplantations, and in studies on viral  
 CC activity in parasitic diseases and neoplasia and in studies on viral  
 CC infection. The peptide can also be used for identifying CTLs which  
 CC bind to it and removing subsets of CTLs from a T-cell composition.  
 CC This peptide is derived from the HLA-B38 antigen and corresponds  
 CC to the amino acid positions 60-84 of that antigen.  
 SQ Sequence 25 AA;

Query Match 53.1%; Score 52; DB 8; Length 25;  
 Best Local Similarity 66.7%; Pred. No. 1.27e+02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;  
 Db 15 yrenlr-lalry 25  
 || : |||||  
 QY 1 YRLAIRRALRY 12

RESULT 11  
 ID R83093 standard; peptide; 25 AA.  
 AC R83093;  
 DT 16-MAY-1996 (first entry)  
 DE HLAB38 CTL modulating peptide (B38.6084).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLAB38.  
 OS Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B7S-84 MHC antigen of the recipient  
 PT host

Example 13; Page 32; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC  
 CC HLAB38. These sequences can be used to extend the period of acceptance  
 CC by a recipient of a transplant from an MHC unmatched donor. The peptides  
 CC are administered to a patient in conjunction with a subtherapeutic amount  
 CC of an immunosuppressant. This is administered to the patient for a  
 CC limited period of time (compared to the lifetime administration for  
 CC current treatments). The peptides particularly modulate (or inhibit) the  
 CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.  
 SQ Sequence 25 AA;

Query Match 53.1%; Score 52; DB 16; Length 25;  
 Best Local Similarity 66.7%; Pred. No. 1.27e+02;  
 Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;  
 Db 15 yrenlr-lalry 25  
 || : |||||  
 QY 1 YRLAIRRALRY 12

RESULT 12  
 ID R03144 standard; protein; 362 AA.

```

AC R03144;
DE 19-MAR-1991 (first entry)
DE Sequence of HLA-B51 antigen.
KW Probe: HLA class I DNA; immunogen.
OS Homo sapiens.
PN EP-354580-A.
PD 14-FEB-1990.
PF 10-AUG-1989.
PR 11-AUG-1988; JP-200758.
PA (OLYU) Olympus Optical Co., Ltd.
PI Kano K, Takiguchi, M.
DR WPI; 90-046289/07.
PT New DNA for class I human leucocyte antigens and derived probes and
PT transformed cells, useful for DNA typing, as immunogens etc.
PS Disclosure; Pages 12-13; 23pp; English.
CC The HLA class I DNA can be used as a source of probes for use in DNA
CC typing. Transformed cells, which are useful as immunogens, can be
CC obtained by introducing these DNAs into eucaryotic cells.
SQ Sequence 362 AA;

Query Match 53.1%; Score 52; DB 2; Length 362;
Best Local Similarity 66.7%; Pred. No. 1.27e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Db 98 yrenlr-ialry 108
   || : |||||
Qy 1 YRLAIRRIALRY 12

RESULT 13
ID R12463 standard; Protein; 362 AA.
AC R12463;
DE 29-AUG-1991 (first entry)
DE HLA-Bw53 exon.
KW Human leucocyte antigen; probe; major histocompatibility complex;
KW MHC; class I.
OS Homo sapiens.
PN J03112487-A.
PD 14-MAY-1991.
PF 22-SEP-1989; 247697.
PR 22-SEP-1989; JP-247697.
PA (OLYU) OLYMPUS OPTICAL KK.
DR WPI; 91-182991/25.
DR N-PSDB; Q12114.
PT HLA-Bw53 gene, DNA probe and transformant cells - used for
PT immunisation, identifying specificity of antiserum etc.
PS Claim 2; Page 1; 11pp; Japanese.
CC Probes comprising part of the sequence encoding the protein can be
CC used to identify Class I genes. The DNA can be expressed for
CC immunisation of animals and prodn. of monoclonal antibodies
CC specific for the HLA-Bw53 antigen. See also J03112485 and
CC J03112486.
SQ Sequence 362 AA;

Query Match 53.1%; Score 52; DB 3; Length 362;
Best Local Similarity 66.7%; Pred. No. 1.27e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Db 98 yrenlr-ialry 108
   || : |||||
Qy 1 YRLAIRRIALRY 12

RESULT 14
ID R03142 standard; protein; 362 AA.
AC R03142;
DE 19-MAR-1991 (first entry)
DE Sequence of HLA-Bw52 antigen.
KW Probe: HLA class I DNA; immunogen.
OS Homo sapiens.
PN EP-354580-A.
PD 14-FEB-1990.
PF 10-AUG-1989.

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PR 11-AUG-1988; JP-200758.
PA (OLYU) Olympus Optical Co., Ltd.
PI Kano K, Takiguchi, M.
DR WPI; 90-046289/07.
PT New DNA for class I human leucocyte antigens and derived probes and
PT transformed cells, useful for DNA typing, as immunogens etc.
PS Disclosure; Page 13; 23pp; English.
CC The HLA class I DNA can be used as a source of probes for use in DNA
CC typing. Transformed cells, which are useful as immunogens, can be
CC obtained by introducing these DNAs into eucaryotic cells.
SQ Sequence 362 AA;

Query Match 53.1%; Score 52; DB 2; Length 362;
Best Local Similarity 66.7%; Pred. No. 1.27e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Db 98 yrenlr-ialry 108
   || : |||||
Qy 1 YRLAIRRIALRY 12

RESULT 15
ID R73966 standard; Protein; 529 AA.
AC R73966;
DE 30-NOV-1995 (first entry)
DE Alpha 2 subunit of a human neuronal nicotinic acetylcholine receptor.
KW Human nNACHr; neuronal nicotinic acetylcholine receptor;
KW neurotransmitter.
OS Homo sapiens.
PN WO9513299-A.
PD 18-MAY-1995.
PF 08-NOV-1994; U12859.
PR 08-NOV-1993; US-149503.
PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
PI Elliott KJ, Ellis SB, Harpold MM;
DR WPI; 95-194036/25.
DR N-PSDB; Q90387.
DR New human neuronal nicotinic acetylcholine receptor alpha2 subunit DNA -
PT used to develop prods. for detection, diagnosis and therapy and for
PT modulating activity.
PS Disclosure; Page 43-46; 54pp; English.
CC DNA encoding the human nNACHr alpha2 subunit was isolated from a
CC human thalamus tissue cDNA library using corresp. rat cDNA. The
CC insert of one clone obtd. was ligated with the insert of another
CC clone to generate a full-length alpha 2 subunit cDNA. The DNA can be
CC used to identify function nNACHrs. Cells contg. the DNA can be used
CC for screening to identify cpds. which modulate the activity of human
CC nNACHrs. The human nNACHr alpha 2 subunit can be used to product
CC antibodies which can be used in immunohistochemistry, diagnosis and
CC therapy. The nucleic acids can be used for analysing disease states
CC and creating animal models.
SQ Sequence 529 AA;

Query Match 53.1%; Score 52; DB 14; Length 529;
Best Local Similarity 50.0%; Pred. No. 1.27e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 257 yafvirlrplfy 268
   | : |||:| |
Qy 1 YRLAIRRIALRY 12

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Search completed: Thu May 22 08:37:16 1997  
Job time : 13 secs.

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W P S R L A I R N E R

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:34:36 1997; MasPar time 3.23 Seconds  
Tabular output not generated. 176.531 Million cell updates/sec

Title: >US-08-653-294-31  
Description: (1-20) from US08653294.pep  
Perfect Score: 154  
Sequence: 1 YRLAIRLNERYLRLNER 20

Scoring table: PAM 150  
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir50  
1:ann1 2:ann2 3:ann3 4:ann4 5:annn1 6:annn2 7:unann3  
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8  
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 28.882; Variance 64.246; scale 0.450

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.	
1	74	48.1	245	10	D49898	cellobiose phosphotr	1.85e+00
2	71	46.1	361	5	S34613	5-exo-hydroxycamphor	4.43e+00
3	70	45.5	279	9	S32869	outo protein - Erwin	5.91e+00
4	70	45.5	768	5	S19263	DNA-directed DNA pol	5.91e+00
5	70	45.5	783	1	JDEC22	DNA-directed DNA pol	5.91e+00
6	68	44.2	253	9	J50595	rod-core linker poly	1.04e+01
7	68	44.2	254	9	S32475	rod-core linker poly	1.04e+01
8	68	44.2	349	4	RGECLG	glnL regulatory prot	1.04e+01
9	68	44.2	1051	14	A35761	cell surface glycopr	1.04e+01
10	68	44.2	1051	13	A40021	integrin VLA-3 alpha	1.04e+01
11	68	44.2	1053	14	I55534	VLA-3 alpha subunit	1.04e+01
12	67	43.5	346	9	G64182	ADP-heptose-lps hept	1.38e+01
13	65	42.2	349	7	S33023	nitrogen regulatory	2.40e+01
14	65	42.2	349	10	A33647	72K crystal protein	2.40e+01
15	65	42.2	818	16	S62790	mismatch DNA recogni	2.40e+01
16	64	41.6	85	10	I40586	hypothetical protein	3.15e+01
17	64	41.6	215	1	LNNTS6	stylar glycoprotein	3.15e+01
18	64	41.6	648	5	A25047	beta-glucuronidase (	3.15e+01
19	64	41.6	771	12	P50299	nitrite reductase (N	3.15e+01
20	64	41.6	1104	12	JH0181	nitrite reductase (N	3.15e+01
21	64	41.6	3224	13	S58884	Ran-binding protein	3.15e+01

22	64	41.6	3224	13	A57545	nucleoporin Nup358 -	3.15e+01
23	63	40.9	115	8	E36811	hypothetical protein	4.13e+01
24	63	40.9	245	16	S43774	Sl1 protein - Chaco	4.13e+01
25	63	40.9	261	8	S24418	dmpE protein - Pseud	4.13e+01
26	63	40.9	485	4	B45343	glycoprotein gp13 pr	4.13e+01
27	63	40.9	597	14	A30814	development-specific	4.13e+01
28	63	40.9	649	10	A49512	alpha-amyrase (EC 3.	4.13e+01
29	63	40.9	3165	16	S15010	hypothetical protein	4.13e+01
30	62	40.3	232	5	S28609	phosphoadenylylsulfa	5.40e+01
31	62	40.3	558	4	MXRRT	RNA 10 protein - ric	5.40e+01
32	62	40.3	818	12	S64251	SAP4 protein - yeast	5.40e+01
33	62	40.3	1155	16	S43275	hypothetical protein	5.40e+01
34	62	40.3	1176	12	A49848	nitrite reductase -	5.40e+01
35	62	40.3	1498	12	S53577	TyB protein - yeast	5.40e+01
36	62	40.3	1547	12	S69842	TyB protein - yeast	5.40e+01
37	61	39.6	108	10	G64386	hypothetical protein	7.04e+01
38	61	39.6	239	5	S34193	3'-phosphoadenosine	7.04e+01
39	61	39.6	354	14	B56392	beta-galactoside alp	7.04e+01
40	61	39.6	372	16	S46344	envelope protein - s	7.04e+01
41	61	39.6	579	13	B45266	MPL-K protein precu	7.04e+01
42	61	39.6	587	11	S54061	probable inorganic p	7.04e+01
43	61	39.6	635	13	A45266	MPL-P protein precu	7.04e+01
44	61	39.6	928	3	RBHU	retinoblastoma-assoc	7.04e+01
45	61	39.6	1502	4	RBYH1	CYC1/CYP3 transcript	7.04e+01

#### ALIGNMENTS

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TITLE			stearothermophilus
ORGANISM			#formal_name Bacillus stearothermophilus
DATE			07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
ACCESSIONS			D49898
REFERENCE			Lai, X.; Ingram, L.O.
#authors			J. Bacteriol. (1993) 175:6441-6450
#journal			Cloning and sequencing of a cellobiose phosphotransferase
#title			system operon from Bacillus stearothermophilus XL-65-6 and functional expression in Escherichia coli.
#cross-references			MUID:94012514
#contents			XL-65-6
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#status			preliminary
#molecule_type			DNA
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#cross-references			NCBIN:138630; NCBIP:138634
#note			sequence extracted from NCBI backbone
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Query Match			48.1%; Score 74; DB 10; Length 245;
Best Local Similarity			50.0%; Pred. No. 1.85e+00;
Matches			8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Db			132 fpvveqlaeryrlpir 147
Qy			1 YRLAIRLNERYLRLAIR 16
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ENTRY			
TITLE			S34613 #type complete
ORGANISM			5-exo-hydroxycamphor dehydrogenase (EC 1.1.1.-) - Pseudomonas
DATE			putida plasmid CAM
ACCESSIONS			S34613; A29844
REFERENCE			S34613
#authors			Aramaki, H.; Koga, H.; Sagara, Y.; Hosoi, M.; Horiuchi, T.
#journal			Biochim. Biophys. Acta (1993) 1174:91-94
#title			Complete nucleotide sequence of the 5-exo-hydroxycamphor

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dehydrogenase gene on the CAM plasmid of Pseudomonas putida
(ATCC 17453).
#accession S34613
#status not compared with conceptual translation
#molecule_type DNA
#residues 1-361 #label ARA
#experimental_source PpG1; ATCC 17453; CAM plasmid
REFERENCE A29844
#authors Koga, H.; Aramaki, H.; Yamaguchi, E.; Takeuchi, K.; Horiuchi,
T.; Gunsalus, I.C.
#journal J. Bacteriol. (1986) 166:1089-1095
#title camR, a negative regulator locus of the cytochrome P-450-cam
hydroxylase operon.
#cross-references MUID:86223770
#accession A29844
#molecule_type DNA
#residues 1-96, 'RAIIV' #label KOG
#note this sequence has been revised in reference S34613
GENETICS
#gene camD
#genome plasmid
#complex homodimer
#description catalyzes formation of 2,5-diketo-camphane from
5-exo-hydroxycamphor
CLASSIFICATION
#superfamily alcohol dehydrogenase; long-chain alcohol
dehydrogenase homology
KEYWORDS NAD; oxidoreductase; zinc
FEATURE
25-350 #domain long-chain alcohol dehydrogenase homology #label
LADH\
40,62,158 #binding_site zinc, catalytic (Cys, His, Cys) #status
predicted\
98,101,104,112 #binding_site zinc, noncatalytic (Cys) #status predicted
SUMMARY #length 361 #molecular-weight 38377 #checksum 992
Query Match 46.1%; Score 71; DB 5; Length 361;
Best Local Similarity 47.4%; Pred. NO. 4.43e+00;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Db 316 qlaarlqdrypladitqr 334
:||||:||||:|
QY 2 RLAIRLNERYRLAIRLN 20
RESULT 3
ENTRY #type complete
TITLE outO protein - Erwinia carotovora subsp. carotovora
ORGANISM #formal_name Erwinia carotovora subsp. carotovora
DATE 08-Dec-1993 #sequence_revision 26-Jul-1996 #text_change
26-Jul-1996
ACCESSIONS S32869; S31758
REFERENCE S32857
#authors Reeves, P.J.; Whitcombe, D.; Wharam, S.; Gibson, M.; Allison,
G.; Bunce, N.; Barallion, R.; Douglas, P.; Mulholland, V.;
Stevens, S.; Walker, D.; Salmond, G.P.C.
#journal Mol. Microbiol. (1993) 8:443-456
#title Molecular cloning and characterization of 13 out genes from
Erwinia carotovora subspecies carotovora: genes encoding
members of a general secretion pathway (GSP) widespread in
gram-negative bacteria.
#accession S32869
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-279 #label REE
#cross-references EMBL:X70049
#note the nucleotide sequence was submitted to the EMBL Data
Library, December 1992
GENETICS
#gene outO
#start_codon GTG
SUMMARY #length 279 #molecular-weight 31131 #checksum 5854

```

```

Query Match 45.5%; Score 70; DB 9; Length 279;
Best Local Similarity 50.0%; Pred. NO. 5.91e+00;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Db 35 yrlpimlerrwrqdiele 52
||||:| | | |
QY 1 YRLAIRLNERYRLAIRLN 18
RESULT 4
ENTRY #type complete
TITLE DNA-directed DNA polymerase (EC 2.7.7.7) (version 1) -
Escherichia coli
ORGANISM #formal_name Escherichia coli
DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
15-Jun-1996
ACCESSIONS S19263; S12820; B36236; JT0943; J00325
REFERENCE S19263
#authors Chen, H.
#submission submitted to the EMBL Data Library, June 1990
#accession S19263
#molecule_type DNA
#residues 1-768 #label CHE
#cross-references EMBL:M35371
REFERENCE S12820
#authors Chen, H.; Lawrence, C.B.; Bryan, S.K.; Moses, R.E.
#journal Nucleic Acids Res. (1990) 18:7185-7186
#title Aphidicolin inhibits DNA polymerase II of Escherichia coli,
an alpha-like DNA polymerase.
#cross-references MUID:91088346
#accession S12820
#status nucleic acid sequence not shown
#molecule_type DNA
#residues 90-768 #label CHE2
#cross-references EMBL:M35371
REFERENCE A36236
#authors Chen, H.; Sun, Y.; Stark, T.; Beattie, W.; Moses, R.E.
#journal DNA Cell Biol. (1990) 9:631-635
#title Nucleotide sequence and deletion analysis of the polB gene of
Escherichia coli.
#cross-references MUID:91083835
#accession B36236
#status preliminary
#molecule_type DNA
#residues 'V', 2-768 #label CH2
#cross-references GB:M35371
GENETICS
#gene polB
#map_position 2 min
#start_codon GTG
CLASSIFICATION #superfamily DNA-directed DNA polymerase II
KEYWORDS DNA synthesis; nucleotidyltransferase
SUMMARY #length 768 #molecular-weight 87931 #checksum 4470
Query Match 45.5%; Score 70; DB 5; Length 768;
Best Local Similarity 50.0%; Pred. NO. 5.91e+00;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Db 231 rmlqkhaeryrlpirl 246
|:|:| | | | | |
QY 2 RLAIRLNERYRLAIRLN 17
RESULT 5
ENTRY #type complete
TITLE DNA-directed DNA polymerase (EC 2.7.7.7) II (version 2) -
Escherichia coli
ORGANISM #formal_name Escherichia coli
DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
19-Oct-1995
ACCESSIONS S15943; S19262; S40576; JQ0780; A38840; JQ0688
REFERENCE S15943
#authors Iwasaki, H.; Ishino, Y.; Toh, H.; Nakata, A.; Shinagawa, H.

```



```

#journal Mol. Gen. Genet. (1991) 226:24-33
#title Escherichia coli DNA polymerase II is homologous to
#cross-references MUID:91238699
#accession SI5943
##molecule_type DNA
##residues 1-783 ##label IWA
##cross-references EMBL:X54847
#accession SI9262
##molecule_type protein
##residues 2-9 ##label IWA2
REFERENCE S40531
#authors Yura, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, A.;
#submisson Fujita, N.; Isono, K.; Mizobuchi, K.; Nakata, A.
#description submitted to the EMBL Data Library, December 1992
#description Systematic sequencing of the Escherichia coli genome:
#analysis of the 0-2.4min region.
#accession S40576
##status preliminary
##molecule_type DNA
##residues 'V', 2-783 ##label YUR
##cross-references EMBL:D10483
REFERENCE JQ0780
#authors Bonner, C.A.; Hays, S.; McEntee, K.; Goodman, M.F.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7663-7667
#title DNA polymerase II is encoded by the DNA damage-inducible dna
#cross-references MUID:91017565
#accession JQ0780
##molecule_type DNA
##residues 1-256, 'DD', 259-271, 'G', 273-458 ##label BON
##cross-references GB:M37727
#accession A38840
##molecule_type protein
##residues 2-9, 'XQ', 12-21, 'H', 23, 'X', 25-28 ##label B02
GENETICS
#gene polB
#map_position 2 min
#start_codon GTG
CLASSIFICATION #superfamily DNA-directed DNA polymerase II
KEYWORDS DNA synthesis; nucleotidyltransferase
FEATURE 2-783
#product DNA-directed DNA polymerase II #status
#experimental #label MAT
SUMMARY #length 783 #molecular-weight 90052 #checksum 2286
Query Match 45.5%; Score 70; DB 1; Length 783;
Best Local Similarity 50.0%; Pred. No. 5.91e+00;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Db 231 rmlqkhaeryrlplrl 246
| : : |||||:|
Qy 2 RLAIRLNERYLRL 17
RESULT 6
ENTRY JS0595 #type complete
TITLE rod-core linker polypeptide cpcG4 - Anabaena sp. (PCC 7120)
ORGANISM #formal_name Anabaena sp.
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
ACCESSIONS JS0595; PS0243
REFERENCE JS0592
#authors Bryant, D.A.; Stirewalt, V.L.; Glauser, M.; Frank, G.;
#journal Sieder, W.; Zuber, H.
#title Gene (1991) 107:91-99
#description A small multigene family encodes the rod-core linker
#cross-references MUID:92077441
#accession JS0595
##molecule_type DNA
##residues 1-253 ##label GRY
##cross-references GB:M80435

```

```

#accession PS0243
##molecule_type protein
##residues 2-23 ##label GRY1
COMMENT Linker polypeptides determine the positions of phycobiliproteins
within the phycobilisome structure.
GENETICS
#gene cpcG4
#feature 2-253
#product rod-core linker polypeptide cpcG4 #status
#experimental #label MAT
SUMMARY #length 253 #molecular-weight 29323 #checksum 5904
Query Match 44.2%; Score 68; DB 9; Length 253;
Best Local Similarity 53.8%; Pred. No. 1.04e+01;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Db 95 yrlvsvnnnyrl 107
| : : |||
Qy 1 YRLAIRLNERYLRL 13
RESULT 7
ENTRY S23475 #type complete
TITLE rod-core linker polypeptide cpcG3 - Fischerella sp.
ORGANISM #formal_name Fischerella sp.
DATE 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change
ACCESSIONS S23475; S16060
REFERENCE S23472
#authors Glauser, M.; Stirewalt, V.L.; Bryant, D.A.; Sieder, W.;
#journal Zuber, H.
#title Eur. J. Biochem. (1992) 205:927-937
#description Structure of the genes encoding the rod-core linker
#title polypeptides of Mastigocladus laminosus phycobilisomes and
#functional aspects of the
#phycobiliprotein/linker-polypeptide interactions.
#accession S23475
##molecule_type DNA
##residues 1-254 ##label GLA
##cross-references EMBL:X59763
#note the source is designated as Mastigocladus laminosus
GENETICS
#gene cpcG3
SUMMARY #length 254 #molecular-weight 29624 #checksum 7870
Query Match 44.2%; Score 68; DB 9; Length 254;
Best Local Similarity 53.8%; Pred. No. 1.04e+01;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Db 95 yrlvsvnnnyrl 107
| : : |||
Qy 1 YRLAIRLNERYLRL 13
RESULT 8
ENTRY RGEGL #type complete
TITLE glnL regulatory protein II - Escherichia coli
ALTERNATE_NAMES ntrB regulatory protein
ORGANISM #formal_name Escherichia coli
DATE 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
ACCESSIONS A30377; S40814; B23970; Q00553
REFERENCE A30377
#authors Miranda-Rios, J.; Sanchez-Pescador, R.; Urdea, M.;
#journal Covarrubias, A.A.
#title Nucleic Acids Res. (1987) 15:2757-2770
#description The complete nucleotide sequence of the glnALG operon of
#cross-references MUID:87174797
#accession A30377
##molecule_type DNA
##residues 1-349 ##label MIR
REFERENCE S40802

```

#authors Plunkett III, G.; Burland, V.; Daniels, D.L.; Blattner, F.R.  
 #journal Nucleic Acids Res. (1993) 21:3391-3398  
 #title Analysis of the Escherichia coli genome. III. DNA sequence of the region from 87.2 to 89.2 minutes.

#accession S40814

##status preliminary; nucleic acid sequence not shown;

translation not shown

##molecule\_type DNA

##residues 1-349 ##label PLU

##cross-references EMBL:L12021

##note the nucleotide sequence was submitted to the EMBL Data Library, October 1993

# REFERENCE

#authors A91533

#journal Rocha, M.; Vazquez, M.; Garciaarrubio, A.; Covarrubias, A.A.

#title Gene (1985) 37:91-99

Nucleotide sequence of the glnA-glnL intercistronic region of

Escherichia coli.

#cross-references MUID:86031370

#accession B23970

##molecule\_type DNA

##residues 1-24 ##label ROC

# GENETICS

#gene glnL; ntrB

#map\_position 87 min

# FUNCTION

#description acts as a signal transducer that responds to the nitrogen level of the cell and modulates the activity of glnG protein; at a low nitrogen level, glnG protein is activated through phosphorylation; at a high nitrogen level, it is deactivated through dephosphorylation  
 #superfamily glnL regulatory protein II  
 #ATP binding; regulatory protein; signal transduction  
 #length 349 #molecular-weight 38556 #checksum 8402

# CLASSIFICATION

## KEYWORDS

## SUMMARY

Query Match 44.2%; Score 68; DB 4; Length 349;

Best Local Similarity 44.4%; Pred. No. 1.04e+01;

Matches 8; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

Db 268 fqtlh-gerylaaxid 284

YRLAIRLNERYLRLAIRL 18

# RESULT

## ENTRY

A35761 #type complete

cell surface glycoprotein b3 precursor - golden hamster

#formal\_name Mesocricetus auratus common\_name golden hamster

12-Oct-1990 #sequence\_revision 12-Oct-1990 #text\_change

31-Dec-1993

## ACCESSIONS

A35761

## REFERENCE

#authors Tsuji, T.; Yamamoto, F.; Miura, Y.; Takio, K.; Titani, K.;

Pawar, S.; Osawa, T.; Hakomori, S.

J. Biol. Chem. (1990) 265:7016-7021

Characterization through cDNA cloning of galactoprotein b3

(Gap b3), a cell surface membrane glycoprotein showing

enhanced expression on oncogenic transformation.

Identification of Gap b3 as a member of the integrin

superfamily.

#cross-references MUID:90216739

#accession A35761

##status preliminary

##molecule\_type mRNA

##residues 1-1051 ##label TSU

##cross-references GB:J05281

## KEYWORDS

glycoprotein

#length 1051 #molecular-weight 116455 #checksum 9974

## SUMMARY

Query Match 44.2%; Score 68; DB 14; Length 1051;

Best Local Similarity 37.5%; Pred. No. 1.04e+01;

Matches 6; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Db . 574 yslplmpdrklmgr 589

QY 1 YRLAIRLNERYLRLAIR 16

# RESULT

## ENTRY

A40021 #type complete

integrin VLA-3 alpha-3 chain precursor - human

fusion regulatory protein FRP2; galactoprotein b3; very late

antigen-3 alpha chain

#formal\_name Homo sapiens #common\_name man

17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change

06-Sep-1996

## ACCESSIONS

A40021; JX0161; C28018; S44356

## REFERENCE

#authors Takada, Y.; Murphy, E.; Pil, P.; Chen, C.; Ginsberg, M.H.;

Hemler, M.E.

J. Cell Biol. (1991) 115:257-266

Molecular cloning and expression of the cDNA for alpha-3

subunit of human alpha-3beta-1 (VLA-3), an integrin-

receptor for fibronectin, laminin, and collagen.

#cross-references MUID:92011866

#accession A40021

##molecule\_type mRNA

##residues 1-1051 ##label TAK

##cross-references GB:M59911

## REFERENCE

JX0161

#authors Tsuji, T.; Hakomori, S.; Osawa, T.

J. Biochem. (1991) 109:659-665

Identification of human galactoprotein b3, an oncogenic

transformation-induced membrane glycoprotein, as VLA-3

alpha subunit: The primary structure of human integrin

alpha 3.

#cross-references MUID:91331981

#accession JX0161

##molecule\_type mRNA

##residues 33-1051 ##label TSU

## REFERENCE

A94151

#authors Takada, Y.; Strominger, J.L.; Hemler, M.E.

Proc. Natl. Acad. Sci. U.S.A. (1987) 84:3239-3243

The very late antigen family of heterodimers is part of a

superfamily of molecules involved in adhesion and

embryogenesis.

#cross-references MUID:87204112

#accession C28018

##molecule\_type protein

##residues 33-46 ##label TA2

## REFERENCE

S44356

#authors Ohta, H.; Tsurudome, M.; Matsumura, H.; Koga, Y.; Morikawa,

S.; Kawano, M.; Kusugawa, S.; Komada, H.; Nishio, M.; Ito,

Y.

EMBO J. (1994) 13:2044-2055

Molecular and biological characterization of fusion

regulatory proteins (FRPs): anti-FRP mAbs induced

HIV-mediated cell fusion via an integrin system.

#accession S44356

##status preliminary

##molecule\_type protein

##residues 33-43, 'X', 45-49 ##label OHT

## GENETICS

#gene GDB:ITGA3

##cross-references GDB:128972

cell adhesion; duplication; glycoprotein; heterodimer; metal

binding; transmembrane protein

## FEATURE

1-32

33-871

#domain signal sequence #status predicted #label SIG\

#product integrin alpha-3 heavy chain #status predicted

#label CHV\

#region calcium/magnesium binding #status predicted\

#region calcium/magnesium binding #status predicted\

#region calcium/magnesium binding #status predicted\

#region calcium/magnesium binding #status predicted\

#product integrin alpha-3 light chain #status predicted

```
992-1019          #label CHL\
#domain transmembrane #status predicted #label TM\
86,107,265,500,511,
573,605,656,697,
841,857,926,935,
969
SUMMARY          #length 1051 #molecular-weight 116611 #checksum 8842
Query Match      44.2%; Score 68; DB 13; Length 1051;
Best Local Similarity 43.8%; Pred. No. 1.04e+01;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Db 574 yslplmpdrplgr 589
|:::|:|:::|
Qy 1 YRLAIRLNERYLRAIR 16

RESULT 11
ENTRY      155534          #type complete
TITLE      VLA-3 alpha subunit - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
ACCESSIONS 155534
REFERENCE  Takeuchi, K.; Hirano, K.; Tsuji, T.; Osawa, T.; Irimura, T.
#authors   J. Cell. Biochem. (1995) 57:371-377
#journal   CDNA cloning of mouse VLA-3 alpha subunit.
#title     #cross-references MUID:95279462
#accession 155534
#status    preliminary; translated from GB/EMBL/DDBJ
#molecule_type mRNA
#residues  1-1053 #label RES
#cross-references GB:D13967; NID:G220634; CDS_PID:G220635
SUMMARY    #length 1053 #molecular-weight 116744 #checksum 976

Query Match      44.2%; Score 68; DB 14; Length 1053;
Best Local Similarity 37.5%; Pred. No. 1.04e+01;
Matches 6; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Db 575 yslplmpdrplgr 590
|:::|:|:::|
Qy 1 YRLAIRLNERYLRAIR 16

RESULT 12
ENTRY      G64182          #type complete
TITLE      ADP-heptose-lps heptosyltransferase II (rfaf) homolog -
ORGANISM   Haemophilus influenzae (strain Rd KW20)
DATE       #formal_name Haemophilus influenzae
18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
G64182
A64000
#authors   Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
Kirkness, E.F.; Krelavage, A.R.; Bult, C.J.; Tomb, J.F.;
Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
J.P.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton,
M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek,
D.N.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann,
J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.;
Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
#journal   Science (1995) 269:496-512
#title     Whole-genome random sequencing and assembly of Haemophilus
infectus Rd.
#accession G64182
#status    preliminary; nucleic acid sequence not shown;
translation not shown
#molecule_type DNA
#residues  1-346 #label TIGR

##cross-references GB:L42023; TIGR:HI1105
#note      named as homolog to a protein from Escherichia coli
SUMMARY    #length 346 #molecular-weight 38847 #checksum 9828

Query Match      43.5%; Score 67; DB 9; Length 346;
Best Local Similarity 52.9%; Pred. No. 1.38e+01;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 70 yrlgkslregydmav 86
|:::|:|:::|
Qy 1 YRLAIRLNERYLRAIR 17

RESULT 13
ENTRY      S53023          #type complete
TITLE      nitrogen regulatory protein B - Salmonella typhimurium
ORGANISM   #formal_name Salmonella typhimurium
DATE       08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
ACCESSIONS S53023
REFERENCE  Kustu, S.G.
#authors   submitted to the EMBL Data Library, March 1995
#submission S53023
#accession  S53023
#status    preliminary
#molecule_type DNA
#residues  1-349 #label KUS
#cross-references EMBL:X85104
CLASSIFICATION #superfamily glnL regulatory protein II
SUMMARY    #length 349 #molecular-weight 38443 #checksum 6851

Query Match      42.2%; Score 65; DB 7; Length 349;
Best Local Similarity 47.1%; Pred. No. 2.40e+01;
Matches 8; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

Db 268 fqltlh-gerylaari 283
|:::|:|:::|
Qy 1 YRLAIRLNERYLRAIR 17

RESULT 14
ENTRY      A43647          #type complete
TITLE      72K crystal protein - Bacillus thuringiensis subsp.
ORGANISM   israelensis
DATE       #formal_name Bacillus thuringiensis subsp. israelensis
03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
A43647
A32256
#authors   Donovan, W.P.; Dankoosik, C.; Gilbert, M.P.
#journal   J. Bacteriol. (1988) 170:4732-4738
#title     Molecular characterization of a gene encoding a 72-kilodalton
mosquito-toxic crystal protein from Bacillus thuringiensis
subsp. israelensis.
#accession A43647
#status    preliminary
#molecule_type DNA
#residues  1-643 #label DON
#cross-references GB:M31737
A32256
#authors   Adams, L.F.; Visick, J.E.; Whiteley, H.R.
#journal   J. Bacteriol. (1989) 171:521-530
#title     A 20-kilodalton protein is required for efficient production
of the Bacillus thuringiensis subsp. israelensis
27-kilodalton crystal protein in Escherichia coli.
#cross-references MUID:89123065
#accession A32256
#status    preliminary; not compared with conceptual translation
#molecule_type DNA
#residues  566-643 #label ADA
GENETICS cryD
#gene      cryD
SUMMARY    #length 643 #molecular-weight 72348 #checksum 6237
```

Query Match 42.2%; Score 65; DB 10; Length 643;  
Best Local Similarity 50.0%; Pred. No. 2.40e+01;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 544 ykllirrvpyrlp 557  
|:|:|:|:|:  
QY 1 YRLAIRLNERYRLA 14

RESULT 15  
ENTRY S62790 #type complete  
TITLE mismatch DNA recognition protein mutS - Thermus aquaticus  
(fragment)  
ORGANISM #formal\_name Thermus aquaticus  
DATE 23-Aug-1996 #sequence\_revision 23-Aug-1996 #text\_change  
23-Aug-1996  
ACCESSIONS S62790  
REFERENCE S62790  
#authors Takamatsu, S.; Kato, R.; Kuramitsu, S.  
#journal Nucleic Acids Res. (1996) 24:640-647  
#title Mismatch DNA recognition protein from an extremely  
thermophilic bacterium, Thermus thermophilus HB8.  
#accession S62790  
##status preliminary  
##residues 1-818 #label TAK  
##cross-references EMBL:D63810  
SUMMARY #length 818 #molecular-weight 91322 #checksum 6755

Query Match 42.2%; Score 65; DB 16; Length 818;  
Best Local Similarity 52.9%; Pred. No. 2.40e+01;  
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 331 rllfrladrlerlatrle 347  
|:|:|:|:|:  
QY 2 RLAIRLNERYRLAIRLN 18

Search completed: Thu May 22 08:35:05 1997  
Job time : 29 secs.

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(TM)

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Release 2.1D John F. Collins, Blocomputing Research Unit.

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:35:21 1997; MasPar time 2.19 Seconds

Tabular output not generated. 99.340 Million cell updates/sec

Title: &gt;US-08-653-294-31

Description: (1-20) from US08653294.pep

Perfect Score: 154

Sequence: 1 YRLAIRLNERYLRLAIRLNER 20

Scoring table: PAM 150

Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-geneseq26

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7

8:part8 9:part9 10:part10 11:part11 12:part12 13:part13

14:part14 15:part15 16:part16 17:part17 18:part18

19:part19

Statistics: Mean 19.740; Variance 84.009; scale 0.235

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	154	100.0	20 16	R92911	HLA-B2702 CTL modul	6.55e-07
2	83	53.9	20 18	R95428	HLA-B2702 84-75-84 pa	1.33e+00
3	83	53.9	20 16	R92907	HLA-B2702 CTL modul	1.33e+00
4	78	50.6	20 16	R92909	HLA-B2702 CTL modul	3.49e+00
5	76	49.4	20 16	R92908	HLA-B2702 CTL modul	5.10e+00
6	72	46.8	20 18	R95430	HLA-B2702 84-757/75-8	1.09e+01
7	71	46.1	20 16	R92910	HLA-B2702 CTL modul	1.31e+01
8	70	45.5	783 5	R24441	E. coli DNA polymerase	1.58e+01
9	70	45.5	783 13	R70841	E. coli polymerase-ii	1.58e+01
10	68	44.2	1019 3	R14118	Human GAP b3 protei	2.29e+01
11	68	44.2	1051 3	R14117	Hamster GAP b3 protei	2.29e+01
12	65	42.2	643 18	R97735	Bacillus thuringiens	3.98e+01
13	65	42.2	643 1	P91462	EHV-4 gC.	5.73e+01
14	63	40.9	485 4	R20796	Novel intestinal onco	5.73e+01
15	63	40.9	597 6	R30168	Pyrococcus furiosus a	5.73e+01
16	63	40.9	649 9	R47504	Sequence encoded by O	5.73e+01
17	63	40.9	3165 8	R38889	T. chalcogramma partl	6.86e+01
18	62	40.3	641 17	R5332	Transglutaminase (fis	6.86e+01
19	62	40.3	641 8	R39520	T. chalcogramma trans	6.86e+01
20	62	40.3	695 17	R65302		

21	62	40.3	696 17	R65303	T. chalcogramma trans	6.86e+01
22	62	40.3	696 8	R39518	Transglutaminase (fis	6.86e+01
23	62	40.3	724 18	R93081	Bacillus thuringiens	6.86e+01
24	62	40.3	1229 10	R34074	CryET5.	6.86e+01
25	61	39.6	635 14	R75940	Human myeloproliferat	8.22e+01
26	61	39.6	635 4	R23970	MPLV env protein with	8.22e+01
27	61	39.6	685 5	R25911	Macrophage tissue tra	8.22e+01
28	61	39.6	687 6	R32074	Bovine transglutamina	8.22e+01
29	61	39.6	816 1	P82112	Human retinoblastoma	8.22e+01
30	61	39.6	816 12	R83584	Retinoblastoma 94KD t	8.22e+01
31	61	39.6	816 11	R38568	Human retinoblastoma	8.22e+01
32	61	39.6	882 10	R51930	Mutated GAL4 protein	8.22e+01
33	61	39.6	928 13	R71681	Recombinant ppl10RB p	8.22e+01
34	61	39.6	928 7	R36534	Retinoblastoma (RB) p	8.22e+01
35	61	39.6	928 13	R71680	Retinoblastoma ppl10R	8.22e+01
36	61	39.6	928 14	R74271	Retinoblastoma tumour	8.22e+01
37	61	39.6	928 1	R05305	Cancer supressing gen	8.22e+01
38	61	39.6	928 1	R06289	Predicted retinoblast	8.22e+01
39	61	39.6	970 1	P90599	Human retinoblastoma	8.22e+01
40	61	39.6	3639 8	R40227	ACVS.	8.22e+01
41	61	39.6	3712 3	R13896	ACV synthetase.	8.22e+01
42	60	39.0	513 13	R77860	S. clavuligerus ORF3	9.83e+01
43	60	39.0	599 13	R72319	Laccase RSLac2 protei	9.83e+01
44	59	38.3	415 15	R76627	Human HRR25-like case	1.18e+02
45	59	38.3	672 2	P71200	Thermostable beta-gal	1.18e+02

## ALIGNMENTS

RESULT 1  
ID R92911 standard; peptide; 20 AA.  
AC R92911:  
DE 16-MAY-1996 (first entry)  
DE HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).  
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
KW class I MHC; HLA-B2702.  
PS Synthetic.  
ON W09525979-A1.  
PD 12-OCT-1995.  
PF 05-APR-1995; U04349.  
PR 05-APR-1994; US-222851.  
PR (STRD ) UNIV LELAND STANFORD JUNIOR.  
PI Clayberger C. Krensky AM, Farham P;  
DR WPI; 95-358582/46.  
PT Extension of acceptance period of transplants from MHC unmatched  
PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
PT host  
PS Example 15; Page 36; 80pp; English.  
CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
CC class I major histocompatibility complex (MHC) antigens. This sequence  
CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC  
CC HLA-B2702. These sequences can be used to extend the period of  
CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
CC The peptides are admistered to a patient in conjunction with a  
CC subtherapeutic amount of an immunosuppressant. This is administered to  
CC the patient for a limited period of time (compared to the lifetime  
CC administration for current treatments). The peptides particularly  
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
CC of the patient.  
SQ Sequence 20 AA;

Query Match 100.0%; Score 154; DB 16; Length 20;

Best Local Similarity 100.0%; Pred.No. 6.55e-07;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlairlneryrlairlner 20

|||||

QY 1 YRLAIRLNERYLRLAIRLNER 20

RESULT 2

ID R95428 standard; peptide; 20 AA.

AC R95428;  
 DE HLA-B\*2702 84-75-84 palindromic.  
 DT HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN W09513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI: 95-194027/25  
 PT Compsns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 12; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B\*2702 84-75-84 palindromic. These sequences can be used to isolate  
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
 CC protein associated with T-cell activation in mammalian T-cells, and is  
 CC also immunologically cross reactive with the heat shock protein Hsc70.  
 CC p74 is found in a limited number of cell types, but is particularly  
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
 CC cell with an amphoteric detergent, and then passed through an affinity  
 CC column containing a covalently bound HLA-B\*2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B\*2702.60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 20 AA;

Query Match 53.9%; Score 83; DB 18; Length 20;  
 Best Local Similarity 65.0%; Pred. No. 1.33e+00;  
 Matches 13; Conservative 2; Mismatches 4; Indels 1; Gaps 1;  
 Db 1 yrlairlner-renlrlalr 19  
 QY 1 YRLAIRLNERYLRLAIRLNER 20  
 ||||| ||||| | : |  
 RESULT 3  
 ID R92907 standard; peptide; 20 AA.  
 AC R92907;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B\*2702 CTL modulating peptide (B2702.84-75/75-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B\*2702.  
 OS Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI: 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096, and R92907-R92914 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 CC I MHC HLA-B\*2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 53.9%; Score 83; DB 16; Length 20;  
 Best Local Similarity 65.0%; Pred. No. 1.33e+00;  
 Matches 13; Conservative 2; Mismatches 4; Indels 1; Gaps 1;  
 Db 1 yrlairlner-renlrlalr 19  
 QY 1 YRLAIRLNERYLRLAIRLNER 20  
 ||||| ||||| | : |  
 RESULT 3  
 ID R92907 standard; peptide; 20 AA.  
 AC R92907;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B\*2702 CTL modulating peptide (B2702.84-75/75-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B\*2702.  
 OS Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI: 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096, and R92907-R92914 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 CC I MHC HLA-B\*2702. These sequences can be used to extend the period of

CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 53.9%; Score 83; DB 16; Length 20;  
 Best Local Similarity 65.0%; Pred. No. 1.33e+00;  
 Matches 13; Conservative 2; Mismatches 4; Indels 1; Gaps 1;  
 Db 1 yrlairlner-renlrlalr 19  
 QY 1 YRLAIRLNERYLRLAIRLNER 20  
 ||||| ||||| | : |  
 RESULT 4  
 ID R92909 standard; peptide; 20 AA.  
 AC R92909;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B\*2702 CTL modulating peptide (B2702.84-75/75-84(T)).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B\*2702.  
 OS Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI: 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096, and R92907-R92913 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 CC I MHC HLA-B\*2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 50.6%; Score 78; DB 16; Length 20;  
 Best Local Similarity 65.0%; Pred. No. 3.49e+00;  
 Matches 13; Conservative 1; Mismatches 5; Indels 1; Gaps 1;  
 Db 1 yrlairlner-renlrlalr 19  
 QY 1 YRLAIRLNERYLRLAIRLNER 20  
 ||||| ||||| | : |  
 RESULT 5  
 ID R92908 standard; peptide; 20 AA.  
 AC R92908;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B\*2702 CTL modulating peptide (B2702.84-75(T)/75-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B\*2702.  
 OS Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI: 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096, and R92907-R92913 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 CC I MHC HLA-B\*2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 50.6%; Score 78; DB 16; Length 20;  
 Best Local Similarity 65.0%; Pred. No. 3.49e+00;  
 Matches 13; Conservative 1; Mismatches 5; Indels 1; Gaps 1;  
 Db 1 yrlairlner-renlrlalr 19  
 QY 1 YRLAIRLNERYLRLAIRLNER 20  
 ||||| ||||| | : |  
 RESULT 5  
 ID R92908 standard; peptide; 20 AA.  
 AC R92908;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B\*2702 CTL modulating peptide (B2702.84-75(T)/75-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B\*2702.  
 OS Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.

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PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
CC I MHC HLA-B*2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;

Query Match 49.4%; Score 76; DB 16; Length 20;
Best Local Similarity 60.0%; Pred. No. 5.10e+00;
Matches 12; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Db 1 yrlatrlner-renlralr 19
QY 1 YRLAIRLNERYLRLAIRLNER 20

RESULT 6
ID R95430 standard; peptide; 20 AA.
AC R95430;
DT 12-NOV-1996 (first entry)
DE HLA-B*2702 84-75T/75-84T palindrome.
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytotoxic; antigen presenting cell.
OS Synthetic.
PN W09513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; U12985.
PR 10-NOV-1993; US-150493.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI: 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 12; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLA-B*2702 84-75T/75-84T palindrome. These sequences can be used to
CC isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface
CC membrane protein associated with T-cell activation in mammalian T-cells,
CC and is also immunologically cross reactive with the heat shock protein
CC Hsc70. p74 is found in a limited number of cell types, but is
CC particularly expressed on B and T cells. p74 can be isolated by lysis of
CC a suitable cell with an amphoteric detergent, and then passed through an
CC affinity column containing a covalently bound HLA-B*2702 palindromic
CC peptide. Compositions comprising the extracellular fragment of p74
CC combined with HLA-B*2702.60-84 (see R95416), induces calcium influx, and
CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity.
CC Candidate compounds can be screened for their effect on the cytolytic
CC activity of T-cells, by combining them with the extracellular portion of
CC p74 and determining the amount of binding between the candidate compound
CC and p74. Modulation of CTL activity can be inhibited in a cellular
CC composition containing T-cells and antigen presenting cells (APCs), by
CC adding to the mix the extracellular portion of p74, in an amount
CC sufficient to compete with p74 for the binding of the p74 ligand.
SQ Sequence 20 AA;

Query Match 46.8%; Score 72; DB 18; Length 20;
Best Local Similarity 72.2%; Pred. No. 1.09e+01;

PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
CC I MHC HLA-B*2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;

Query Match 46.1%; Score 71; DB 16; Length 20;
Best Local Similarity 60.0%; Pred. No. 1.31e+01;
Matches 12; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Db 1 yrlatrlner-renlralr 19
QY 1 YRLAIRLNERYLRLAIRLNER 20

RESULT 8
ID R24441 standard; Protein; 783 AA.
AC R24441;
DT 08-DEC-1992 (first entry)
DE E. coli DNA polymerase II.
KW Expression plasmid; industrial production.
OS Escherichia coli.
PN J04141088-A.
PD 14-MAY-1992.
PF 02-OCT-1990; 263125.
PR 02-OCT-1990; JP-263125.
PA (TAKI ) TAKARA SHUZO CO LTD.
DR WPI: 92-212759/26.
DR N-PSDB: 025440.
PT Novel Escherichia coli DNA polymerase II - contains specific
PT aminoacid sequence, obcd. by culturing DNA of recombinant plasmid
PT introduced transformant etc.
PS Disclosure; Fig 1; 8pp; Japanese.
CC The sequence is E. coli DNA polymerase II. The DNA encoding this
CC sequence can be introduced into expression plasmids which can then be
CC used to transform cells such that the new polymerase can be collected
CC from the culture on an industrial scale.
SQ Sequence 783 AA;

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Query Match 45.5%; Score 70; DB 5; Length 783;  
 Best Local Similarity 50.0%; Pred. No. 1.58e+01;  
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 231 rmlqkhaeryrlprl 246  
 QY 2 RLAIRLNERYRLAIRL 17

RESULT 9  
 ID R70841 standard; Protein; 783 AA.  
 AC R70841;  
 DT 31-AUG-1995 (first entry)  
 DE E. coli polymerase-II.  
 KW DNA-polymerase; DNA sequencing; 3'-5' exonuclease; replication;  
 KW enzyme engineering; protein engineering; mutagenesis.  
 OS Escherichia coli.  
 PN WO9504162-A.  
 PD 09-FEB-1995.  
 PF 01-AUG-1994; U08610.  
 PR 02-AUG-1993; US-101593.  
 PA (UYAL-) UNIV ALBERTA.  
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 PI Goodman MF, Reha-Krantz LJ;  
 DR WPI; 95-082243/11.  
 DR N-PSDB; Q85427.  
 PT Variant DNA polymerase(s) for DNA sequencing - having reduced  
 PT 3'-5' exonuclease activity or having enhanced DNA replication  
 PT activity  
 PS Disclosure; Page 28-31; 45pp; English.  
 CC The E. coli DNA-polymerase-II (given in R70841) may be engineered  
 CC by mutagenesis of the encoding DNA (Q85427) for use with novel  
 CC combinations of deoxynucleotides and chain-terminating  
 CC nucleotides in new DNA sequencing protocols. Variants pref.  
 CC include D156A and/or E158A mutations.  
 SQ Sequence 783 AA;

Query Match 45.5%; Score 70; DB 13; Length 783;  
 Best Local Similarity 50.0%; Pred. No. 1.58e+01;  
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 231 rmlqkhaeryrlprl 246  
 QY 2 RLAIRLNERYRLAIRL 17

RESULT 10  
 ID R14118 standard; Protein; 1019 AA.  
 AC R14118;  
 DT 10-DEC-1991 (first entry)  
 DE Human GAP b3 protein.  
 KW Galactoprotein b3; carcinoma; cancer; tumour.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Modified -site 54  
 FT /label= N-glycosylation  
 FT Modified -site 85  
 FT /label= N-glycosylation  
 FT Binding-site 136..144  
 FT /label= divalent cation binding site  
 FT Binding-site 209..217  
 FT /label= divalent cation binding site  
 FT Modified -site 233  
 FT /label= N-glycosylation  
 FT Binding-site 283..291  
 FT /label= divalent cation binding site  
 FT Binding-site 346..354  
 FT /label= divalent cation binding site  
 FT Binding-site 407..415  
 FT /label= divalent cation binding site  
 FT Modified -site 468  
 FT /label= N-glycosylation  
 FT Modified -site 479

FT /label= N-glycosylation  
 FT Modified -site 541  
 FT /label= N-glycosylation  
 FT Modified -site 573  
 FT /label= N-glycosylation  
 FT Modified -site 624  
 FT /label= N-glycosylation  
 FT Modified -site 665  
 FT /label= N-glycosylation  
 FT Modified -site 809  
 FT /label= N-glycosylation  
 FT Modified -site 825  
 FT /label= N-glycosylation  
 FT Cleavage-site 840..841  
 FT Modified -site 894  
 FT /label= N-glycosylation  
 FT Modified -site 903  
 FT /label= N-glycosylation  
 FT Modified -site 937  
 FT /label= N-glycosylation  
 FT Domain 960..987  
 FT /label= transmembrane domain  
 PN WO9113983-A.  
 PD 19-SEP-1991.  
 PF 08-APR-1991; U01606.  
 PR 12-MAR-1990; US-491910.  
 PA (BIOM-) BIOMERBRANE INST.  
 PI Tsuji T, Yamamoto F, Hakomori S;  
 DR WPI; 91-295637/40.  
 DR N-PSDB; Q13822.  
 PT DNA sequences encoding galactoprotein b3 - produced using DNA  
 PT constructs also antibodies to Gap b3 used to detect tumours that  
 PT result in elevated expression of protein.  
 PS Disclosure; Fig 6; 46pp; English.  
 CC The sequence was deduced from 3 overlapping clones isolated from  
 CC a human T24 cell line cDNA library. The DNA can be used to express  
 CC the Gap b3 protein which is a transformation-dependent cell surface  
 CC glycoprotein. The C-terminal 32 AA segment is likely to constitute  
 CC the cytoplasmic domain with the longer 959 AA residue segment  
 CC forming a glycosylated extracellular domain. The N-terminal region  
 CC has seven homologous repeats, three of which include the putative  
 CC metal binding sequences. Each repeat consists of a long (21-28 AA)  
 CC stretch followed by a short (5 AA) stretch. The alignment of  
 CC glycine and hydrophobic residues in each repeat shows a similar  
 CC pattern, especially the presence of XXXGAP (X= a hydrophobic AA) at  
 CC the end of most of the longer stretches (except for the 2nd and 7th  
 CC repeats. The protein may be used to produce antibodies and these,  
 CC or the DNA sequences, can be used to detect and quantify levels of  
 CC Gap b3 protein or mRNA in biological samples. A high level of the  
 CC protein is indicative of certain cancers.  
 CC See also R14117.  
 SQ Sequence 1019 AA;

Query Match 44.2%; Score 68; DB 3; Length 1019;  
 Best Local Similarity 43.8%; Pred. No. 2.29e+01;  
 Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Db 542 yslplrmprlprlgr 557  
 QY 1 YRLAIRLNERYLRLAIR 16

RESULT 11  
 ID R14117 standard; Protein; 1051 AA.  
 AC R14117;  
 DT 10-DEC-1991 (first entry)  
 DE Hamster GAP b3 protein.  
 KW Galactoprotein b3; carcinoma; cancer; tumour.  
 OS Cricetulus griseus.  
 FH Key Location/Qualifiers  
 FT Peptide 1..32  
 FT /label= signal sequence  
 FT Cleavage-site 32..33



FT Protein 33..1051  
 FT /label= mature gap b3  
 FT Peptide 33..50  
 FT /note= "confirmed by Edman degradation"  
 FT Binding-site 315 323  
 FT /label= divalent cation binding site  
 FT Binding-site 346..354  
 FT /label= divalent cation binding site  
 FT Binding-site 406..415  
 FT /label= divalent cation binding site  
 FT Modified-site 468  
 FT /label= N-glycosylation  
 FT Modified-site 479  
 FT /label= N-glycosylation  
 FT Modified-site 541  
 FT /label= N-glycosylation  
 FT Peptide 544..572  
 FT /note= "confirmed by Edman degradation"  
 FT Modified-site 573  
 FT /label= N-glycosylation  
 FT Modified-site 624  
 FT /label= N-glycosylation  
 FT Modified-site 665  
 FT /label= N-glycosylation  
 FT Peptide 755..784  
 FT /note= "confirmed by Edman degradation"  
 FT Modified-site 809  
 FT /label= N-glycosylation  
 FT Cleavage-site 840..841  
 FT Modified-site 891  
 FT /label= N-glycosylation  
 FT Modified-site 902  
 FT /label= N-glycosylation  
 FT Modified-site 937  
 FT /label= N-glycosylation  
 FT Domain 960..987  
 FT /label= transmembrane domain  
 PN W09113983-A.  
 PD 19-SEP-1991.  
 PF 08-APR-1991; U01606.  
 PR 12-MAR-1990; US-491910.  
 PA (BIOM-) BIOMEMBRANE INST.  
 PI Tsuji T, Yamamoto F, Hakomori S;  
 DR WPI; 91-295637/40.  
 DT N-PSDB; Q13821.  
 PR DNA sequences encoding galactoprotein b3 - produced using DNA  
 PT constructs also antibodies to Gap b3 used to detect tumours that  
 result in elevated expression of protein.  
 PS Disclosure; Fig 4; 46pp; English.  
 CC The sequence was deduced from 3 overlapping clones isolated from  
 CC a hamster Nilp cDNA library. The DNA can be used to express the  
 CC Gap b3 protein which is a transformation-dependent cell surface  
 CC glycoprotein. The C-terminal 32 AA segment is likely to constitute  
 CC the cytoplasmic domain with the longer 959 AA residue segment  
 CC forming a glycosylated extracellular domain. The protein may be  
 CC used to produce antibodies and these, or the DNA sequences, can be  
 CC used to detect and quantify levels of Gap b3 protein or mRNA in  
 CC biological samples. A high level of the protein is indicative of  
 CC certain cancers.  
 CC See also R14118.  
 SQ Sequence 1051 AA;

Query Match 44.2%; Score 68; DB 3; Length 1051;  
 Best Local Similarity 37.5%; Pred. No. 2.29e+01;  
 Matches 6; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Db 574 yslplmpdrklgm 589  
 |:::|:|:|:  
 QY 1 YRLAIRLNERVLAIR 16

RESULT 12  
 ID R97735 standard; Protein; 643 AA.

AC R97735;  
 DT 19-NOV-1996 (first entry)  
 DE Bacillus thuringiensis ssp. israelensis CryIVD protein.  
 KW CryIVD; toxic protein; crystal toxin; expression construct;  
 KW transformed cyanobacteria; phycocyanin beta; cpCB; promoter;  
 KW insecticide; dipteran larvae; mosquito; blackfly.  
 OS Bacillus thuringiensis.  
 PN US5518897-A.  
 PD 21-MAY-1996.  
 PF 04-MAY-1992; 877876.  
 PR 04-MAY-1992; US-877876.  
 PR 28-JAN-1994; US-188581.  
 PA (UYNE-) UNIV MEMPHIS STATE.  
 PI Murphy RC, Stevens SE;  
 DR WPI; 96-259063/26.  
 DR N-PSDB; T29774.  
 PT New DNA construct for expressing cryIV D protein in cyanobacteria -  
 PT under control of a phycocyanin beta promoter, useful for control of  
 PT dipteran larvae in water  
 PS Example 1; Columns 9-14; 20pp; English.  
 CC The present sequence is the B. thuringiensis ssp. israelensis CryIVD  
 CC toxic protein, the DNA of which was used in the prepn. of a claimed  
 CC DNA construct for the expression of CryIVD in cyanobacteria,  
 CC comprising the CryIVD DNA under the control of phycocyanin beta  
 CC (cpCB) promoter. Cyanobacteria (which may be adapted for growth in  
 CC fresh or brackish water) transformed with the construct can be used  
 CC as insecticides for controlling dipteran larvae, esp. those of  
 CC mosquitoes and blackflies, that live in water. The percentage of  
 CC Culex pipiens (mosquito) larvae surviving after 4 days with  
 CC cyanobacteria transformed with the claimed DNA construct as their  
 CC only food source was 51 %, compared to 94 % for those fed with  
 CC cyanobacteria transformed with an empty plasmid. In the  
 CC cyanobacteria, CryIVD is efficiently expressed under the control of  
 CC the strong cpCB promoter, even though the CryIVD gene contains 19  
 CC AUA which are generally poorly translated (if at all) in  
 CC cyanobacteria.  
 SQ Sequence 643 AA;

Query Match 42.2%; Score 65; DB 18; Length 643;  
 Best Local Similarity 50.0%; Pred. No. 3.98e+01;  
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 544 yklirrvpyrpl 557  
 |::|:|:  
 QY 1 YRLAIRLNERVLA 14

RESULT 13  
 ID P91462 standard; protein; 643 AA.  
 AC P91462;  
 DT 09-JAN-1990 (first entry).  
 DE 67-kD protein toxin.  
 KW cryd ; Bacillus thuringiensis; biopesticide.  
 OS Bacillus thuringiensis var. israelensis.  
 PN W08907605-A.  
 PD 24-AUG-1989.  
 PF 17-FEB-1989; U00663.  
 PR 19-FEB-1988; US-158176.  
 PA (ECOG) Ecogen Inc.  
 PI Donovan WP.  
 DR WPI; 89-263682/36.  
 DR N-PSDB; N90712.  
 PT Bacillus thuringiensis var israelensis cry D toxin gene and proteins  
 PT - used for producing insecticide compsns. active against Dipteran species  
 PS claim 2; fig 2; 58pp; English.  
 CC The 67kD protein encoded by the gene has insecticidal activity against  
 CC dipteran larvae.  
 SQ Sequence 643 AA;

Query Match 42.2%; Score 65; DB 1; Length 643;  
 Best Local Similarity 50.0%; Pred. No. 3.98e+01;  
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 544 ykllirvrvpyrlp 557  
 :| | | | |  
 QY 1 YRLAIRLNERVRLA 14

RESULT 14  
 ID R20796 standard; Protein; 485 AA.

AC R20796;  
 DT 19-MAY-1992 (first entry)  
 DE EHV-4 gC.  
 KW Equine herpes virus-4; glycoprotein gC; antigenic; vaccine;  
 KW alphaherpesvirus; respiratory disease; cellular attachment;  
 KW pathogenic.

OS Equine herpesvirus-4.  
 FH Key Location/Qualifiers  
 FT Peptide 1..32  
 FT /label= signal\_peptide  
 FT Protein 33..485  
 FT /label= EHV-4\_gC  
 FT Domain 33..444  
 FT /note= "external domain contg. 11 N-linked  
 FT glycosylation sites."

FT Domain 445..468  
 FT /note= "transmembrane domain"

FT Domain 469..485

FT /note= "hydrophilic cytoplasmic domain"

FT Misc-difference 409

FT /note= "antigenic site"

PN W09201057-A.

PD 23-JAN-1992.

PR 04-JUL-1991; G01091.

PF 06-JUL-1990; GB-014950.

PA (UNIU ) UNIV OF GLASGOW.

PA (EQUI-) EQUINE VIROLOGY RES FOUN.

PI Nicolson L, Onions DE;

DR WPI; 92-056872/07.

DR N-PSDB; Q20995.

PT Nucleic acid sequence encoding EHV-4 gH or gC protein - used to

PT produce a vaccine for protection of horses against EHV-4

PT Infection

PS Claim 7; Page 23; 29pp; English.

CC The sequence (SEQ ID no 2) was deduced from the nucleic acid  
 CC sequence obtd. by screening a BamHI library constructed from EHV-4  
 CC infected equine dermal cells (NBL-6). The gC protein is homologous  
 CC to its gC counterpart of other herpesviruses and is characterised  
 CC by conserved regions within the gC homologues (see feature table).  
 CC gC homologues comprise inter alia conserved amino acids in the  
 CC C-terminal half positioned around six sites of cysteine conservation  
 CC at residues 256, 318, 357, 361, 390 and 416, in this sequence, implying  
 CC some degree of conservation of secondary and tertiary structure  
 CC between gC homologues, presumably involving disulphide bonding.  
 CC EHV-4 gC has at Asp 409 a site capable of eliciting an immune  
 CC response. Vaccines derived from this sequence can be prepd., and  
 CC they may be used to protect horses against EHV-4 infection,  
 CC inducing a higher level of immunity and less side-effects than  
 CC other live virus vaccines.  
 CC See also R20795.

SQ Sequence 485 AA;

Query Match 40.9%; Score 63; DB 4; Length 485;

Best Local Similarity 70.0%; Pred. No. 5.73e+01;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 120 yrleihngr 129

||| | | | |

QY 1 YRLAIRLNER 10

RESULT 15

ID R30168 standard; Protein; 597 AA.

AC R30168;

DT 18-MAY-1993 (first entry)

DE Novel intestinal oncofetal gene product.

KW oncofoetal; onco-foetal; onco-fetal; intestine; gastrointestinal;  
 KW cancer; tumour; growth; benign; malignant; neoplasm; metastasis.  
 OS Homo sapiens.  
 PN US5171850-A.  
 PD 15-DEC-1992.  
 PF 31-AUG-1988; 239084.  
 PR 31-AUG-1988; US-239084.  
 PA (ONTA-) ONTARIO CANCER INST.  
 PI Buick RN, Fillmus JE;  
 DR WPI; 93-008640/01.  
 DR N-PSDB; Q33008.

PT DNA or RNA molecule encoding intestinal onco-foetal gene - useful  
 PT for detecting neoplastic cells, esp. intestinally-originating  
 PT prim. and metastatic tumours

PS Claim 1; Fig 8; 12pp; English.

CC This sequence represents the novel intestinal oncofoetal gene  
 CC product. It can be used to produce antibodies for detecting the  
 CC intestinal oncofetal gene product. The encoding DNA and RNA can be  
 CC used as probes for screening samples for the intestinal oncofetal  
 CC gene or gene transcripts for detection of neoplastic cells, esp.  
 CC intestinally-originating primary and metastatic tumours.

SQ Sequence 597 AA;

Query Match 40.9%; Score 63; DB 6; Length 597;

Best Local Similarity 46.2%; Pred. No. 5.73e+01;

Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 75 kmeekyqltarln 87

||| | | | |

QY 6 RLNERYLALRLN 18

Search completed: Thu May 22 08:35:34 1997

Job time : 13 secs.

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(TW)

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Release 2.1D John F. Collins, BioComputing Research Unit.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:32:44 1997; MasPar time 2.31 Seconds

Tabular output not generated.  
183.472 Million cell updates/sec

Title: >US-08-653-294-26  
Description: (1-20) from US08653294.pep  
Perfect Score: 154  
Sequence: 1 YRLAIRLNERENRIALRY 20

Scoring table: PAM 150  
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot34

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 31.472; Variance 50.872; scale 0.619

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	77	50.0	359	1B01_PANTR	CHLA CLASS I HISTOCOMP	7.49e-02
2	77	50.0	362	HLAH_HUMAN	HLA CLASS I HISTOCOMP	7.49e-02
3	77	50.0	362	1B47_HUMAN	HLA CLASS I HISTOCOMP	7.49e-02
4	77	50.0	362	1B53_HUMAN	HLA CLASS I HISTOCOMP	7.49e-02
5	77	50.0	362	1B01_GORGO	CLASS I HISTOCOMPATIB	7.49e-02
6	77	50.0	362	1B54_HUMAN	HLA CLASS I HISTOCOMP	7.49e-02
7	77	50.0	362	1B60_HUMAN	HLA CLASS I HISTOCOMP	7.49e-02
8	77	50.0	362	1B15_HUMAN	HLA CLASS I HISTOCOMP	7.49e-02
9	77	50.0	362	1B62_HUMAN	HLA CLASS I HISTOCOMP	7.49e-02
10	77	50.0	362	1B03_GORGO	CLASS I HISTOCOMPATIB	7.49e-02
11	77	50.0	362	1B49_HUMAN	HLA CLASS I HISTOCOMP	7.49e-02
12	77	50.0	362	1B61_HUMAN	HLA CLASS I HISTOCOMP	7.49e-02
13	77	50.0	362	1B52_HUMAN	HLA CLASS I HISTOCOMP	7.49e-02
14	77	50.0	362	1B02_GORGO	CLASS I HISTOCOMPATIB	7.49e-02
15	77	50.0	365	1A23_HUMAN	HLA CLASS I HISTOCOMP	7.49e-02
16	77	50.0	365	1A24_HUMAN	HLA CLASS I HISTOCOMP	7.49e-02
17	73	47.4	365	1A25_HUMAN	HLA CLASS I HISTOCOMP	3.43e-01
18	73	47.4	365	1A32_HUMAN	HLA CLASS I HISTOCOMP	3.43e-01
19	70	45.5	362	1B42_HUMAN	HLA CLASS I HISTOCOMP	1.04e+00
20	70	45.5	362	1B41_HUMAN	HLA CLASS I HISTOCOMP	1.04e+00
21	70	45.5	362	1B05_HUMAN	HLA CLASS I HISTOCOMP	1.04e+00
22	70	45.5	3712	1 ACV5_CEPAC	DELTA-(L-ALPHA-AMINO	1.04e+00

23	69	44.8	388	7	PAM_STRPV	PLASMINOGEN-BINDING P	1.49e+00
24	67	43.5	380	10	VINT_BBP21	INTEGRASE	3.05e+00
25	66	42.9	847	8	REL_STRCO	GTP PYROPHOSPHOKINASE	4.33e+00
26	66	42.9	882	3	ENV_SIVML	ENVELOPE POLYPROTEIN	6.13e+00
27	65	42.2	798	5	ITB7_HUMAN	INTEGRIN BETA-7 SUBUN	6.13e+00
28	65	42.2	806	5	ITB7_MOUSE	INTEGRIN BETA-7 SUBUN	6.13e+00
29	65	42.2	852	2	CLPB_CORGL	CLPB PROTEIN	6.13e+00
30	64	41.6	337	3	DFRA_VITV1	DIHYDROFLAVONOL-4-RED	8.65e+00
31	64	41.6	365	1	1A04_GORGO	CLASS I HISTOCOMPATIB	8.65e+00
32	64	41.6	517	6	NCAP_SENDZ	NUCLEOCAPSID PROTEIN	8.65e+00
33	64	41.6	880	3	ENV_SIVML	ENVELOPE POLYPROTEIN	8.65e+00
34	64	41.6	881	3	ENV_SIVMK	ENVELOPE POLYPROTEIN	8.65e+00
35	63	40.9	250	10	UNG_HCMVA	URACIL-DNA GLYCOSYLAS	1.21e+01
36	63	40.9	351	2	CBIG_SALTY	CBIG PROTEIN	1.21e+01
37	63	40.9	433	4	HEM2_SPIOL	DELTA-AMINOLEVULINIC	1.21e+01
38	63	40.9	443	11	YV16_MYCLE	PROBABLE SENSOR-LIKE	1.21e+01
39	63	40.9	485	10	VGLC_HSVE4	GLYCOPROTEIN C PRECUR	1.21e+01
40	63	40.9	517	6	NCAP_SENDE	NUCLEOCAPSID PROTEIN	1.21e+01
41	63	40.9	711	5	HGFL_HUMAN	HEPATOCTE GROWTH FAC	1.21e+01
42	62	40.3	370	5	HUPK_RHILV	HUPK PROTEIN	1.70e+01
43	62	40.3	380	11	YXEP_BACSU	HYPOTHEICAL 41.6 KD	1.70e+01
44	62	40.3	524	6	NCAP_SENDS	NUCLEOCAPSID PROTEIN	1.70e+01
45	62	40.3	661	8	RDGC_DRONE	SERINE/THREONINE PROT	1.70e+01

## ALIGNMENTS

RESULT 1  
ID 1B01\_PANTR STANDARD; PRT; 359 AA.

AC P13750;  
DT 01-JAN-1990 (REL. 13, CREATED)  
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)  
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)

DE CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR (FRAGMENT).

OS PAN TROGLODYTES (CHIMPANZEE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

ON EUTHERIA; PRIMATES.

RP SEQUENCE FROM N.A.

RX MEDLINE; 89030641.

RA MAYER W.B., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,

RA KLEIN J.;

RL EMBO J. 7:2765-2774(1988).

RN [2]

RP REVISIONS.

RA MAYER W.;

RL SUBMITTED (FEB-1989) TO EMBL/GENBANK/DBJ DATA BANKS.

CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO

CC THE IMMUNE SYSTEM.

CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

CC MICROGLOBULIN).

DR EMBL; X13115; G755776; -.

DR PIR; S03537; S03537.

DR HSP; P03989; IHS.

DR PROSITE; PS00290; IG\_MHC.

KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.

FT NON\_TER 1

FT SIGNAL <1 20

FT CHAIN 21 359

FT CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN.

FT DOMAIN 21 110

FT DOMAIN 111 202

FT DOMAIN 203 294

FT DOMAIN 295 305

FT TRANSMEM 306 329

FT DOMAIN 330 359

FT DISULFID 121 184

FT DISULFID 223 279

FT CARBOHYD 106 106

SEQ SEQUENCE 359 AA; 40173 MW; 5395FFC9 CRC32;

Query Match

50.0%; Score 77; DB 1; Length 359;

```

Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 95 rentrialry 104
QY 11 RENLRIALRY 20

RESULT 2
ID HLA_HUMAN STANDARD; PRT; 362 AA.
AC P01893;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, H ALPHA CHAIN PRECURSOR
DE (HLA-AR) (HLA-12.4).
GN HLAH.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RX MEDLINE: 82151002.
RA MALISSEN M., MALISSEN B., JORDAN B.R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 79:893-897(1982).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; V00526; G386873; ALT_INIT.
DR PIR; A02189; HLH12.
DR HSSP; P03989; 1HSA.
DR MIM; 142925.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 227 283
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40850 MW; 5610F63 CRC32;

Query Match 50.0%; Score 77; DB 5; Length 362;
Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 rentrialry 108
QY 11 RENLRIALRY 20

RESULT 3
ID LB47_HUMAN STANDARD; PRT; 362 AA.
AC P30487;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RX MEDLINE: 89235215.
RA PARHAM P., LAWLER D.A., LOMEN C.E., ENNIS P.D.;

Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 rentrialry 108
QY 11 RENLRIALRY 20

RESULT 4
ID LB53_HUMAN STANDARD; PRT; 362 AA.
AC P30490;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RX MEDLINE: 89080265.
RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
RA TAKIGUCHI M.;
RL J. IMMUNOL. 142:306-311(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M22799; G553538; ALT SEQ.
DR EMBL; M22793; G553538; JOINED.
DR EMBL; M22794; G553538; JOINED.
DR EMBL; M22795; G553538; JOINED.
DR EMBL; M22796; G553538; JOINED.
DR EMBL; M22797; G553538; JOINED.
DR EMBL; M22798; G553538; JOINED.
DR PIR; B30345; B30345.
DR PIR; B30548; B30548.
DR HSSP; P03989; 1HSA.
DR MIM; 142830.
DR PROSITE; PS00290; IG_MHC.

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J. IMMUNOL. 142:3937-3950(1989).
[2]
RN REVISIONS TO 78.
RX MEDLINE: 93056529.
RA HILDEBRAND W.H., MADRIGAL J.A., BELICH M.P., ZEMMOUR J., WARD F.E.,
RA WILLIAMS R.C., PARHAM P.;
RL J. IMMUNOL. 149:3563-3568(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M24037; G407191.
DR HSSP; P03989; 1HSA.
DR MIM; 142830.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 309
FT TRANSMEM 310 333
FT DOMAIN 334 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40581 MW; E996F82F CRC32;

Query Match 50.0%; Score 77; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 rentrialry 108
QY 11 RENLRIALRY 20

RESULT 4
ID LB53_HUMAN STANDARD; PRT; 362 AA.
AC P30490;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RX MEDLINE: 89080265.
RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
RA TAKIGUCHI M.;
RL J. IMMUNOL. 142:306-311(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M22799; G553538; ALT SEQ.
DR EMBL; M22793; G553538; JOINED.
DR EMBL; M22794; G553538; JOINED.
DR EMBL; M22795; G553538; JOINED.
DR EMBL; M22796; G553538; JOINED.
DR EMBL; M22797; G553538; JOINED.
DR EMBL; M22798; G553538; JOINED.
DR PIR; B30345; B30345.
DR PIR; B30548; B30548.
DR HSSP; P03989; 1HSA.
DR MIM; 142830.
DR PROSITE; PS00290; IG_MHC.

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KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 115 206 ALPHA CHAIN BW-52(B-5) B*5201.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-1.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-2.
FT TRANSMEM 309 332 EXTRACELLULAR ALPHA-3.
FT DOMAIN 333 362 CONNECTING PEPTIDE.
FT CARBOHYD 110 110 CYTOPLASMIC TAIL.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40521 MW; 3B436FEB CRC32;

Query Match 50.0%; Score 77; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renltrialry 108
QY 11 RENLIRIALRY 20

RESULT 5
ID 1B01_GORGO STANDARD; PRT: 362 AA.
AC P30379;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECURSOR.
OS GORILLA GORILLA GORILLA (LOWLAND GORILLA).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92078860.
RA LAWLER D.A., WARREN E., TAYLOR P., PARHAM P.;
RL J. EXP. MED. 174:1491-1509(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL: X60255; G228666; -.
DR PIR: JH0539; JH0539.
DR HSP: P03989; 1HSA.
DR PROSITE: PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114 CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT TRANSMEM 309 332 EXTRACELLULAR ALPHA-3.
FT DOMAIN 333 362 CONNECTING PEPTIDE.
FT CARBOHYD 110 110 CYTOPLASMIC TAIL.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40170 MW; 2E33E2B8 CRC32;

Query Match 50.0%; Score 77; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renltrialry 108
QY 11 RENLIRIALRY 20

RESULT 6
ID 1B54_HUMAN STANDARD; PRT: 362 AA.
AC P30491;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 B*5301 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91067476.
RA HAYASHI H., Ooba T., NAKAYAMA S., SEKIMATA M., KANO K.,
RA TAKIGUCHI M.;
RL IMMUNOGENETICS 32:195-199(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL: M58636; G187757; -.
DR PIR: A45834; A45834.
DR HSP: P03989; 1HSA.
DR MIM: I42830; -.
DR PROSITE: PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 115 206 ALPHA CHAIN BW-53 B*5301.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT TRANSMEM 309 332 EXTRACELLULAR ALPHA-3.
FT DOMAIN 333 362 CONNECTING PEPTIDE.
FT CARBOHYD 110 110 CYTOPLASMIC TAIL.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40495 MW; 2BDC746E CRC32;

Query Match 50.0%; Score 77; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renltrialry 108
QY 11 RENLIRIALRY 20

RESULT 7
ID 1B60_HUMAN STANDARD; PRT: 362 AA.
AC P18465;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5701 ALPHA
DE CHAIN PRECURSOR (BW57.1).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90207291.
RA ENNIS P.D.; ZEMMOUR J., SALTER R.D., PARHAM P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.

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CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 DR EMBL; M32318; G307222; -.  
 DR EMBL; X55711; G32181; -.  
 DR PIR; S12622; S12622.  
 DR PIR; D35997; D35997.  
 DR HSSP; P03989; 1HSA.  
 DR MIM; 142830; -.  
 DR PROSITE; PS00290; IG\_MHC.  
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 24  
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 FT ALPHA CHAIN B-27 (B-17) B\*5701.  
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.  
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.  
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.  
 FT DOMAIN 299 308 CONNECTING PEPTIDE.  
 FT TRANSMEM 309 332  
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.  
 FT CARBOHYD 110 110 BY SIMILARITY.  
 FT DISULFID 125 188 BY SIMILARITY.  
 FT DISULFID 227 283 BY SIMILARITY.  
 SQ SEQUENCE 362 AA; 40224 MW; D91DF8DD CRC32;

Query Match 50.0%; Score 77; DB 1; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 7.49e-02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 rentrialry 108  
 |||||  
 QY 11 RENLRALRY 20

RESULT 8  
 ID 1B15\_HUMAN STANDARD; PRT; 362 AA.  
 AC P10317;  
 DT 01-MAR-1989 (REL. 10, CREATED)  
 DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)  
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)  
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B\*2702 ALPHA CHAIN  
 DE PRECURSOR (B-27K) (B27.2).  
 GN HLAB.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 86220133.  
 RA SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;  
 RL EMBO J. 5:547-552(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA PARHAM P., ARNETT K.L., ADAMS E.J.;  
 RL SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RN [3]  
 RP SEQUENCE OF 86-107 AND 171-181.  
 RX MEDLINE; 86042671.  
 RA VEGA M.A., EZQUERRA A., ROJO S., APARICIO P., BRAGADO R.,  
 RA LOPEZ DE CASTRO J.A.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 82:7394-7398(1985).  
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 CC EMBL; X03664; G871296; -.  
 DR EMBL; X03667; G871296; JOINED.  
 DR EMBL; L38504; G896271; -.  
 DR PIR; B25092; HLHUBK.  
 DR HSSP; P03989; 1HSA.  
 DR MIM; 142830; -.  
 DR PROSITE; PS00290; IG\_MHC.  
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 24

FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 FT ALPHA CHAIN B-27 B\*2702.  
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.  
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.  
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.  
 FT DOMAIN 299 308 CONNECTING PEPTIDE.  
 FT TRANSMEM 309 332  
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.  
 FT CARBOHYD 110 110 BY SIMILARITY.  
 FT DISULFID 125 188 BY SIMILARITY.  
 FT DISULFID 227 283 BY SIMILARITY.  
 SQ SEQUENCE 362 AA; 40397 MW; 9798F0BB CRC32;

Query Match 50.0%; Score 77; DB 1; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 7.49e-02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 rentrialry 108  
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 QY 11 RENLRALRY 20

RESULT 9  
 ID 1B62\_HUMAN STANDARD; PRT; 362 AA.  
 AC P10319;  
 DT 01-MAR-1989 (REL. 10, CREATED)  
 DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)  
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)  
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-58(B-17) B\*5801 ALPHA  
 DE CHAIN PRECURSOR.  
 GN HLAB.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 86008247.  
 RA WAYS J.P., COPPIN H.L., PARHAM P.;  
 RL J. BIOL. CHEM. 260:11924-11933(1985).  
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 CC EMBL; M11799; G386885; -.  
 DR PIR; A23895; HLHUB8.  
 DR HSSP; P03989; 1HSA.  
 DR MIM; 142830; -.  
 DR PROSITE; PS00290; IG\_MHC.  
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 24  
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 FT ALPHA CHAIN BW-58(B-17) B\*5801.  
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.  
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.  
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.  
 FT DOMAIN 299 308 CONNECTING PEPTIDE.  
 FT TRANSMEM 309 332  
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.  
 FT CARBOHYD 110 110 BY SIMILARITY.  
 FT DISULFID 125 188 BY SIMILARITY.  
 FT DISULFID 227 283 BY SIMILARITY.  
 SQ SEQUENCE 362 AA; 40337 MW; 3E5E7534 CRC32;

Query Match 50.0%; Score 77; DB 1; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 7.49e-02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 rentrialry 108  
 |||||  
 QY 11 RENLRALRY 20

RESULT 10

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ID 1B03_GORGO STANDARD; PRT; 362 AA.
AC P30381;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0103 ALPHA CHAIN PRECURSOR.
OS GORILLA GORILLA GORILLA (LOWLAND GORILLA).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92078660.
RA LAWLER D.A., WARREN E., TAYLOR P., PARHAM P.;
RL J. EXP. MED. 174:1491-1509(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; X60254; G22870; -.
DR PIR; JH0541; JH0541.
DR HSSP; P03989; 1HSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
FT SEQUENCE 362 AA; 40248 MW; FEA6A941 CRC32;
Query Match 50.0%; Score 77; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 99 renltrialry 108
QY 11 renltrialry 20
RESULT 11
ID 1B49_HUMAN STANDARD; PRT; 362 AA.
AC P18464;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90207291.
RA ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89080265.
RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
RA TAKIGUCHI M.;
RL J. IMMUNOL. 142:306-311(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89233295.
RA POHLA H., KUON W., TABACZEWSKI P., DOERNER C., WEISS E.H.;

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RL IMMUNOGENETICS 29:297-307(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M32319; G307223; -.
DR EMBL; M22792; G553533; ALT_SEQ.
DR EMBL; M22786; G553533; JOINED.
DR EMBL; M22787; G553533; JOINED.
DR EMBL; M22788; G553533; JOINED.
DR EMBL; M22789; G553533; JOINED.
DR EMBL; M22790; G553533; JOINED.
DR EMBL; M22791; G553533; JOINED.
DR EMBL; L41087; G735902; -.
DR PIR; A30345; A30345.
DR PIR; A30548; A30548.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT SEQUENCE 362 AA; 40566 MW; 4D846F30 CRC32;
Query Match 50.0%; Score 77; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 99 renltrialry 108
QY 11 renltrialry 20
RESULT 12
ID 1B61_HUMAN STANDARD; PRT; 362 AA.
AC P30497;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5702 ALPHA CHAIN
DE PRECURSOR (BW57.2).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93056508.
RA MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
RA LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETIL-ERLER M.L.,
RA MARTELL R.W., DU TOIT E.D., PARHAM P.;
RL J. IMMUNOL. 149:3411-3415(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; X61707; G32187; -.
DR PIR; S16774; S16774.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.

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FT SIGNAL 1 24  
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 FT ALPHA CHAIN B-57(B-17) B\*5702.  
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.  
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.  
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.  
 FT DOMAIN 299 308 CONNECTING PEPTIDE.  
 FT TRANSMEM 309 332  
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.  
 FT CARBOHYD 110 110 BY SIMILARITY.  
 FT DISULFID 125 188 BY SIMILARITY.  
 FT DISULFID 227 283 BY SIMILARITY.  
 SQ SEQUENCE 362 AA; 40342 MW; 628C2156 CRC32;

Query Match 50.0%; Score 77; DB 1; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 7.49e-02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renltrialy 108  
 |||||  
 QY 11 RENLRIALRY 20

RESULT 13  
 ID 1B52\_HUMAN STANDARD; PRT; 362 AA.  
 AC P30489;  
 DT 01-APR-1993 (REL. 25, CREATED)  
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)  
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)  
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B\*5104 ALPHA CHAIN  
 DE PRECURSOR.  
 GN HLAB.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 92269955.  
 RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,  
 RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;  
 RL NATURE 357:326-329(1992).  
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 THE IMMUNE SYSTEM.  
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 MICROGLOBULIN).  
 CC EMBL; Z15143; G28235; -.  
 DR HSSP; P03989; IHSA.  
 DR MIM; 142830; -.  
 DR PROSITE; PS00290; IG\_MHC.  
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 24  
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 FT ALPHA CHAIN B-51(B-5) B\*5104.  
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.  
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.  
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.  
 FT DOMAIN 299 308 CONNECTING PEPTIDE.  
 FT TRANSMEM 309 332  
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.  
 FT CARBOHYD 110 110 BY SIMILARITY.  
 FT DISULFID 125 188 BY SIMILARITY.  
 FT DISULFID 227 283 BY SIMILARITY.  
 SQ SEQUENCE 362 AA; 40560 MW; F22F08AB CRC32;

Query Match 50.0%; Score 77; DB 1; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 7.49e-02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renltrialy 108  
 |||||  
 QY 11 RENLRIALRY 20

RESULT 14  
 ID 1B02\_GORGO STANDARD; PRT; 362 AA.  
 AC P30380;  
 DT 01-APR-1993 (REL. 25, CREATED)  
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)  
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)  
 DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECURSOR.  
 DE GORILLA GORILLA (LOWLAND GORILLA).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 92078860.  
 RA LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;  
 RL J. EXP. MED. 174:1491-1509(1991).  
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 THE IMMUNE SYSTEM.  
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 MICROGLOBULIN).  
 CC EMBL; X60693; G22868; -.  
 DR FIR; JH0540; JH0540.  
 DR HSSP; P03989; IHSA.  
 DR PROSITE; PS00290; IG\_MHC.  
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 24  
 FT CHAIN 25 362 CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 FT GOGO-B0102 ALPHA CHAIN.  
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.  
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.  
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.  
 FT DOMAIN 299 308 CONNECTING PEPTIDE.  
 FT TRANSMEM 309 332  
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.  
 FT DISULFID 125 188 BY SIMILARITY.  
 FT DISULFID 227 283 BY SIMILARITY.  
 FT CARBOHYD 110 110 BY SIMILARITY.  
 SQ SEQUENCE 362 AA; 40204 MW; 3CF119AD CRC32;

Query Match 50.0%; Score 77; DB 1; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 7.49e-02;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renltrialy 108  
 |||||  
 QY 11 RENLRIALRY 20

RESULT 15  
 ID 1A23\_HUMAN STANDARD; PRT; 365 AA.  
 AC P30447;  
 DT 01-APR-1993 (REL. 25, CREATED)  
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) ALPHA CHAIN  
 DE PRECURSOR.  
 GN HLA.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A. (A\*2301).  
 RX MEDLINE; 92104637.  
 RA LITTLE A.-M., MADRIGAL J.A., PARHAM P.;  
 RL IMMUNOGENETICS 35:41-45(1992).  
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 THE IMMUNE SYSTEM.  
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 MICROGLOBULIN).  
 CC EMBL; M64742; G187618; -.  
 DR HSSP; P01892; 1HHG.  
 DR MIM; 142800; -.



```

DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 365 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN A-23(A9).
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 365 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 365 AA; 40732 MW; BIC21094 CRC32;

Query Match 50.0%; Score 77; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 7.49e-02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 rentrialry 108
Oy 11 RENLRYALRY 20

```

Search completed: Thu May 22 08:32:51 1997  
Job time : 7 secs.

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WISREH (TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:33:09 1997; MasPar time 3.22 Seconds  
Tabular output not generated. 176.841 Million cell updates/sec

Title: >US-08-653-294-26  
Description: (1-20) from US08653294.pep  
Perfect Score: 154  
Sequence: 1 YRLAIRLNERENLRALRY 20

Scoring table: PAM 150  
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir50  
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3  
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8  
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 30.116; Variance 61.232; scale 0.492

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	77	50.0	273	13	I38509 MHC class I histocomp	5.91e-01
2	77	50.0	274	13	I54463 MHC HLA-B*51 chain -	5.91e-01
3	77	50.0	354	13	I59308 class I histocompati	5.91e-01
4	77	50.0	354	13	I80168 class I histocompati	5.91e-01
5	77	50.0	354	13	I80167 class I histocompati	5.91e-01
6	77	50.0	355	13	I80171 class I histocompati	5.91e-01
7	77	50.0	355	13	I80169 class I histocompati	5.91e-01
8	77	50.0	359	2	HLHU12 MHC class I histocom	5.91e-01
9	77	50.0	362	6	JH0539 MHC class I histocom	5.91e-01
10	77	50.0	362	6	B30345 MHC class I histocom	5.91e-01
11	77	50.0	362	13	I84486 transmembrane glycop	5.91e-01
12	77	50.0	362	6	JH0540 class I histocompati	5.91e-01
13	77	50.0	362	6	S24434 class I histocompati	5.91e-01
14	77	50.0	362	6	A30345 MHC class I histocom	5.91e-01
15	77	50.0	362	13	I37521 HLA-B*57.2 antigen -	5.91e-01
16	77	50.0	362	13	I59633 MHC HLA-B transmembr	5.91e-01
17	77	50.0	362	6	JH0541 class I histocompati	5.91e-01
18	77	50.0	362	13	I84490 lymphocyte antigen -	5.91e-01
19	77	50.0	362	13	I62045 gene HLA-B*1517 prot	5.91e-01
20	77	50.0	362	6	A45834 MHC class I histocom	5.91e-01
21	77	50.0	362	2	HLHUB8 MHC class I histocom	5.91e-01

22	77	50.0	362	13	I37120 MHC class I HLA-B*51	5.91e-01
23	77	50.0	363	16	S07113 class I histocompati	5.91e-01
24	77	50.0	363	13	I36957 MHC ChLA chain - chi	5.91e-01
25	77	50.0	363	6	S02537 class I histocompati	5.91e-01
26	77	50.0	364	6	D35997 MHC class I histocom	5.91e-01
27	77	50.0	365	13	I54493 HLA-A protein - huma	5.91e-01
28	77	50.0	365	13	I54416 HLA-AW24 protein - h	5.91e-01
29	73	47.4	274	2	HLHU32 MHC class I histocom	2.08e+00
30	73	47.4	364	6	A35997 MHC class I histocom	2.08e+00
31	70	45.5	362	6	A45850 MHC class I histocom	5.22e+00
32	70	45.5	362	6	S25415 class I histocompati	5.22e+00
33	70	45.5	362	13	I61861 MHC HLA-B*44.2 chain	5.22e+00
34	70	45.5	362	13	I54442 MHC HLA-B13 precursor	5.22e+00
35	70	45.5	3712	2	YGCEVC alpha-aminoadipyl-cy	5.22e+00
36	69	44.8	388	7	A49545 plasminogen-binding	7.06e+00
37	66	42.9	88	16	S60814 M protein precursor	1.72e+01
38	66	42.9	408	7	S30283 protein M precursor	1.72e+01
39	66	42.9	436	7	S30284 M protein precursor	1.72e+01
40	66	42.9	881	4	VCLJG3 env polyprotein - si	1.72e+01
41	65	42.2	763	11	S17998 gene COX1 intron 4 p	2.30e+01
42	65	42.2	798	7	A40526 integrin beta-7 chai	2.30e+01
43	65	42.2	806	7	A46271 integrin beta-7 chai	2.30e+01
44	65	42.2	869	8	A47665 env protein gp120(cl	2.30e+01
45	64	41.6	881	8	S03068 env protein - human	3.06e+01

ALIGNMENTS

RESULT 1  
ENTRY I38509 #type fragment  
TITLE MHC class I histocompatibility antigen - human (fragment)  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 06-Sep-1996  
ACCESSIONS I38509  
REFERENCE I38509  
#authors Cerobb, N.; Choi, J.W.; Riu, K.Z.; Yang, S.Y.  
#journal Tissue Antigens (1994) 44:271-273  
#title HLA-B\*5105: a newly identified B51 IEF variant.  
#cross-references MUID:95176331  
#accession I38509  
#status preliminary; translated from GB/EMBL/DBDJ  
#molecule\_type mRNA  
#residues 1-273 #label RES  
#cross-references EMBL:U06697; NID:g469544; CDS\_PID:g469545  
GENETICS  
#note gene name HLA-B  
SUMMARY #length 273 #checksum 6533

Query Match 50.0%; Score 77; DB 13; Length 273;  
Best Local Similarity 100.0%; Pred. No. 5.91e-01;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 74 renirialry 83  
|||||||  
Qy 11 RENLRALRY 20

RESULT 2  
ENTRY I54463 #type fragment  
TITLE MHC HLA-B\*38 chain - human (fragment)  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 07-Jun-1996  
ACCESSIONS I54463  
REFERENCE I54463  
#authors Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.;  
Weiss, E.; Schmidt, H.  
#journal Immunogenetics (1989) 30:200-207  
#title Genetic and serological heterogeneity of the supertypic HLA-B  
locus specificities Bw4 and Bw6.  
#cross-references MUID:89379286  
#accession I54463

```

##status      preliminary; translated from GB/EMBL/DBDJ
##molecule_type DNA
##residues    1-274 ##label RES
##cross-references GB:M29864; NID:g187674; CDS_PID:g187675
SUMMARY      #length 274 #checksum 1031

```

```

Query Match      50.0%; Score 77; DB 13; Length 274;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 75 renltrialy 84
|||||
QY 11 RENLRIALRY 20

```

```

RESULT 3
ENTRY class I histocompatibility antigen - pygmy chimpanzee
TITLE (fragment)
ORGANISM #formal_name Pan paniscus #common_name pygmy chimpanzee,
         bonobo
DATE 31-May-1996 #sequence_revision 31-May-1996 #text_change
ACCESSIONS I59308
REFERENCE #formal_name Pan paniscus #common_name pygmy chimpanzee,
#authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
         A.L.; Bontröpp, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession I59308
##status preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-354 ##label RES
##cross-references EMBL:U05575; NID:g454767; CDS_PID:g454768
SUMMARY #length 354 #checksum 3211

```

```

Query Match      50.0%; Score 77; DB 13; Length 354;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 91 renltrialy 100
|||||
QY 11 RENLRIALRY 20

```

```

RESULT 4
ENTRY class I histocompatibility antigen - chimpanzee (fragment)
TITLE #formal_name Pan troglodytes #common_name chimpanzee
ORGANISM #formal_name Pan troglodytes #common_name chimpanzee
DATE 24-May-1996 #sequence_revision 24-May-1996 #text_change
ACCESSIONS I80168
REFERENCE #formal_name Pan troglodytes #common_name chimpanzee,
#authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
         A.L.; Bontröpp, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession I80168
##status preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-354 ##label RES
##cross-references EMBL:U05579; NID:g454775; CDS_PID:g454776
SUMMARY #length 354 #checksum 5067

```

```

Query Match      50.0%; Score 77; DB 13; Length 354;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 91 renltrialy 100
|||||
QY 11 RENLRIALRY 20

```

```

RESULT 5
ENTRY class I histocompatibility antigen - pygmy chimpanzee
TITLE (fragment)
ORGANISM #formal_name Pan paniscus #common_name pygmy chimpanzee,
         bonobo
DATE 24-May-1996 #sequence_revision 24-May-1996 #text_change
ACCESSIONS I80167
REFERENCE #formal_name Pan paniscus #common_name pygmy chimpanzee,
#authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
         A.L.; Bontröpp, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession I80167
##status preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-354 ##label RES
##cross-references EMBL:U05578; NID:g454773; CDS_PID:g454774
SUMMARY #length 354 #checksum 3983

```

```

Query Match      50.0%; Score 77; DB 13; Length 354;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 91 renltrialy 100
|||||
QY 11 RENLRIALRY 20

```

```

RESULT 6
ENTRY class I histocompatibility antigen - chimpanzee (fragment)
TITLE #formal_name Pan troglodytes #common_name chimpanzee
ORGANISM #formal_name Pan troglodytes #common_name chimpanzee
DATE 24-May-1996 #sequence_revision 24-May-1996 #text_change
ACCESSIONS I80171
REFERENCE #formal_name Pan troglodytes #common_name chimpanzee,
#authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
         A.L.; Bontröpp, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession I80171
##status preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-355 ##label RES
##cross-references EMBL:U05582; NID:g454781; CDS_PID:g454782
SUMMARY #length 355 #checksum 6021

```

```

Query Match      50.0%; Score 77; DB 13; Length 355;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 91 renltrialy 100
|||||
QY 11 RENLRIALRY 20

```

```

RESULT 7
ENTRY class I histocompatibility antigen - chimpanzee (fragment)
TITLE #formal_name Pan troglodytes #common_name chimpanzee
ORGANISM #formal_name Pan troglodytes #common_name chimpanzee
DATE 24-May-1996 #sequence_revision 24-May-1996 #text_change
ACCESSIONS I80169
REFERENCE #formal_name Pan troglodytes #common_name chimpanzee,
#authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
         A.L.; Bontröpp, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
SUMMARY #length 355 #checksum 6021

```

```

#title      A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession  I80169
#status     preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues_type 1-355 ##label RES
#cross-references EMBL:U05580; NID:g454777; CDS_PID:g454778
SUMMARY     #length 355 #checksum 4603

Query Match      50.0%; Score 77; DB 13; Length 355;
Best Local Similarity 100.0%; Pred. No. 5,91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 renrtrialry 100
|||||
Qy 11 RENRTRIALRY 20

RESULT 8
ENTRY   HLH012      #type complete
TITLE   MHC class I histocompatibility antigen HLA alpha chain
ORGANISM #formal_name Homo sapiens #common_name man
DATE     05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change
15-Jun-1996
ACCESSIONS A02189
REFERENCE   A02189
#authors   Malissen, M.; Malissen, B.; Jordan, B.R.
#journal   Proc. Natl. Acad. Sci. U.S.A. (1982) 79:893-897
#title     Exon/intron organization and complete nucleotide sequence of
           an HLA gene.
#cross-references MUID:82151002
#accession  A02189
#molecule_type DNA
#residues_type 1-359 ##label MAL
COMMENT    The seven exons correspond approximately to the domain structure of
           this chain.
GENETICS   #map_position 6p21.3
#introns   22/1; 112/1; 204/1; 296/1; 335/1; 346/1
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
KEYWORDS    duplication; glycoprotein; heterodimer; transmembrane
           protein; transplantation antigen
FEATURE     1-21      #domain signal sequence #status predicted #label SIG\
22-359      #product class I histocompatibility antigen HLA alpha
           chain #status predicted #label MAT\
22-304      #domain extracellular #status predicted #label EX1\
22-111      #domain alpha-1 #label EX1\
112-203      #domain alpha-2 #label EX2\
217-282      #domain immunoglobulin homology #label IMM\
305-329      #domain transmembrane #status predicted #label TMM\
335-359      #domain intracellular #status predicted #label INN\
107          #binding_site carbohydrate (Asn) (covalent) #status
           predicted\
224-280      #disulfide_bonds #status predicted
SUMMARY     #length 359 #molecule-weight 40548 #checksum 2195

Query Match      50.0%; Score 77; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 5,91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 96 renrtrialry 105
|||||
Qy 11 RENRTRIALRY 20

RESULT 9
ENTRY   JH0539      #type complete
TITLE   class I histocompatibility antigen Gogo-B0101 heavy chain
           precursor - lowland gorilla
ORGANISM #formal_name Gorilla gorilla #common_name lowland

```

```

gorilla
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
26-Apr-1996
ACCESSIONS JH0539
REFERENCE   JH0534
#authors   Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
#journal   J. Exp. Med. (1991) 174:1491-1509
#title     Gorilla class I major histocompatibility complex alleles:
           comparison to human and chimpanzee class I.
#cross-references MUID:92078860
#accession  JH0539
#molecule_type DNA
#residues   1-362 ##label LAW
#cross-references EMBL:X60255
#experimental_source EBV-transformed B cell
GENETICS    25/1; 115/1; 207/1; 299/1; 338/1; 349/1
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
FEATURE     1-24      #domain signal sequence #label SIG\
25-362      #product class I histocompatibility antigen heavy chain,
           Gogo-B0101 #status predicted #label CLA\
25-114      #domain alpha-1 #label AL1\
115-206      #domain alpha-2 #label AL2\
207-298      #domain alpha-3 #label AL3\
220-285      #domain immunoglobulin homology #label IMM\
299-362      #domain intracellular #label INT
SUMMARY     #length 362 #molecule-weight 40170 #checksum 7327

Query Match      50.0%; Score 77; DB 6; Length 362;
Best Local Similarity 100.0%; Pred. No. 5,91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renrtrialry 108
|||||
Qy 11 RENRTRIALRY 20

RESULT 10
ENTRY   B30345      #type complete
TITLE   MHC class I histocompatibility antigen HLA-Bw52 precursor -
           human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change
26-Apr-1996
ACCESSIONS B30345
REFERENCE   A30345
#authors   Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham,
           P.; Kano, K.; Takiguchi, M.
#journal   J. Immunol. (1989) 142:306-311
#title     HLA-B*51 and HLA-B*52 differ by only two amino acids which are
           in the helical region of the alpha-1 domain.
#cross-references MUID:89080265
#accession  B30345
#status     preliminary
#molecule_type DNA
#residues   1-362 ##label HAY
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
FEATURE     220-285      #domain immunoglobulin homology #label IMM
SUMMARY     #length 362 #molecule-weight 40521 #checksum 9891

Query Match      50.0%; Score 77; DB 6; Length 362;
Best Local Similarity 100.0%; Pred. No. 5,91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renrtrialry 108
|||||
Qy 11 RENRTRIALRY 20

```

```

RESULT 11
ENTRY   I84486      #type complete
TITLE   transmembrane glycoprotein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE    02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS I84486
REFERENCE  I38421
#authors  Hildebrand, W.H.; Domana, J.D.; Shen, S.Y.; Lau, M.;
          Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
          Bias, W.B.; Parham, P.
#journal  Tissue Antigens (1994) 43:209-218
#title    HLA-B*15: a widespread and diverse family of HLA-B alleles.
#cross-references MUID:94367483
#accession I84486
#status   preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-362 #label RES
#cross-references GB:L15005; NID:g493154; CDS_PID:g493155
GENETICS
#note     gene name HLA-B*1513
#length 362 #molecular-weight 40378 #checksum 9463
SUMMARY
Query Match 50.0%; Score 77; DB 13; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renltrialy 108
    |||||
QY 11 RENLRIALRY 20

RESULT 12
ENTRY   JH0540      #type complete
TITLE   class I histocompatibility antigen Gogo-B0102 heavy chain
ORGANISM #formal_name Gorilla gorilla #common_name lowland
          gorilla
DATE    30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
ACCESSIONS JH0540
REFERENCE  JH0534
#authors  Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
#journal  J. Exp. Med. (1991) 174:1491-1509
#title    Gorilla class I major histocompatibility complex alleles:
          comparison to human and chimpanzee class I.
#cross-references MUID:92078860
#accession JH0540
#molecule_type DNA
#residues 1-362 #label LAW
#cross-references EMBL:X60693
#experimental_source EBV-transformed B cell
GENETICS
#introns  25/1; 115/1; 207/1; 299/1; 338/1; 349/1
CLASSIFICATION #superfamily class I histocompatibility antigen;
               immunoglobulin homology
FEATURE
1-24      #domain signal sequence #label SIG\
25-362    #product class I histocompatibility antigen heavy chain,
          Gogo-B0102 #status predicted #label CLA\
25-114    #domain alpha-1 #label AL1\
115-206   #domain alpha-2 #label AL2\
207-298   #domain alpha-3 #label AL3\
220-288   #domain immunoglobulin homology #label IMM\
299-362   #domain intracellular #label INT
SUMMARY   #length 362 #molecular-weight 40204 #checksum 7312

Query Match 50.0%; Score 77; DB 6; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renltrialy 108
    |||||
QY 11 RENLRIALRY 108

RESULT 13
ENTRY   S24434      #type complete
TITLE   class I histocompatibility antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE    22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
ACCESSIONS S24434
REFERENCE  S24027
#authors  Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford,
          E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.;
          Ghm, S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L.
#journal  Nature (1992) 357:329-333
#title    New recombinant HLA-B alleles in a tribe of South American
          Amerindians indicate rapid evolution of MHC class I loci.
#cross-references MUID:92269956
#accession S24434
#status   preliminary
#molecule_type mRNA
#residues 1-362 #label WAT
CLASSIFICATION #superfamily immunoglobulin homology
FEATURE
220-285   #domain immunoglobulin homology #label IMM
SUMMARY   #length 362 #molecular-weight 40462 #checksum 9855

Query Match 50.0%; Score 77; DB 6; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renltrialy 108
    |||||
QY 11 RENLRIALRY 20

RESULT 14
ENTRY   A30345      #type complete
TITLE   MHC class I histocompatibility antigen HLA-B51 precursor -
          human
ORGANISM #formal_name Homo sapiens #common_name man
DATE    29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change
ACCESSIONS A30345; I68746
REFERENCE  A30345
#authors  Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham,
          P.; Kano, K.; Takiguchi, M.
#journal  J. Immunol. (1989) 142:306-311
#title    HLA-B51 and HLA-B*52 differ by only two amino acids which are
          in the helical region of the alpha-1 domain.
#cross-references MUID:89080265
#accession A30345
#status   preliminary
#molecule_type mRNA
#residues 1-362 #label HAY
REFERENCE  I5457
#authors  Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss,
          E.H.
#journal  Immunogenetics (1989) 29:297-307
#title    Allelic variation in HLA-B and HLA-C sequences and the
          evolution of the HLA-B alleles.
#cross-references MUID:89233295
#accession I68746
#status   preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-362 #label RES
#cross-references GB:L41087; NID:g735900; CDS_PID:g735902
GENETICS
#gene     GDB:HLA-B
#cross-references GDB:I20048
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
               immunoglobulin homology

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FEATURE
220-285      #domain immunoglobulin homology #label IMM
SUMMARY      #length 362 #molecular-weight 40566 #checksum 9719

Query Match      50.0%; Score 77; DB 6; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renlrialy 108
|||||
QY 11 RENLRIALRY 20

RESULT 15
ENTRY      I37521      #type complete
TITLE      HLA-B*57.2 antigen - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
          02-Jul-1996
ACCESSIONS I37521
REFERENCE   I37476
#authors   Madrigal, J.A.; Belich, M.P.; Hildebrand, W.H.; Benjamin,
          R.J.; Little, A.M.; Zemmour, J.; Ennis, P.D.; Ward, F.E.;
          Petzl-Erler, M.L.; Du Toit, E.D.; Parham, P.
#journal   J. Immunol. (1992) 149:3411-3415
#title     Distinctive HLA-A,B antigens of black populations formed by
          interallelic conversion.
#cross-references MUID:93056508
#accession I37521
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-362 #label RES
#cross-references EMBL:X61707; NID:g32186; CDS_PID:g32187
SUMMARY    #length 362 #molecular-weight 40342 #checksum 7369

Query Match      50.0%; Score 77; DB 13; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.91e-01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 renlrialy 108
|||||
QY 11 RENLRIALRY 20

Search completed: Thu May 22 08:33:25 1997
Job time : 16 secs.

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W P S R L H (TM)  
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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu May 22 08:33:42 1997; MasPar time 2.21 Seconds  
98.639 Million cell updates/sec  
Tabular output not generated.  
Title: >US-08-653-294-26  
Description: (1-20) from US08653294.pep  
Perfect Score: 154  
Sequence: 1 YRLAIRLNRERLRLRY 20

Scoring table: PAM 150  
Gap 15  
Searched: 92623 seqs, 10896596 residues  
Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Database: a-geneseq26  
1:part1 2:part3 3:part4 4:part5 5:part6 6:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19

Statistics: Mean 21.097; Variance 80.944; scale 0.261  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Match %	Length	Pred. No.
1	154	100.0	20 18	R95428
2	154	100.0	20 16	R92907
3	147	95.5	20 16	R92909
4	147	95.5	20 16	R92908
5	140	90.9	20 16	R92910
6	131	85.1	20 18	R95430
7	83	53.9	20 16	R92911
8	77	50.0	10 16	R83062
9	77	50.0	10 18	R95413
10	77	50.0	10 8	R41208
11	77	50.0	15 16	R92912
12	77	50.0	25 18	R95422
13	77	50.0	25 18	R95416
14	77	50.0	25 8	R41205
15	77	50.0	25 16	R83093
16	77	50.0	25 8	R48286
17	77	50.0	25 16	R83090
18	77	50.0	362 2	R03142
19	77	50.0	362 2	R03144
20	77	50.0	362 3	R12463

21	75	48.7	10 16	R83094	HLA-B2702 CTL modul	4.72e+00
22	75	48.7	10 18	R95425	HLA-B2702.75-84 (D)	4.72e+00
23	70	45.5	10 18	R95426	HLA-B2702.75-84 (T)	1.30e+01
24	70	45.5	10 16	R83096	HLA-B2702 CTL modul	1.30e+01
25	70	45.5	10 16	R83095	HLA-B2702 CTL modul	1.30e+01
26	70	45.5	20 18	R95415	HLA-B7.84-75-84 Palin	1.30e+01
27	70	45.5	20 16	R92913	HLA-B7 CTL modul	1.30e+01
28	70	45.5	3639 8	R40227	ACVS	1.30e+01
29	70	45.5	3712 3	R13896	ACV synthetase	1.30e+01
30	65	42.2	879 4	R24126	SVYmac239 env gene pr	3.49e+01
31	64	41.6	97 4	R21601	Putative transposito	4.25e+01
32	64	41.6	116 7	R38670	268-D	4.25e+01
33	63	40.9	485 4	R20796	EHV-4 9C	5.16e+01
34	63	40.9	705 10	R66598	Human L5/3 tumour sup	5.16e+01
35	63	40.9	705 10	R66597	Human L5/3 tumour sup	5.16e+01
36	63	40.9	711 10	R66602	Human L5/3 tumour sup	5.16e+01
37	63	40.9	713 10	R66603	Encoded by full-lengt	5.16e+01
38	63	40.9	15281 9	R44929	T. niveum Cyclosporin	5.16e+01
39	61	39.6	10 8	R41212	Peptide fragment of C	7.60e+01
40	61	39.6	10 18	R95423	HLA-B2705.75-84	7.60e+01
41	61	39.6	10 16	R83075	HLA-B2702 CTL modul	7.60e+01
42	61	39.6	25 18	R95417	HLA-B2705.60-84	7.60e+01
43	61	39.6	25 16	R83091	HLA-B2702 CTL modul	7.60e+01
44	61	39.6	362 2	P70155	Sequence encoded by g	7.60e+01
45	61	39.6	630 3	R12230	TrpE/androgen recept	7.60e+01

ALIGNMENTS

RESULT 1  
ID R95428 standard; peptide; 20 AA.  
AC R95428;  
DT 12-NOV-1996 (first entry)  
DE HLA-B2702 84-75-84 palindrome.  
KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;  
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
KW Cytolysis; antigen presenting cell.  
OS Synthetic.  
PN W09513288-A1.  
PD 18-MAY-1995.  
PF 10-NOV-1994; U12985.  
PR 10-NOV-1993; US-150493.  
PA (STRD) UNIV LELAND STANFORD JUNIOR.  
PI Clayberger C. Krensky AM;  
DR WPI; 95-194027/35.  
PT Compsns. comprising lymphoid surface membrane proteins - which may  
PT inhibit cytolytic activity and differentiation of CTLs.  
PS Example; Page 12; 29pp; English.  
CC R95413, and R95415-R95431 represent palindromes and fragments of  
CC human-leucocyte-associated antigens. These sequences can be used to isolate  
CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
CC protein associated with T-cell activation in mammalian T-cells, and is  
CC also immunologically cross reactive with the heat shock protein Hsc70.  
CC p74 is found in a limited number of cell types, but is particularly  
CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
CC cell with an amphoteric detergent, and then passed through an affinity  
CC column containing a covalently bound HLA-B2702 palindromic peptide.  
CC Compositions comprising the extracellular fragment of p74 combined with  
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxic. Candidate  
CC compounds can be screened for their effect on the cytotoxic activity of  
CC T-cells, by combining them with the extracellular portion of p74 and  
CC determining the amount of binding between the candidate compound and p74.  
CC Modulation of CTL activity can be inhibited in a cellular composition  
CC containing T-cells and antigen presenting cells (APCs), by adding to the  
CC mix the extracellular portion of p74, in an amount sufficient to compete  
CC with p74 for the binding of the p74 ligand.  
SQ Sequence 20 AA;

Query Match 100.0%; Score 154; DB 18; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.21e-07;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 YRLAIRLNRERENLRALRY 20  
 ||||| ||||| ||||| ||||| |||||

QY 1 YRLAIRLNRERENLRALRY 20

# RESULT 2

ID R92907 standard; peptide; 20 AA.

AC R92907;

DT 16-MAY-1996 (first entry)

DE HLA-B\*2702 CTL modulating peptide (B2702.84-75/75-84).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW Immunosuppressant; graft versus host disorder; transplantation; therapy;

KW Class I MHC; HLA-B\*2702.

OS Synthetic.

PN WO9526979-A1.

PD 12-OCT-1995.

PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM, Parham P;

DR WPI; 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient

PT host

PS Example 15; Page 36; 80pp; English.

CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of

CC class I major histocompatibility complex (MHC) antigens. This sequence

CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class

CC I MHC HLA-B\*2702. These sequences can be used to extend the period of

CC acceptance by a recipient of a transplant from an MHC unmatched donor.

CC The peptides are administered to a patient in conjunction with a

CC subtherapeutic amount of an immunosuppressant. This is administered to

CC the patient for a limited period of time (compared to the lifetime

CC administration for current treatments). The peptides particularly

CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)

CC of the patient.

CC Sequence 20 AA;

# Query Match

Best Local Similarity 100.0%; Score 154; DB 16; Length 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 YRLAIRLNRERENLRALRY 20

||||| ||||| ||||| ||||| |||||

QY 1 YRLAIRLNRERENLRALRY 20

# RESULT 3

ID R92909 standard; peptide; 20 AA.

AC R92909;

DT 16-MAY-1996 (first entry)

DE HLA-B\*2702 CTL modulating peptide (B2702.84-75/75-84(T)).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW Immunosuppressant; graft versus host disorder; transplantation; therapy;

KW Class I MHC; HLA-B\*2702.

OS Synthetic.

PN WO9526979-A1.

PD 12-OCT-1995.

PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM, Parham P;

DR WPI; 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient

PT host

PS Example 15; Page 36; 80pp; English.

CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of

CC class I major histocompatibility complex (MHC) antigens. This sequence

CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class

CC I MHC HLA-B\*2702. These sequences can be used to extend the period of

CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 CC Sequence 20 AA;

# Query Match

Best Local Similarity 95.5%; Score 147; DB 16; Length 20;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 YRLAIRLNRERENLRALRY 20

||||| ||||| ||||| ||||| |||||

QY 1 YRLAIRLNRERENLRALRY 20

# RESULT 4

ID R92908 standard; peptide; 20 AA.

AC R92908;

DT 16-MAY-1996 (first entry)

DE HLA-B\*2702 CTL modulating peptide (B2702.84-75(T)/75-84).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW Immunosuppressant; graft versus host disorder; transplantation; therapy;

KW Class I MHC; HLA-B\*2702.

OS Synthetic.

PN WO9526979-A1.

PD 12-OCT-1995.

PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM, Parham P;

DR WPI; 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient

PT host

PS Example 15; Page 36; 80pp; English.

CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of

CC class I major histocompatibility complex (MHC) antigens. This sequence

CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class

CC I MHC HLA-B\*2702. These sequences can be used to extend the period of

CC acceptance by a recipient of a transplant from an MHC unmatched donor.

CC The peptides are administered to a patient in conjunction with a

CC subtherapeutic amount of an immunosuppressant. This is administered to

CC the patient for a limited period of time (compared to the lifetime

CC administration for current treatments). The peptides particularly

CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)

CC of the patient.

CC Sequence 20 AA;

# Query Match

Best Local Similarity 95.0%; Score 147; DB 16; Length 20;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 YRLAIRLNRERENLRALRY 20

||||| ||||| ||||| ||||| |||||

QY 1 YRLAIRLNRERENLRALRY 20

# RESULT 5

ID R92910 standard; peptide; 20 AA.

AC R92910;

DT 16-MAY-1996 (first entry)

DE HLA-B\*2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW Immunosuppressant; graft versus host disorder; transplantation; therapy;

KW Class I MHC; HLA-B\*2702.

OS Synthetic.

PN WO9526979-A1.

PD 12-OCT-1995.

PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.

(STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 CC I MHC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 CC Sequence 20 AA;  
 SQ

Query Match 90.9%; Score 140; DB 16; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 3.05e-06;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 yrlairlnrerlnrlalr 20  
 QY 1 YRLAIRLNRERENRLIALR 20

RESULT 6  
 ID R95430 standard; peptide; 20 AA.  
 AC R95430;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B2702 84-75/75-84 palindromic.  
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN WO9513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI; 95-194027/25.  
 PT Compsns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 12; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B2702 84-75/75-84 palindromic.  
 CC Isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface  
 CC membrane protein associated with T-cell activation in mammalian T-cells,  
 CC and is also immunologically cross reactive with the heat shock protein  
 CC Hsc70. p74 is found in a limited number of cell types, but is  
 CC particularly expressed on B and T cells. p74 can be isolated by lysis of  
 CC a suitable cell with an amphoteric detergent, and then passed through an  
 CC affinity column containing a covalently bound HLA-B2702 palindromic  
 CC peptide. Compositions comprising the extracellular fragment of p74  
 CC combined with HLA-B2702 60-84 (see R95416), induces calcium influx, and  
 CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis.  
 CC Candidate compounds can be screened for their effect on the cytolytic  
 CC activity of T-cells, by combining them with the extracellular portion of  
 CC p74 and determining the amount of binding between the candidate compound  
 CC and p74. Modulation of CTL activity can be inhibited in a cellular  
 CC composition containing T-cells and antigen presenting cells (APCs), by  
 CC adding to the mix the extracellular portion of p74, in an amount  
 CC sufficient to compete with p74 for the binding of the p74 ligand.  
 CC Sequence 20 AA;  
 SQ

Query Match 85.1%; Score 131; DB 18; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 2.39e-05;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 yrlairlnrerlnrlalr 19  
 QY 1 YRLAIRLNRERENRLIALR 19

RESULT 7  
 ID R92911 standard; peptide; 20 AA.  
 AC R92911;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN WO9526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC  
 CC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 CC Sequence 20 AA;  
 SQ

Query Match 53.9%; Score 83; DB 16; Length 20;  
 Best Local Similarity 65.0%; Pred. No. 9.02e-01;  
 Matches 13; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Db 1 yrlairlnrerlnrlalr 20  
 QY 1 YRLAIRLNRERENRLIALR 19

RESULT 8  
 ID R83062 standard; peptide; 10 AA.  
 AC R83062;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.75-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN WO9526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Claim 15; Page 9; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC  
 CC HLA-B2702. These sequences can be used to extend the period of

CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 10 AA;

Query Match 50.0%; Score 77; DB 16; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 renltrialry 10  
 QY 11 RENLRIALRY 20

## RESULT 9

ID R95413 standard; peptide; 10 AA.  
 AC R95413; 12-NOV-1996 (first entry)  
 DE Alpha-helix of HLA-B2702.  
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW Cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN WO9513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI; 95-194027/25.

PT Compens. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 11; 29pp; English.  
 CC This sequence represents the alpha-helix of the  
 CC human-leucocyte-associated antigen B2702 (HLA-B2702). This sequence,  
 CC epitopes, and palindromes of it (such as R95428) can be used to isolate  
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
 CC protein associated with T-cell activation in mammalian T-cells, and is  
 CC also immunologically cross reactive with the heat shock protein Hsc70.  
 CC p74 is found in a limited number of cell types, but is particularly  
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
 CC cell with an amphoteric detergent, and then passed through an affinity  
 CC column containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B2702-60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 10 AA;

Query Match 50.0%; Score 77; DB 18; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 renltrialry 10  
 QY 11 RENLRIALRY 20

## RESULT 10

ID R41208 standard; peptide; 10 AA.  
 AC R41208;  
 DT 15-MAR-1994 (first entry)

DE Peptide fragment of Class I HLA peptide.  
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;  
 KW Parasitic disease; cytotoxic T lymphocyte; modulation.  
 OS Synthetic.  
 PN WO9317699-A.  
 PD 16-SEP-1993.  
 PF 25-FEB-1993; U01758.  
 PR 02-MAR-1992; US-844716.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger CA, Krensky AM;  
 DR WPI; 93-303134/38.  
 PT New peptide(s) based on Class I HLA antigen domains - used for  
 PT modulating cytotoxic T-lymphocyte activity towards targets  
 PS Claim 11; Page 54; 61pp; English.  
 CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)  
 CC activity, either by inhibition or stimulation. It can be used  
 CC for inhibiting CTL toxicity in transplantations, for inducing CTL  
 CC activity in parasitic diseases and neoplasia and in studies on viral  
 CC infection. The peptide can also be used for identifying CTLs which  
 CC bind to it and removing subsets of CTLs from a T-cell composition.  
 CC This peptide sequence is more commonly found within larger peptide  
 CC compounds of not more than 30 amino acids in length.  
 SQ Sequence 10 AA;

Query Match 50.0%; Score 77; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 renltrialry 10  
 QY 11 RENLRIALRY 20

## RESULT 11

ID R92912 standard; peptide; 15 AA.  
 AC R92912;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.70-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW Immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.

OS Synthetic.  
 PN WO9526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC corresponds to residues 70-84 of the alpha-1 domain of the class I MHC  
 CC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 15 AA;

Query Match 50.0%; Score 77; DB 16; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 renltrialry 15  
 QY 11 RENLRIALRY 20

CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents  
 CC HLA-B2702.60-84. These sequences can be used to isolate the protein p74  
 CC from a T-cell lysate. p74 is a T-cell surface membrane protein  
 CC associated with T-cell activation in mammalian T-cells, and is also  
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is  
 CC found in a limited number of cell types, but is particularly expressed on  
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an  
 CC amphoteric detergent, and then passed through an affinity column  
 CC containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC this sequence, induces calcium influx, and inhibits cytotoxic T  
 CC lymphocyte (CTL) differentiation or cytotoxicity. Candidate compounds can  
 CC be screened for their effect on the cytolytic activity of T-cells, by  
 CC combining them with the extracellular portion of p74 and determining the  
 CC amount of binding between the candidate compound and p74. Modulation of  
 CC CTL activity can be inhibited in a cellular composition containing  
 CC T-cells and antigen presenting cells (APCs), by adding to the mix the  
 CC extracellular portion of p74, in an amount sufficient to compete with p74  
 CC for the binding of the p74 ligand.  
 SQ Sequence 25 AA;

Query Match 50.0%; Score 77; DB 18; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 renltrialy 25  
 |||||  
 QY 11 RENLRIALRY 20

## RESULT 14

ID R41205 standard; peptide; 25 AA.  
 AC R41205;  
 DT 15-MAR-1994 (first entry)  
 DE Peptide fragment of Class I HLA peptide.  
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;  
 KW Parasitic disease; cytotoxic T lymphocyte; modulation.  
 OS Synthetic.  
 PN W09317699-A.  
 PD 16-SEP-1993.  
 PF 25-FEB-1993; U01758.  
 PR 02-MAR-1992; US-844716.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI; 93-303134/38.  
 PT New peptide(s) based on Class I HLA antigen domains - used for  
 PT modulating cytotoxic T-lymphocyte activity towards targets  
 PS Claim 8; Page 53; 61pp; English.  
 CC The peptide (or a fragment of at least 10 amino acids, joined at at  
 CC least one terminus to a sequence other than that of wild type HLA  
 CC antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity,  
 CC either by inhibition or stimulation. It can be used for  
 CC inhibiting CTL toxicity in transplantations, for inducing CTL  
 CC activity in parasitic diseases and neoplasia and in studies on viral  
 CC infection. The peptide can also be used for identifying CTLs which  
 CC bind to it and removing subsets of CTLs from a T-cell composition.  
 SQ Sequence 25 AA;

Query Match 50.0%; Score 77; DB 8; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 renltrialy 25  
 |||||  
 QY 11 RENLRIALRY 20

## RESULT 15

ID R83093 standard; peptide; 25 AA.  
 AC R83093;  
 DT 16-MAY-1996 (first entry)  
 DE HLAB38 CTL modulating peptide (B38.6084).

CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC a T-cell lysate. p74 is a T-cell surface membrane protein associated  
 CC with T-cell activation in mammalian T-cells, and is also immunologically  
 CC cross reactive with the heat shock protein Hsc70. p74 is found in a  
 CC limited number of cell types, but is particularly expressed on B and T  
 CC cells. p74 can be isolated by lysis of a suitable cell with an  
 CC amphoteric detergent, and then passed through an affinity column  
 CC containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 25 AA;

Query Match 50.0%; Score 77; DB 18; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 renltrialy 25  
 |||||  
 QY 11 RENLRIALRY 20

## RESULT 13

ID R95416 standard; peptide; 25 AA.  
 AC R95416;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B2702.60-84.  
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN W09513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI; 95-194027/25.  
 PT Compns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 9; 29pp; English.

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLAB38.  
 OS Synthetic.  
 PN WO9526979-A1.  
 PD 12-OCT-1995.  
 PR 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 13: Page 32: 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC  
 CC HLAB38. These sequences can be used to extend the period of acceptance  
 CC by a recipient of a transplant from an MHC unmatched donor. The peptides  
 CC are administered to a patient in conjunction with a subtherapeutic amount  
 CC of an immunosuppressant. This is administered to the patient for a  
 CC limited period of time (compared to the lifetime administration for  
 CC current treatments). The peptides particularly modulate (or inhibit) the  
 CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.  
 SQ Sequence 25 AA:

Query Match 50.0%; Score 77; DB 16; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 renlralry 25  
 Qy 11 RENLRLALRY 20  
 |||||

Search completed: Thu May 22 08:33:50 1997  
 Job time : 8 secs.

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WISHLH (TM)

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:35:52 1997; MasPar time 2.11 Seconds

Tabular output not generated. 120.401 Million cell updates/sec

Title: >US-08-653-294-36  
Description: (1-12) from US08653294.pep  
Perfect Score: 98  
Sequence: 1 YRLAIRRLRY 12

Scoring table: PAM 150  
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot34  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 28.088; Variance 37.415; scale 0.751

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	63	64.3	375	HRMA_PSESY	HRMA PROTEIN.	4.00e-01
2	57	58.2	281	STRF_STRGR	STREPTOMYCIN BIOSYNTH	5.20e+00
3	57	58.2	348	HLAF_MACMU	HLA CLASS I HISTOCOMP	5.20e+00
4	57	58.2	477	BGL2_BACSU	PROBABLE BETA-GLUCOSI	5.20e+00
5	56	57.1	495	ACH3_BOVIN	NEURONAL ACETYLCHOLIN	7.83e+00
6	56	57.1	496	ACH3_CHICK	NEURONAL ACETYLCHOLIN	7.83e+00
7	56	57.1	499	ACH3_RAT	NEURONAL ACETYLCHOLIN	7.83e+00
8	56	57.1	502	ACH3_HUMAN	NEURONAL ACETYLCHOLIN	7.83e+00
9	56	57.1	1151	GRR1_YEAST	GRR1 PROTEIN.	7.83e+00
10	55	56.1	212	YCD4_YEAST	HYPOTHETICAL 23.6 KD	1.17e+01
11	55	56.1	491	ACHE_BOVIN	ACETYLCHOLINE RECEPTO	1.17e+01
12	55	56.1	493	ACHE_HUMAN	ACETYLCHOLINE RECEPTO	1.17e+01
13	55	56.1	583	RUB2_BRANA	RUBISCO SUBUNIT BINDI	1.17e+01
14	55	56.1	844	DN44_HUMAN	DNA LIGASE IV (EC 6.5	1.17e+01
15	55	56.1	1420	AP04_MACMU	APOLIPROTEIN(A) (EC	1.17e+01
16	54	55.1	298	RT03_ACACA	MITOCHONDRIAL RIBOSOM	1.74e+01
17	54	55.1	493	ACHE_MOUSE	ACETYLCHOLINE RECEPTO	1.74e+01
18	54	55.1	494	ACHE_RAT	ACETYLCHOLINE RECEPTO	1.74e+01
19	54	55.1	500	ACH4_DROME	ACETYLCHOLINE RECEPTO	1.74e+01
20	54	55.1	651	YHK_ECOLI	HYPOTHETICAL 73.1 KD	1.74e+01
21	54	55.1	699	PTGA_BACSU	PTS SYSTEM, GLUCOSE-S	1.74e+01
22	54	55.1	850	RN12_YEAST	RN12 PROTEIN.	1.74e+01

23	54	55.1	880	8	8PAl_SULAC	DNA-DIRECTED RNA POLY	1.74e+01
24	54	55.1	1748	7	POLR_ELV	RNA REPLICASE POLYPRO	1.74e+01
25	53	54.1	334	1	BI0B_BREFL	BIOTIN SYNTHETASE (EC	2.58e+01
26	53	54.1	347	10	VAL1_SLCV	ALL PROTEIN.	2.58e+01
27	53	54.1	454	1	ACH5_CHICK	NEURONAL ACETYLCHOLIN	2.58e+01
28	53	54.1	508	7	PGKD_TRYBB	PHOSPHOGLYCERATE KINA	2.58e+01
29	53	54.1	547	6	MERA_STAAD	MERCURIC REDUCTASE (E	2.58e+01
30	53	54.1	622	1	ACH4_CHICK	NEURONAL ACETYLCHOLIN	2.58e+01
31	53	54.1	852	2	CLPB_CORGL	CLPB PROTEIN.	2.58e+01
32	53	54.1	959	6	MSH1_YEAST	MUTS PROTEIN HOMOLOG	2.58e+01
33	53	54.1	1281	6	MDR3_CRIGR	MULTIDRUG RESISTANCE	2.58e+01
34	53	54.1	1858	10	VGNB_CPSMV	GENOME POLYPROTEIN B	2.58e+01
35	53	54.1	3391	7	POLG_DEN27	GENOME POLYPROTEIN (C	2.58e+01
36	53	54.1	3391	7	POLG_DEN26	GENOME POLYPROTEIN (C	2.58e+01
37	52	53.1	122	8	RL17_CHLTR	50S RIBOSOMAL PROTEIN	3.79e+01
38	52	53.1	161	11	YD95_YEAST	HYPOTHETICAL 18.9 KD	3.79e+01
39	52	53.1	362	1	1B49_HUMAN	HLA CLASS I HISTOCOMP	3.79e+01
40	52	53.1	362	1	1B62_HUMAN	HLA CLASS I HISTOCOMP	3.79e+01
41	52	53.1	362	1	1B52_HUMAN	HLA CLASS I HISTOCOMP	3.79e+01
42	52	53.1	473	1	BGLB_MICBI	THERMOSTABLE BETA-GLU	3.79e+01
43	52	53.1	609	7	PRXC_CURIN	VANADIUM CHLOROPEROXI	3.79e+01
44	52	53.1	682	7	PRC_ECOLI	TAIL-SPECIFIC PROTEAS	3.79e+01
45	52	53.1	948	7	PMA3_ARATH	PLASMA MEMBRANE ATPAS	3.79e+01

ALIGNMENTS

RESULT 1  
ID HRMA\_PSESY STANDARD; PRT; 375 AA.  
AC Q08370;  
DT 01-NOV-1995 (REL. 32, CREATED)  
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
DE HRMA PROTEIN.  
GN HRMA.  
OC PSEUDOMONAS SYRINGAE (PV. SYRINGAE).  
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;  
OC PSEUDOMONADACEAE.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PSS61;  
RA HUANG H.C., HUTCHESON S.W., COLLIER A.;  
RL MOL. PLANT MICROBE INTERACT. 4:469-476(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PSS61;  
RX MEDLINE; 94100578.  
RA HEU S., HUTCHESON S.W.;  
RL MOL. PLANT MICROBE INTERACT. 6:553-564(1993).  
CC -!- FUNCTION: UNKNOWN. MAY SERVE A REGULATORY FUNCTION.  
KW HYPERSENSITIVE RESPONSE.  
SQ SEQUENCE 375 AA; 41458 MW; 733EB06 CRC32;

Query Match 64.3%; Score 63; DB 5; Length 375;  
Best Local Similarity 58.3%; Pred. No. 4.00e-01;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 174 yrlestrktlsy 185  
Oy 1 YRLAIRRLRY 12

RESULT 2  
ID STRF\_STRGR STANDARD; PRT; 281 AA.  
AC P09397;  
DT 01-MAR-1989 (REL. 10, CREATED)  
DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)  
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)  
DE STREPTOMYCIN BIOSYNTHESIS PROTEIN STRF.  
GN STRF.  
OS STREPTOMYCES GRISEUS.  
OC PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=N2-3-11;  
 RX MEDLINE; 91375432.  
 RA MANSOURI K., PIEPERSBERG W.;  
 RL MOL. GEN. GENET. 228:459-469(1991).  
 CC -!- FUNCTION: MAY BE INVOLVED IN THE FORMATION OF N-METHYL-L-  
 CC GLUCOSAMINE.  
 CC -!- PATHWAY: STREPTOMYCIN BIOSYNTHESIS.  
 CC -!- SIMILARITY: LOW, TO THE AMINO-TERMINAL DOMAIN OF GLUCOSE-6-  
 CC PHOSPHATE ISOMERASE.  
 DR EMBL; Y00459; E11412; ALT\_INIT.  
 DR PIR; S17776; S17776.  
 KW STREPTOMYCIN BIOSYNTHESIS.  
 SQ SEQUENCE 281 AA; 31726 MW; 75CEB24C CRC32;  
 Db 234 rlaarllamr 243  
 QY 2 RLAIIRLALR 11  
 Query Match 58.2%; Score 57; DB 9; Length 281;  
 Best Local Similarity 70.0%; Pred. No. 5.20e+00;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 RESULT 3  
 ID HLA\_F MACNU STANDARD; PRT; 348 AA.  
 AC P33617;  
 DT 01-FEB-1994 (REL. 28, CREATED)  
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, F ALPHA CHAIN PRECURSOR (HLA F  
 DE ANTIGEN) (LEUKOCYTE ANTIGEN F).  
 GN HLA\_F.  
 OS MACACA MULATTA (RHESUS MACAQUE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 93246295.  
 RA OTTING N., BONTROP R.E.;  
 RL IMMUNOGENETICS 38:141-145(1993).  
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 DR EMBL; Z21819; G38569; -.  
 DR PIR; S29990; S29990.  
 DR HSSP; P03989; 1HSA.  
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 21  
 FT CHAIN 22 348  
 FT DOMAIN 22 113  
 FT DOMAIN 114 205  
 FT DOMAIN 206 297  
 FT DOMAIN 298 307  
 FT TRANSMEM 308 331  
 FT DOMAIN 332 348  
 FT DISULFID 124 187  
 FT DISULFID 226 282  
 FT CARBOHYD 109 109  
 SQ SEQUENCE 348 AA; 39300 MW; 3A375142 CRC32;

Query Match 58.2%; Score 57; DB 5; Length 348;  
 Best Local Similarity 54.5%; Pred. No. 5.20e+00;  
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 Db 98 rvaalrllly 108  
 QY 2 RLAIIRLALR 12

RESULT 4  
 ID BGL2\_BACSU STANDARD; PRT; 477 AA.  
 AC P42403;  
 DT 01-NOV-1995 (REL. 32, CREATED)  
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
 DE PROBABLE BETA-GLUCOSIDASE (EC 3.2.1.21) (GENTIOBIASE) (CELLOBIASE)  
 DE (BETA-D-GLUCOSIDE GLUCOHYDROLASE) (AMYGALASE).  
 GN YCKE.  
 OS BACILLUS SUBTILIS.  
 OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE; 95219080.  
 RA FUJISHIMA Y., YAMANE K.;  
 RL MICROBIOLOGY 141:277-279(1995).  
 RN [2]  
 RP SEQUENCE OF 461-477 FROM N.A.  
 RX MEDLINE; 88298684.  
 RA VOSMAN B., KUIKEN G., KOOISTRA J., VENEMA G.;  
 RL J. BACTERIOL. 170:3703-3710(1988).  
 CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-  
 CC GLUCOSE RESIDUES WITH RELEASE OF BETA-D-GLUCOSE.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF GLYCOSYL HYDROLASES.  
 DR EMBL; D30762; G710632; -.  
 DR EMBL; M21672; -; NOT\_ANNOTATED\_CDS.  
 DR SUBTILIST; BG1181; YCKE.  
 DR PROSITE; PS00572; GLYCOSYL\_HYDROL\_F1.1.  
 DR PROSITE; PS00653; GLYCOSYL\_HYDROL\_F1.2.  
 KW HYPOTHETICAL PROTEIN: HYDROLASE; GLYCOSIDASE; CELLULOSE DEGRADATION.  
 FT ACT\_SITE 170 170  
 FT ACT\_SITE 378 378  
 FT ACT\_SITE 378 378  
 SQ SEQUENCE 477 AA; 55140 MW; E92CD679 CRC32;  
 Query Match 58.2%; Score 57; DB 1; Length 477;  
 Best Local Similarity 54.5%; Pred. No. 5.20e+00;  
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 Db 360 rlgllrlrly 370  
 QY 2 RLAIIRLALR 12  
 RESULT 5  
 ID ACH3\_BOVIN STANDARD; PRT; 495 AA.  
 AC Q07263;  
 DT 01-OCT-1994 (REL. 30, CREATED)  
 DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)  
 DE NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR.  
 OS BOS TAURUS (BOVINE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; ARTIODACTYLA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 92319195.  
 RA CRIADO M., ALAMO L., NAVARRO A.;  
 RL NEUROCHEM. RES. 17:281-287(1993).  
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN  
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND  
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA  
 CC MEMBRANE.  
 CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT  
 CC TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.  
 DR EMBL; X57032; G237763; -.  
 DR PROSITE; PS00236; NEUROTR\_ION\_CHANNEL.  
 KW RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;  
 FT TRANSMEMBRANE; MULTIGENE FAMILY.  
 FT SIGNAL 1 21  
 FT SIGNAL 1 21



FT CHAIN 22 495 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3.  
 FT DOMAIN 22 230 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 231 255 POTENTIAL.  
 FT TRANSMEM 263 281 POTENTIAL.  
 FT TRANSMEM 296 318 POTENTIAL.  
 FT DOMAIN 319 467 CYTOPLASMIC (BY SIMILARITY).  
 FT TRANSMEM 468 487 POTENTIAL.  
 FT DISULFID 149 163 BY SIMILARITY.  
 FT DISULFID 213 214 ASSOCIATED WITH RECEPTOR ACTIVATION  
 (BY SIMILARITY).  
 FT CARBOHYD 45 45 POTENTIAL.  
 FT CARBOHYD 162 162 POTENTIAL.  
 SQ SEQUENCE 495 AA; 56914 MW; 63BE4C2E CRC32;

Query Match 57.1%; Score 56; DB 1; Length 495;  
 Best Local Similarity 58.3%; Pred. No. 7.83e+00; Gaps 0;  
 Matches 7; Conservative 2; Mismatches 3; Indels 0;

Db 223 yslirrlpfy 234  
 | | | | | | | |  
 QY 1 YRLAIRRLRY 12

RESULT 6  
 ID ACH3\_CHICK STANDARD; PRT; 496 AA.  
 AC P09481;  
 DT 01-MAR-1989 (REL. 10, CREATED)  
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)  
 DE NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR.  
 OS GALLUS GALLUS (CHICKEN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;  
 OC GALLIFORMES.  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 91009210.  
 RA COUTURIER S., ERKMAN L., VALERA S., RUNGGER D., BERTRAND S.,  
 RA BOULTER J., BALLIVET M., BERTRAND D.,  
 RL J. BIOL. CHEM. 265:17560-17567(1990).  
 [2]  
 RP SEQUENCE OF 81-496 FROM N.A.  
 RX MEDLINE; 88283624.  
 RA NEF P., ONEYER C., ALLIOT C., COUTURIER S., BALLIVET M.;  
 RL EMO J. 7:595-601(1988).  
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN  
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND  
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA  
 CC MEMBRANE.  
 CC -1- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT  
 CC TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (ALSO CALLED BETA). A  
 CC FUNCTIONAL RECEPTOR SEEMS TO CONSIST OF TWO ALPHA-CHAINS AND  
 CC THREE NON-ALPHA CHAINS.  
 CC -1- DEVELOPMENTAL STAGE: HIGH LEVELS IN THE DEVELOPING CILIARY AND  
 CC SUPERIOR CERVICAL GANGLIA.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.  
 DR EMBL; M37336; G211045; -;  
 DR EMBL; X07345; G871036; -;  
 DR EMBL; X07346; G871036; JOINED.  
 DR EMBL; X07347; G871036; JOINED.  
 DR PIR; S00378; ACCH3N.  
 DR PROSITE; PS00236; NEUROTR\_ION\_CHANNEL.  
 KW POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;  
 KW TRANSMEMBRANE; MULTIGENE FAMILY.  
 FT SIGNAL 1 22  
 FT CHAIN 23 496 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3.  
 FT DOMAIN 23 231 EXTRACELLULAR.  
 FT TRANSMEM 232 256  
 FT TRANSMEM 264 282  
 FT TRANSMEM 298 319  
 FT DOMAIN 320 468  
 FT TRANSMEM 469 488 CYTOPLASMIC.  
 FT DISULFID 150 164 BY SIMILARITY.

FT DISULFID 214 215 ASSOCIATED WITH RECEPTOR ACTIVATION  
 (BY SIMILARITY).  
 FT CARBOHYD 46 46 POTENTIAL.  
 FT CARBOHYD 163 163 PROBABLE.  
 SQ SEQUENCE 496 AA; 57027 MW; 883D3EA9 CRC32;  
 Query Match 57.1%; Score 56; DB 1; Length 496;  
 Best Local Similarity 58.3%; Pred. No. 7.83e+00;  
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 224 yslirrlpfy 235  
 | | | | | | | |  
 QY 1 YRLAIRRLRY 12

RESULT 7  
 ID ACH3\_RAT STANDARD; PRT; 499 AA.  
 AC P04757;  
 DT 13-AUG-1987 (REL. 05, CREATED)  
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR.  
 GN ACRA3.  
 OS RATTUS NORVEGICUS (RAT).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 86118671.  
 RA BOULTER J., EVANS K., GOLDMAN D., MARTIN G., TRECO D., HEINEMANN S.,  
 RA PATRICK J.;  
 RL NATURE 319:368-374(1986).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 88041184.  
 RA BOULTER J., CONNOLLY J., DENERIS E.S., GOLDMAN D.J., HEINEMANN S.F.,  
 RA PATRICK J.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 84:7763-7767(1987).  
 [3]  
 RP SEQUENCE OF 1-21 FROM N.A.  
 RX TISSUE-LIVER;  
 RX MEDLINE; 94193711.  
 RA YANG X., MCDONOUGH J., FYODOROV D., MORRIS M., WANG F.,  
 RA DENERIS E.S.;  
 RL J. BIOL. CHEM. 269:10252-10264(1994).  
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN  
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND  
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA  
 CC MEMBRANE.  
 CC -1- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES  
 CC OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-3 SUBUNIT CAN BE  
 CC COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.  
 DR EMBL; X03440; G758258; -;  
 DR EMBL; L31621; G468916; -;  
 DR EMBL; U04961; G484069; -;  
 DR PIR; A24572; A24572.  
 DR PROSITE; PS00236; NEUROTR\_ION\_CHANNEL.  
 KW RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;  
 KW TRANSMEMBRANE; MULTIGENE FAMILY.  
 FT SIGNAL 1 25  
 FT CHAIN 26 499 POTENTIAL.  
 FT DOMAIN 26 234 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3.  
 FT TRANSMEM 235 259 EXTRACELLULAR.  
 FT TRANSMEM 267 285  
 FT TRANSMEM 301 322  
 FT DOMAIN 323 471 CYTOPLASMIC.  
 FT TRANSMEM 472 491  
 FT DISULFID 153 167 BY SIMILARITY.  
 FT DISULFID 217 218 ASSOCIATED WITH RECEPTOR ACTIVATION  
 (BY SIMILARITY).  
 FT CARBOHYD 49 49 POTENTIAL.

FT CARBOHYD 166 166 PROBABLE.  
SQ SEQUENCE 499 AA; 56997 MW; E561713C CRC32;

Query Match 57.1%; Score 56; DB 1; Length 499;

Best Local Similarity 58.3%; Pred. No. 7.83e+00; Mismatches 2; Indels 0; Gaps 0;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 227 yslvrrrlplfy 238  
| | | | | | | | | |  
QY 1 YRLAIRRIALRY 12

RESULT 8  
ID ACH3\_HUMAN STANDARD; PRT; 502 AA.  
AC P3297;  
DT 01-OCT-1993 (REL. 27, CREATED)  
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR.  
GN CHRNA3.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 90245296.  
RA FORNASARI D., CHINI B., TARRONI P., CLEMENTI F.;  
RL NEUROSCI. LETT. 111:351-356(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE-THYMUS;  
RX MEDLINE; 91114756.  
RA MIHOVILOVIC M., ROSES A.D.;  
RL EXP. NEUROL. 111:175-180(1991).  
RN [3]  
RP SEQUENCE OF 29-502 FROM N.A.  
RC TISSUE-BRAIN;  
RA ANAND R., LINDSTROM J.;  
RL SUBMITTED (JUN-1990) TO EMBL/GENBANK/DBJ DATA BANKS.  
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA MEMBRANE.  
CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.  
DR EMBL; M86383; G177898; -.  
DR EMBL; X52239; G35090; -.  
DR EMBL; M37981; G189253; -.  
DR EMBL; X53559; G34986; -.  
DR PIR; A37040; A37040.  
DR PIR; S24595; S24595.  
DR MIM; I18503; -.  
KW PROSITE; PS00236; NEUROTR\_ION\_CHANNEL.  
KW RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;  
KW TRANSMEMBRANE; MULTIGENE FAMILY.  
FT SIGNAL 1 28 POTENTIAL.  
FT CHAIN 29 502 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3.  
FT DOMAIN 29 237 EXTRACELLULAR.  
FT TRANSMEM 238 262  
FT TRANSMEM 270 288  
FT TRANSMEM 304 325  
FT DOMAIN 326 474  
FT TRANSMEM 475 494 CYTOPLASMIC.  
FT DISULFID 136 170  
FT DISULFID 220 221 BY SIMILARITY.  
FT CARBOHYD 52 52 ASSOCIATED WITH RECEPTOR ACTIVATION  
FT CARBOHYD 169 169 (BY SIMILARITY).  
FT CONFLICT 5 13 POTENTIAL.  
FT CONFLICT 99 99 VSLPLACRA -> ALAAPCAVAP (IN REF. 2).  
FT CONFLICT 131 132 D -> G (IN REF. 1).  
FT DD -> TT (IN REF. 1).

FT CONFLICT 234 234 I -> S (IN REF. 1).  
FT CONFLICT 429 429 L -> V (IN REF. 1).  
SQ SEQUENCE 502 AA; 57245 MW; 75D79DEC CRC32;

Query Match 57.1%; Score 56; DB 1; Length 502;

Best Local Similarity 58.3%; Pred. No. 7.83e+00; Mismatches 2; Indels 0; Gaps 0;

Db 230 yslvrrrlplfy 241  
| | | | | | | | | |  
QY 1 YRLAIRRIALRY 12

RESULT 9  
ID GRRL\_YEAST STANDARD; PRT; 1151 AA.  
AC P24814;  
DT 01-MAR-1992 (REL. 21, CREATED)  
DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)  
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
DE GRRL PROTEIN.  
GN GRRL OR COT2 OR CAT80 OR YJR090C OR J1885.  
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYETES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 92017785.  
RA FLICK J.S., JOHNSTON M.;  
RL MOL. CELL. BIOL. 11:5101-5112(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-S288C;  
RX HUANG M.-E., MANUS V., CHUAT J.-C., GALIBERT F.;  
RL YEAST 12:869-875(1996).  
CC -!- FUNCTION: PROBABLY CONSTITUTES THE PRIMARY RESPONSE ELEMENT REQUIRED FOR THE GENERATION OR INTERPRETATION OF THE SIGNAL THAT INDUCES GLUCOSE REPRESSION. IS NOT AN ESSENTIAL PROTEIN.  
CC -!- PATHWAY: NECESSARY FOR THE GLUCOSE REPRESSION PATHWAY.  
CC -!- INDUCTION: IS EXPRESSED CONSTITUTIVELY AT LOW LEVELS.  
CC -!- SUBCELLULAR LOCATION: ASSOCIATED WITH THE PARTICULATE FRACTION. PROBABLY FORMS A COMPLEX BY PROTEIN-PROTEIN INTERACTIONS VIA ITS LEUCINE-RICH SEGMENT.  
CC -!- SIMILARITY: THE REPEATED LEUCINE-RICH (LRR) SEGMENT IS FOUND IN MANY PROTEINS. NUMBER IN THIS PROTEIN: 12.  
DR EMBL; M59247; G171617; -.  
DR EMBL; Z49590; G1015784; -.  
DR EMBL; L47993; G1019709; -.  
DR PIR; A41529; A41529.  
DR LISTA; SC00406; GRRL.  
DR SGD; L0000730; GRRL.  
KW GLUCOSE METABOLISM; REPEAT; LEUCINE-REPEAT.  
FT DOMAIN 38 49 POLY-ASN.  
FT DOMAIN 1045 1124 ASN-RICH.  
FT DOMAIN 409 726 LEUCINE-RICH REPEATS.  
FT REPEAT 409 434 LRR 1.  
FT REPEAT 435 460 LRR 2.  
FT REPEAT 461 486 LRR 3.  
FT REPEAT 487 512 LRR 4.  
FT REPEAT 513 548 LRR 5.  
FT REPEAT 549 567 LRR 6.  
FT REPEAT 568 593 LRR 7.  
FT REPEAT 594 619 LRR 8.  
FT REPEAT 620 645 LRR 9.  
FT REPEAT 646 670 LRR 10.  
FT REPEAT 671 699 LRR 11.  
FT REPEAT 700 726 LRR 12.  
SQ SEQUENCE 1151 AA; 132733 MW; 8C0DF89 CRC32;

Query Match 57.1%; Score 56; DB 4; Length 1151;  
Best Local Similarity 41.7%; Pred. No. 7.83e+00;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 386 yrlmikrinf 397



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#accession D49898
#status preliminary
#molecule_type DNA
#residues 1-245 #label LAI
#cross-references NCBI:138630; NCBI:138634
#note sequence extracted from NCBI backbone
SUMMARY #length 245 #molecular-weight 27430 #checksum 647

Query Match 93.9%; Score 46; DB 10; Length 245;
Best Local Similarity 83.3%; Pred. No. 1.13e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 142 yrlpir 147
| | | | |
QY 1 YRLAIR 6

RESULT 3
ENTRY #type complete
TITLE hypothetical protein Tfl - fission yeast (Schizosaccharomyces
ORGANISM pombe)
#formal_name Schizosaccharomyces pombe
DATE 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change
30-Sep-1993
ACCESSIONS A36373
REFERENCE A36373
#authors Levin, H.L.; Weaver, D.C.; Boeke, J.D.
#journal Mol. Cell. Biol. (1990) 10:6791-6798
#title Two related families of retrotransposons from
Schizosaccharomyces pombe.
#cross-references MUID:91061791
#accession A36373
#status preliminary
#molecule_type DNA
#residues 1-1330 #label LEV
#cross-references GB:M38526
SUMMARY #length 1330 #molecular-weight 154795 #checksum 1686

Query Match 93.9%; Score 46; DB 11; Length 1330;
Best Local Similarity 83.3%; Pred. No. 1.13e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 408 yrlpir 413
| | | | |
QY 1 YRLAIR 6

RESULT 4
ENTRY #type complete
TITLE Tf2 protein, Retrotransposon - fission yeast
(Schizosaccharomyces pombe)
ORGANISM #formal_name Schizosaccharomyces pombe
DATE 03-May-1994 #sequence_revision 03-May-1994 #text_change
03-May-1994
ACCESSIONS JN0791
REFERENCE JN0791
#authors Weaver, D.C.; Shpakovski, G.V.; Caputo, E.; Levin, H.L.;
Boeke, J.D.
#journal Gene (1993) 131:135-139
#title Sequence analysis of closely related retrotransposon families
from fission yeast.
#accession JN0791
#molecule_type DNA
#residues 1-1333 #label WEA
#cross-references GB:L10324
GENETICS
#status preliminary
#molecule_type mRNA
#residues 1-2616 #label HON
#cross-references GB:U29153
SUMMARY #length 1333 #molecular-weight 154915 #checksum 3353

Query Match 93.9%; Score 46; DB 11; Length 1333;
Best Local Similarity 83.3%; Pred. No. 1.13e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 411 yrlpir 416
| | | | |
QY 1 YRLAIR 6

RESULT 5
ENTRY #type complete
TITLE host specificity protein J - phage lambda
ORGANISM #formal_name phage lambda
DATE 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change
31-Dec-1993
ACCESSIONS D43009; A43015; A04374
REFERENCE A4614
#authors Daniels, D.
#submission submitted to the Nucleic Acid Sequence Database, September
1982
#accession D43009
#molecule_type DNA
#residues 1-1132 #label DAN
REFERENCE A92891
#authors Sanger, F.; Coulson, A.R.; Hong, G.F.; Hill, D.F.; Petersen,
G.B.
#journal J. Mol. Biol. (1982) 162:729-773
#title Nucleotide sequence of bacteriophage lambda DNA.
#cross-references MUID:83189071
#accession A43015
#molecule_type DNA
#residues 1-1132 #label SAN
COMMENT Gene J protein makes up the distal fiber of the phage tail. It is
responsible for adsorption to the host during infection and
determines host specificity. It specifically binds to the lambda
receptor protein of E. coli K12. This receptor protein encoded by
E. coli gene lamB is an outer membrane protein that functions in
the transport of maltose and maltodextrins.
J protein serves as the initiator of tail polymerization. There
are 2-4 copies of protein J per mature phage.
GENETICS
#gene J
#map_position 31.97-38.97
CLASSIFICATION #superfamily phage lambda host specificity protein J
SUMMARY #length 1132 #molecular-weight 124421 #checksum 1868

Query Match 91.8%; Score 45; DB 4; Length 1132;
Best Local Similarity 66.7%; Pred. No. 1.78e+01;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 688 yrlpir 693
| | | | |
QY 1 YRLAIR 6

RESULT 6
ENTRY #type complete
TITLE nudel protein precursor - fruit fly (Drosophila melanogaster)
ORGANISM #formal_name Drosophila melanogaster
DATE 27-Oct-1995 #sequence_revision 27-Oct-1995 #text_change
19-Jan-1996
ACCESSIONS A57096
REFERENCE A57096
#authors Hong, C.C.; Hashimoto, C.
#journal Cell (1995) 82:785-794
#title An unusual mosaic protein with a protease domain, encoded by
the nudel gene, is involved in defining embryonic
dorsoventral polarity in Drosophila.
#accession A57096
#status preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues 1-2616 #label HON
#cross-references GB:U29153
CLASSIFICATION #superfamily LDL receptor ligand-binding repeat homology
KEYWORDS extracellular protein
FEATURE

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891-929      #domain LDL receptor ligand-binding repeat homology
2421-2457    #label LDL1\
             #domain LDL receptor ligand-binding repeat homology
             #label LDL3
SUMMARY      #length 2616 #molecular-weight 292372 #checksum 9962

Query Match      91.8%; Score 45; DB 12; Length 2616;
Best Local Similarity 83.3%; Pred. No. 1.78e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 2609 yrleir 2614
   ||| ||
QY 1 YRLAIR 6

RESULT 7
ENTRY      S27852      #type complete
TITLE      hypothetical protein DGF-1 - Trypanosoma cruzi
ORGANISM   #formal_name Trypanosoma cruzi
DATE       17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
30-Sep-1993
ACCESSIONS S27852
REFERENCE   #authors Wincker, P.; Murta-Dovales, A.C.; Goldenberg, S.
             #submission submitted to the EMBL Data Library, April 1992
             #description Nucleotide sequence of a representative member of a
             Trypanosoma cruzi dispersed gene family.
             #accession S27852
             #molecule_type DNA
             #residues 1-3229 #label WIN
             #cross-references EMBL:M90534
SUMMARY      #length 3229 #molecular-weight 334929 #checksum 5768

Query Match      91.8%; Score 45; DB 12; Length 3229;
Best Local Similarity 66.7%; Pred. No. 1.78e+01;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1266 yrleir 1271
   ||| ||
QY 1 YRLAIR 6

RESULT 8
ENTRY      A48450      #type complete
TITLE      probable cell-surface protein (cysteine-rich repeat motif) -
             Trypanosoma cruzi
ORGANISM   #formal_name Trypanosoma cruzi
DATE       01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change
03-Mar-1995
ACCESSIONS A48450
REFERENCE   #authors Wincker, P.; Murto-Dovales, A.C.; Goldenberg, S.
             #journal Mol. Biochem. Parasitol. (1992) 55:217-220
             #title Nucleotide sequence of a representative member of a
             Trypanosoma cruzi dispersed gene family.
             #cross-references MUID:93063053
             #accession A48450
             #status preliminary; not compared with conceptual translation
             #molecule_type DNA
             #residues 1-3229 #label WIN
             #cross-references NCBI:P118407
             #note sequence extracted from NCBI backbone
SUMMARY      #length 3229 #molecular-weight 334929 #checksum 5768

Query Match      91.8%; Score 45; DB 12; Length 3229;
Best Local Similarity 66.7%; Pred. No. 1.78e+01;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1266 yrleir 1271
   ||| ||
QY 1 YRLAIR 6

```

```

RESULT 9
ENTRY      JN0448      #type complete
TITLE      t-complex polypeptide Tcpl-1 - Arabidopsis thaliana
ORGANISM   #formal_name Arabidopsis thaliana #common_name mouse-ear
             cress
DATE       30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
30-Sep-1993
ACCESSIONS JN0448
REFERENCE   #authors Mori, M.; Murata, K.; Kubota, H.; Yamamoto, A.; Matsushiro,
             A.; Morita, T.
             #journal Gene (1992) 122:381-382
             #title Cloning of a cDNA encoding the Tcpl-1 (t complex polypeptide
             1) homologue of Arabidopsis thaliana.
             #accession JN0448
             #molecule_type mRNA
             #residues 1-545 #label MOR
             #cross-references DDBJ:D11351
SUMMARY      #length 545 #molecular-weight 59229 #checksum 1573

Query Match      89.8%; Score 44; DB 11; Length 545;
Best Local Similarity 83.3%; Pred. No. 2.79e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 124 yrleir 129
   ||| ||
QY 1 YRLAIR 6

RESULT 10
ENTRY      JC4696      #type complete
TITLE      alpha,alpha-trehalose-phosphate synthase (EC 2.4.1.-) -
             Rhizobium sp.
ORGANISM   #formal_name Rhizobium sp.
DATE       10-May-1996 #sequence_revision 19-Jul-1996 #text_change
19-Jul-1996
ACCESSIONS JC4696
REFERENCE   #authors Maruta, K.; Hattori, K.; Nakada, T.; Kubota, M.; Sugimoto,
             T.; Kurimoto, M.
             #journal Biosci. Biotechnol. Biochem. (1996) 60:717-720
             #title Cloning and sequencing of trehalose biosynthesis genes from
             Rhizobium sp. M-11.
             #accession JC4696
             #molecule_type DNA
             #residues 1-772 #label MAR
             #cross-references DDBJ:D78001
COMMENT      This enzyme belongs to alpha-amylase family. It catalyzes the
             conversion of maltodextrins to maltotriose by
             forming alpha,alpha-1,1-glucosidic linkage by an intramolecular
             transglucosylation.

GENETICS
#gene      MTSase
KEYWORDS   glycosyltransferase; hexosyltransferase
SUMMARY      #length 772 #molecular-weight 84859 #checksum 8061

Query Match      89.8%; Score 44; DB 8; Length 772;
Best Local Similarity 83.3%; Pred. No. 2.79e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 8 yrleir 13
   ||| ||
QY 1 YRLAIR 6

RESULT 11
ENTRY      S31175      #type complete
TITLE      hypothetical protein 2 - midge (Chironomus thummi) transposon
             NLR1Cth
ORGANISM   #formal_name Chironomus thummi
DATE       30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
30-Sep-1993
ACCESSIONS S31175

```

```

REFERENCE S31174
#authors Blinov, A.G.; Sobanov, Y.V.; Bogachev, S.S.; Donchenko, A.P.;
#journal Filippova, M.A. (1993) 237:412-420
#title Mol. Gen. Genet. The Chironomus thummi genome contains a non-LTR
#accession S31175
#status not compared with conceptual translation
#molecule_type DNA
#residues 1-883 #molecular-weight 102009 #checksum 5809
SUMMARY #length 883 #molecular-weight 102009 #checksum 5809
Query Match 89.8%; Score 44; DB 12; Length 883;
Best Local Similarity 83.3%; Pred. No. 2.79e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 803 yklair 808
QY 1 YRLAIR 6

RESULT 12
ENTRY S42144 #type complete
TITLE ribosomal protein L5.e - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES protein YPL14w; protein YPL13lw; ribosomal protein YLL1;
ORGANISM ribosomal protein YL3
#formal_name Saccharomyces cerevisiae
DATE 03-May-1994 #sequence_revision 27-Jan-1995 #text_change
06-Sep-1996
ACCESSIONS S42144; S48089; S11574; S69053; A38724
REFERENCE S42144
#authors Deshmukh, M.; Tsay, Y.F.; Paulovich, A.G.; Woolford Jr., J.L.
#journal Mol. Cell. Biol. (1993) 13:2835-2845
#title Yeast ribosomal protein L1 is required for the stability of
newly synthesized 5S rRNA and the assembly of 60S ribosomal
subunits.
#accession S42144
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-297 #label DES
#cross-references EMBL:L01796
#note the nucleotide sequence was submitted to the EMBL Data
Library, September 1992
REFERENCE A38724
#authors Tang, B.; Nazar, R.N.
#journal J. Biol. Chem. (1991) 266:6120-6123
#title Structure of the yeast ribosomal 5 S RNA-binding
protein YL3.
#cross-references M01D:91177855
#accession S14172
#status not compared with conceptual translation
#molecule_type DNA
#residues 1-111,'R',113-297 #label TAN
REFERENCE S48088
#authors Tang, B.; Nazar, R.N.
#journal J. Biol. Chem. (1992) 267:17738-17742
#title Unbalanced regulation of the ribosomal 5 S RNA-binding
protein in Saccharomyces cerevisiae expressing mutant 5 S
rRNAs.
#accession S48089
#status translation not shown
#molecule_type DNA
#residues 1-111,'R',113-297 #label TA2
#cross-references EMBL:M94864
REFERENCE S11574
#authors Nazar, R.N.; Yaguchi, M.; Willick, G.E.; Rollin, C.F.; Roy,
C.
#journal Eur. J. Biochem. (1979) 102:573-582
#title The 5-S RNA binding protein from yeast (Saccharomyces
cerevisiae) ribosomes. Evolution of the eukaryotic 5-S RNA
binding protein.
#cross-references M01D:80112896
#accession S11574
#molecule_type protein

```

---

```

#residues 2-31;209-256 #label NAZ
#note the sequence from the summary and Fig. 5 is inconsistent
with that from tables 2 and 3 in having 17-Tyr
REFERENCE S69040
#authors Hall, J.; DePaulo, T.; Ahmed, A.; Bussey, H.; Fortin, N.;
Friesen, J.D.; Storms, R.K.; Vo, D.H.; Wang, Y.; Winnett,
E.
#submission submitted to the EMBL Data Library, December 1995
#description The sequence of Saccharomyces cerevisiae chromosome XVI left
arm.
#accession S69053
#molecule_type DNA
#residues 1-297 #label HAL
#cross-references EMBL:U43703
GENETICS LISTA:RPL1
#gene
#map_position 16L
CLASSIFICATION #superfamily rat ribosomal protein L5
KEYWORDS protein biosynthesis; ribosome; RNA binding
FEATURE
2-297 #product ribosomal protein L5.e #status experimental
#label MAT
SUMMARY #length 297 #molecular-weight 33714 #checksum 4118
Query Match 87.8%; Score 43; DB 7; Length 297;
Best Local Similarity 66.7%; Pred. No. 4.33e+01;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 49 yrlvvr 54
QY 1 YRLAIR 6

RESULT 13
ENTRY BVAS1 #type complete
TITLE aroM protein - Emericella nidulans
ALTERNATE_NAMES biosynthetic dehydroquinase
CONTAINS 3-dehydroquininate dehydratase (EC 4.2.1.10); 3-dehydroquininate
synthase (EC 4.6.1.3); 3-phosphoshikimate
1-carboxyvinyltransferase (EC 2.5.1.19); shikimate
5-dehydrogenase (EC 1.1.1.25); shikimate kinase (EC
2.7.1.71)
ORGANISM #formal_name Emericella nidulans, Aspergillus nidulans
DATE 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
18-Aug-1995
ACCESSIONS A24962; A24042
REFERENCE A24962
#authors Charles, I.G.; Keyte, J.W.; Brammar, W.J.; Smith, M.;
Hawkins, A.R.
#journal Nucleic Acids Res. (1986) 14:2201-2213
#title The isolation and nucleotide sequence of the complex AROM
locus of Aspergillus nidulans.
#cross-references M01D:86176723
#accession A24962
#molecule_type DNA
#residues 1-1603 #label DUN
REFERENCE A24042
#authors Charles, I.G.; Keyte, J.W.; Brammar, W.J.; Hawkins, A.R.
#journal Nucleic Acids Res. (1985) 13:8119-8128
#title Nucleotide sequence encoding the biosynthetic dehydroquinase
function of the penta-functional AROM locus of Aspergillus
nidulans.
#cross-references M01D:86067221
#accession A24042
#molecule_type DNA
#residues 844-1048,'G',1050-1093,'N',1095-1458,'T',1460-1474
#label CHA
GENETICS
#gene aroM
CLASSIFICATION #superfamily aroI protein; 3-dehydroquininate dehydratase
homology; 3-dehydroquininate synthase homology;
3-phosphoshikimate 1-carboxyvinyltransferase homology;
shikimate dehydrogenase homology; shikimate kinase homology

```

## KEYWORDS

aromatic amino acid biosynthesis; ATP binding; carbon-oxygen lyase; hydro-lyase; multifunctional enzyme; NADP; oxidoreductase; phosphorus-oxygen lyase; phosphotransferase; transferase

## FEATURE

7-372 #domain 3-dehydroquinase synthase homology #label DQS\  
407-835 #domain 3-phosphoshikimate 1-carboxyvinyltransferase homology #label PSK\  
863-982 #domain shikimate kinase homology #label SKI\  
1037-1277 #domain 3-dehydroquinase dehydratase homology #label DDD\  
1344-1567 #domain shikimate dehydrogenase homology #label SKD

## SUMMARY

#length 1603 #molecular-weight 175079 #checksum 7102

## Query Match

87.8%; Score 43; DB 1; Length 1603;

Best Local Similarity 83.3%; Pred. No. 4.33e+01;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1141 yrlafr 1146

||||:|

Qy 1 YRLAIR 6

## RESULT 14

ENTRY W8BPT3 #type complete  
TITLE gene 18.7 protein - phage T3  
ORGANISM #formal\_name phage T3  
#note host Escherichia coli  
DATE 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 07-Apr-1994  
ACCESSIONS E23476  
REFERENCE A94339  
#authors Yamada, M.; Fujisawa, H.; Kato, H.; Hamada, K.; Minagawa, T.  
#journal Virology (1986) 151:350-361  
#title Cloning and sequencing of the genetic right end of bacteriophage T3 DNA.  
#cross-references MUID:86209997

## #accession E23476

## #molecule\_type DNA

## #residues 1-83 #label YAM

## REFERENCE A94344

#authors Yamada, M.; Fujisawa, H.; Kato, H.; Hamada, K.; Minagawa, T.  
#journal Virology (1986) 154:246  
#contents annotation; erratum; corrections to coding regions

## GENETICS

## #gene 18.7

## CLASSIFICATION #superfamily phage T7 gene 18.7 protein

SUMMARY #length 83 #molecular-weight 9393 #checksum 4304

## Query Match

85.7%; Score 42; DB 4; Length 83;

Best Local Similarity 66.7%; Pred. No. 6.68e+01;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 20 yrlsik 25

||||:

Qy 1 YRLAIR 6

## RESULT 15

ENTRY D49804 #type complete  
TITLE p25, CP-capsid protein - citrus tristeza closterovirus CTV  
ORGANISM #common\_name citrus tristeza closterovirus CTV  
DATE 11-Oct-1994 #sequence\_revision 11-Oct-1994 #text\_change 11-Oct-1994

## ACCESSIONS

## REFERENCE D49804

## #authors

Pappu, H.R.; Karasev, A.V.; Anderson, E.J.; Pappu, S.S.; Half, M.E.; Febres, V.J.; Eckloff, R.M.; McCaffery, M.; Boyko, V.; Gowda, S.; Dolla, V.V.; Koonin, E.V.; Gumpf, D.J.; Cline, K.C.; Garnsey, S.M.; Dawson, W.O.; Lee, R.F.; Niblett, C.L.

Virology (1994) 199:35-46

#journal Nucleotide sequence and organization of eight 3' open reading

#cross-references MUID:94160579  
#contents T36, severe quick decline isolate  
#accession D49804

## #status preliminary

## #molecule\_type genomic RNA

## #residues 1-223 #label PAP

## #cross-references NCBIN:144092; NCBIP:144102

## #note sequence extracted from NCBI backbone

## SUMMARY #length 223 #molecular-weight 24890 #checksum 4316

## Query Match

85.7%; Score 42; DB 16; Length 223;

Best Local Similarity 66.7%; Pred. No. 6.68e+01;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 85 yrlavk 90

||||:

Qy 1 YRLAIR 6

Search completed: Thu May 22 08:31:55 1997

Job time : 19 secs.

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WISREH (TM)

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:27:58 1997; MasPar time 1.97 Seconds  
Tabular output not generated. 64.764 Million cell updates/sec

Title: >US-08-653-294-5  
Description: (1-6) from US08653294.pep  
Perfect score: 53  
Sequence: 1 RILLRY 6

Scoring table: PAM 150  
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot34  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 23.812; Variance 26.364; scale 0.903

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	48	90.6	830	5	HMT1_SCHPO	HEAVY METAL TOLERANCE
2	48	90.6	832	11	YC26_YEAST	PUTATIVE 95.7 KD TRAN
3	47	88.7	139	10	VPRE_HUMAN	IMMUNOGLOBULIN IOTA C
4	47	88.7	142	10	VPR1_MOUSE	IMMUNOGLOBULIN IOTA C
5	47	88.7	142	10	VPR2_MOUSE	IMMUNOGLOBULIN IOTA C
6	47	88.7	225	2	CBQI_SALTY	COBALT TRANSPORT PROT
7	47	88.7	496	6	MMSA_FSEAE	METHYLMALONATE-SEMIAL
8	46	86.8	328	4	HA1Q_MOUSE	H-2 CLASS I HISTOCOMP
9	46	86.8	338	1	IB20_HUMAN	HLA CLASS I HISTOCOMP
10	46	86.8	346	7	PP12_TRYBB	SERINE/THREONINE PROT
11	46	86.8	361	1	IB14_HUMAN	HLA CLASS I HISTOCOMP
12	46	86.8	362	4	HA13_MOUSE	H-2 CLASS I HISTOCOMP
13	46	86.8	362	1	IB18_HUMAN	HLA CLASS I HISTOCOMP
14	46	86.8	362	1	IB45_HUMAN	HLA CLASS I HISTOCOMP
15	46	86.8	362	1	IB16_HUMAN	HLA CLASS I HISTOCOMP
16	46	86.8	362	1	IB29_HUMAN	HLA CLASS I HISTOCOMP
17	46	86.8	362	1	IB19_HUMAN	HLA CLASS I HISTOCOMP
18	46	86.8	365	6	MEFX_HUMAN	MYOCYTE-SPECIFIC ENHA
19	46	86.8	368	4	HA1Q_MOUSE	H-2 CLASS I HISTOCOMP
20	46	86.8	411	6	LYOX_MOUSE	PROTEIN-LYSINE 6-OXID
21	46	86.8	411	6	LYOX_RAT	PROTEIN-LYSINE 6-OXID
22	46	86.8	417	6	LYOX_HUMAN	PROTEIN-LYSINE 6-OXID

23	46	86.8	420	6	LYOX_CHICK	PROTEIN-LYSINE 6-OXID
24	46	86.8	515	6	MEF2_DROME	MYOCYTE-SPECIFIC ENHA
25	46	86.8	1626	9	TOPB_HUMAN	DNA TOPOISOMERASE II,
26	45	84.9	217	9	TER4_ECOLI	TETRACYCLINE REPRESSO
27	45	84.9	218	9	TER8_PASPI	TETRACYCLINE REPRESSO
28	45	84.9	298	9	RT03_ACACA	MITOCHONDRIAL RIBOSOM
29	45	84.9	1203	9	SDC1_CABEL	ZINC FINGER PROTEIN S
30	44	83.0	168	11	YZDC_ECOLI	VERY HYPOTHETICAL 20.
31	44	83.0	217	11	XJ17_YEAST	HYPOTHETICAL 24.5 KD
32	44	83.0	338	4	GALE_NEIGO	UDP-GLUCOSE 4-EPIHERA
33	44	83.0	402	11	YG34_YEAST	HYPOTHETICAL 45.3 KD
34	44	83.0	410	1	ATIN_VZVD	ALPHA TRANS-INDUCING
35	44	83.0	607	11	YN92_YEAST	PUTATIVE TRANSCRIPTIO
36	44	83.0	633	5	KS62_MOUSE	RIBOSOMAL PROTEIN S6
37	44	83.0	724	5	KS61_MOUSE	RIBOSOMAL PROTEIN S6
38	44	83.0	740	5	KS62_HUMAN	RIBOSOMAL PROTEIN S6
39	44	83.0	752	5	KS6A_CHICK	RIBOSOMAL PROTEIN S6
40	44	83.0	817	8	RRPO_CRV	PROBABLE RNA-DIRECTED
41	44	83.0	817	8	RRPO_TBSVC	PROBABLE RNA-DIRECTED
42	44	83.0	817	8	RRPO_CNV	PROBABLE RNA-DIRECTED
43	44	83.0	1174	11	XJ11_YEAST	HYPOTHETICAL 135.1 KD
44	44	83.0	1216	1	ATC2_YEAST	PROBABLE CALCIUM-TRAN
45	44	83.0	1741	8	RPC1_GIALA	DNA-DIRECTED RNA POLY

ALIGNMENTS

RESULT 1  
ID HMT1\_SCHPO STANDARD; PRT; 830 AA.  
AC Q02592;  
DT 01-JUL-1993 (REL. 26, CREATED)  
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
DE HEAVY METAL TOLERANCE PROTEIN PRECURSOR.  
GN HMT1.  
OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SP223;  
RX MEDLINE; 93010938.  
RA ORTIZ D.F., KREPEL L., SPEISER D.M., SCHEEL G., MCDONALD G.,  
OW D.W.;  
RL EMBO J. 11:3491-3499(1992).  
CC -!- FUNCTION: INVOLVED IN METAL TOLERANCE. PROBABLY INVOLVED IN THE  
TRANSPORT OF METAL-BOUND PHYTOCHELATIONS. COMPARTMENTALIZES  
CADMIUM WITHIN VACUOLES, THEREBY PROTECTING CELLS FROM CADMIUM  
TOXICITY.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. VACUOLAR.  
CC -!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY  
(ABC TRANSPORTERS). BELONGS TO THE MDR SUBFAMILY.  
DR EMBL; Z14055; G4972; -.  
DR PIR; S25198; S25198.  
DR PROSITE; PS00211; ABC\_TRANSPORTER.  
KW CADMIUM; METAL-BINDING; TRANSMEMBRANE; SIGNAL; ATP-BINDING;  
GLYCOPROTEIN; CADMIUM RESISTANCE.  
FT SIGNAL 1 27  
FT CHAIN 28 830 HEAVY METAL TOLERANCE PROTEIN.  
FT TRANSMEM 10 31 POTENTIAL.  
FT TRANSMEM 52 71 POTENTIAL.  
FT TRANSMEM 88 108 POTENTIAL.  
FT TRANSMEM 126 146 POTENTIAL.  
FT TRANSMEM 403 423 POTENTIAL.  
FT TRANSMEM 490 511 POTENTIAL.  
FT NP\_BIND 617 624 ATP (POTENTIAL).  
FT CARBOHYD 150 150 POTENTIAL.  
FT CARBOHYD 350 350 POTENTIAL.  
SQ SEQUENCE 830 AA; 94007 MW; 32AA6381 CRC32;

Query Match 90.6%; Score 48; DB 5; Length 830;  
Best local similarity 83.3%; Pred. No. 5.28e+00;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 628 rllrlf 633  
|||||  
QY 1 RILLY 6

RESULT 2  
ID YC26 YEAST STANDARD; PRT; 832 AA.  
AC P25611;  
DT 01-MAY-1992 (REL. 22, CREATED)  
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)  
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
DE PUTATIVE 95.7 KD TRANSCRIPTIONAL REGULATORY PROTEIN IN PAU3  
DE 3'REGION.  
GN YCR106W.  
OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.  
RN [1]  
RP SEQUENCE OF 1-517 FROM N.A.  
RA VAN DER LINDEN C.G., MAURER C.T.C., PLANTA R.J.,  
RA VAN VLIET-REEDIJK J.C.;  
RL SUBMITTED (MAR-1992) TO EMBL/GENBANK/DBJ DATA BANKS.  
RN [2]  
RP SEQUENCE OF 130-832 FROM N.A.  
RA GRENSON M., JAUNIAUX J.-C., URRESTARAZU L.A.;  
RL SUBMITTED (MAR-1992) TO EMBL/GENBANK/DBJ DATA BANKS.  
RN [3]  
RP PRESENCE OF A ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR CLUSTER.  
RX MEDLINE; 92350247  
RA BORK P., OZOUNIS C., SANDER C., SCHARF M., SCHNEIDER R.,  
RA SONNHAMMER E.;  
RL NATURE 358:287-287(1992).  
CC -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).  
CC -!- SIMILARITY: CONTAINS A ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR  
CC CLUSTER DOMAIN.  
DR EMBL; X59720; E264733; -  
DR PIR; S19418; S19418.  
DR PROSITE; PS00463; ZN2\_CY6\_FUNGAL.  
KW HYPOTHETICAL PROTEIN; TRANSCRIPTION REGULATION; DNA-BINDING;  
KW NUCLEAR PROTEIN; ZINC; METAL-BINDING.  
FT DNA\_BIND 15 42 ZN(2)-CYS(6), FUNGAL-TYPE.  
SQ SEQUENCE 832 AA; 95689 MW; 77275669 CRC32;

Query Match 90.6%; Score 48; DB 11; Length 832;  
Best Local Similarity 83.3%; Pred. No. 5.28e+00;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 629 rllrlf 634  
|||||  
QY 1 RILLY 6

RESULT 3  
ID VPRE\_HUMAN STANDARD; PRT; 139 AA.  
AC P12018;  
DT 01-OCT-1989 (REL. 12, CREATED)  
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)  
DT 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)  
DE IMMUNOGLOBULIN IOTA CHAIN PRECURSOR (V(PREB) PROTEIN) (FRAGMENT).  
GN VPREB.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 88196069.  
RA BAUER S.R., KUDO A., MELCHERS F.;  
RL EMBO J. 7:111-116(1988).  
CC -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR  
CC COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS  
CC COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY  
CC STEPS OF B-CELL DIFFERENTIATION.  
CC -!- SIMILARITY: TO MOUSE V(PREB)1 AND V(PREB)2.  
CC -!- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.

CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
DR EMBL; M34927; G340305; -  
DR PIR; S00258; S00258.  
DR HSP; P01703; IBL.  
DR MIM; I46770; -  
KW IMMUNOGLOBULIN FOLD; B-CELL; SIGNAL.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 139 IMMUNOGLOBULIN IOTA CHAIN.  
FT DOMAIN 20 41 FRAMEWORK 1.  
FT DOMAIN 42 56 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 57 70 FRAMEWORK 2.  
FT DOMAIN 71 81 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 82 115 FRAMEWORK 3.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 139 139  
SQ SEQUENCE 139 AA; 15948 MW; EIDA1049 CRC32;

Query Match 88.7%; Score 47; DB 10; Length 139;  
Best Local Similarity 83.3%; Pred. No. 8.61e+00;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 66 rllrlf 71  
|||||  
QY 1 RILLY 6

RESULT 4  
ID VPRL\_MOUSE STANDARD; PRT; 142 AA.  
AC P13372;  
DT 01-JAN-1990 (REL. 13, CREATED)  
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)  
DT 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)  
DE IMMUNOGLOBULIN IOTA CHAIN PRECURSOR (V(PREB)1 PROTEIN).  
GN VPREB1.  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-DBA/2J X C57BL/6;  
RX MEDLINE; 88029315.  
RA KUDO A., MELCHERS F.;  
RL EMBO J. 6:2267-2272(1987).  
CC -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR  
CC COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS  
CC COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY  
CC STEPS OF B-CELL DIFFERENTIATION.  
CC -!- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.  
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
DR EMBL; X05556; G55410; -  
DR EMBL; X05557; G55414; -  
DR PIR; A28344; A28344.  
DR HSP; P01607; IFGV.  
KW IMMUNOGLOBULIN FOLD; B-CELL; SIGNAL.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 142 V(PREB)1 PROTEIN.  
FT DOMAIN 20 41 FRAMEWORK 1.  
FT DOMAIN 42 56 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 57 70 FRAMEWORK 2.  
FT DOMAIN 71 81 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 82 115 FRAMEWORK 3.  
FT DISULFID 41 115 BY SIMILARITY.  
SQ SEQUENCE 142 AA; 16125 MW; 45C58A1B CRC32;

Query Match 88.7%; Score 47; DB 10; Length 142;  
Best Local Similarity 83.3%; Pred. No. 8.61e+00;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 66 rllrlf 71  
|||||  
QY 1 RILLY 6

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RESULT 5
ID VPR2_MOUSE STANDARD; PRT; 142 AA.
AC P13373;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
DE IMMUNOGLOBULIN OMEGA CHAIN PRECURSOR (V(PREB)2 PROTEIN).
GN VPBE2.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DBA/2J X C57BL/6;
RX MEDLINE; 88029315.
RA KUDO A., MELCHERS F.;
RL EMBO J. 6:2267-2272(1987).
CC -1- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
CC COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS
CC COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY
CC STEPS OF B-CELL DIFFERENTIATION.
CC -1- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
DR EMBL; X05563; G55416; -.
DR PIR; B28344; B28344.
DR HSSP; P01607; 1FGV.
KW IMMUNOGLOBULIN FOLD; B-CELL; SIGNAL.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 142 V(PREB)2 PROTEIN.
FT DOMAIN 20 41 FRAMEWORK 1.
FT DOMAIN 42 56 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 57 70 FRAMEWORK 2.
FT DOMAIN 71 81 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 82 115 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
SQ SEQUENCE 142 AA; 16052 MW; 6AE40A3B CRC32;

Query Match 88.7%; Score 47; DB 10; Length 142;
Best Local Similarity 83.3%; Pred. No. 8.61e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 56 rllry 71
   1:||||
Qy 1 RILLY 6

RESULT 6
ID CBIQ_SALTY STANDARD; PRT; 225 AA.
AC Q05598;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE COBALT TRANSPORT PROTEIN CBIQ.
GN CBIQ.
OS SALMONELLA TYPHIMURIUM.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC ENTEROBACTERIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LT2;
RX MEDLINE; 93273696.
RA ROTH J.R., LAWRENCE J.G., RUBENFELD M., KIEFFER-HIGGINS S.,
RA CHURCH G.M.;
RL J. BACTERIOL. 175:3303-3316(1993).
CC -1- FUNCTION: MAY BE INVOLVED WITH COBALT TRANSPORT IN ASSOCIATION
CC WITH COBALAMIN BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- PATHWAY: COBALAMIN BIOSYNTHESIS.
DR EMBL; L12006; G154434; -.
DR SYGENE; SG10049; CBIQ.
KW COBALAMIN BIOSYNTHESIS; TRANSPORT; COBALT TRANSPORT; TRANSMEMBRANE.
FT TRANSMEM 22 42 POTENTIAL.
FT TRANSMEM 65 85 POTENTIAL.

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FT TRANSMEM 90 110 POTENTIAL.
FT TRANSMEM 122 142 POTENTIAL.
FT TRANSMEM 150 170 POTENTIAL.
SQ SEQUENCE 225 AA; 25983 MW; E926FA4B CRC32;

Query Match 88.7%; Score 47; DB 2; Length 225;
Best Local Similarity 66.7%; Pred. No. 8.61e+00;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 202 rvlmry 207
   1:||||
Qy 1 RILLY 6

RESULT 7
ID MMSA_PSEAE STANDARD; PRT; 496 AA.
AC P28810;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
DE METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE (ACYLATING) (EC 1.2.1.27)
DE (MMSDH).
GN MMSA.
OS PSEUDOMONAS AERUGINOSA.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC PSEUDOMONADACEAE.
RN [1]
RP SEQUENCE FROM N.A.; AND SEQUENCE OF 1-29.
RC STRAIN-PAO / ATCC 15692;
RX MEDLINE; 92317087.
RA STEELE M.I., LORENZ D., HATTER K., PARK A., SOKATCH J.R.;
RA J. BIOL. CHEM. 267:13585-13592(1992).
CC -1- CATALYTIC ACTIVITY: 2-METHYL-3-OXOPROPANATE + COA + NAD(+) -
CC PROPHANOL-COA + CO(2) + NADH.
CC -1- SUBUNIT: HOMODIMER.
CC -1- PATHWAY: DISTAL VALINE METABOLIC PATHWAY.
CC -1- INDUCTION: BY VALINE.
CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
DR EMBL; M84911; G151362; -.
DR PIR; B42902; B42902.
DR PIR; S27602; S27602.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS.
DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU.
KW OXIDOREDUCTASE; NAD.
FT INIT_MET 0 0
FT ACT_SITE 281 281 BY SIMILARITY.
SQ SEQUENCE 496 AA; 53532 MW; 4D33C45B CRC32;

Query Match 88.7%; Score 47; DB 6; Length 496;
Best Local Similarity 66.7%; Pred. No. 8.61e+00;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 67 rvlmry 72
   1:||||
Qy 1 RILLY 6

RESULT 8
ID HA1Q_MOUSE STANDARD; PRT; 328 AA.
AC P14428;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-Q ALPHA CHAIN (FRAGMENT).
GN H2-K.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85206119.
RA MORITA T., DELARBRE C., KRESS M., KOURILSKY P., GACHELIN G.;
RL IMMUNOGENETICS 21:367-383(1985).

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CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 DR EMBL; M14827; G387471; -.  
 DR HSP; P01901; IYAA.  
 DR PROSITE; PS00290; IG\_MHC.  
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN.  
 FT NON\_TER 1  
 FT DOMAIN <1 71  
 FT DOMAIN 72 163  
 FT DOMAIN 164 255  
 FT DOMAIN 256 265  
 FT DOMAIN 266 289  
 FT TRANSMEM 290 328  
 FT DOMAIN 329 338  
 FT CYTOPLASMIC TAIL.  
 FT DISULFID 82 145  
 FT DISULFID 184 240  
 FT CARBOHYD 67 67  
 FT CARBOHYD 157 157  
 FT POTENTIAL.  
 SQ SEQUENCE 328 AA; 36855 MW; 3845B867 CRC32;

Query Match 86.8%; Score 46; DB 4; Length 328;

Best Local Similarity 83.3%; Pred. No. 1.39e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 60 rllly 65

QY 1 rllly 6

RESULT 9  
 ID 1B20\_HUMAN STANDARD; PRT; 338 AA.  
 AC P30467;  
 DT 01-APR-1993 (REL. 25, CREATED)  
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)  
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)  
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B\*2707 ALPHA CHAIN  
 DE (B27-HS).  
 GN HLAB.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 91268545.  
 RA CHOO Y.S., FAN L.A., HANSEN J.A.;  
 RL J. IMMUNOL. 147:174-180(1991).  
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 DR EMBL; M62852; G187761; -.  
 DR HSP; P03989; ILSA.  
 DR MIM; I42830; -.  
 DR PROSITE; PS00290; IG\_MHC.  
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN.  
 FT DOMAIN 1 90  
 FT DOMAIN 91 182  
 FT DOMAIN 183 274  
 FT DOMAIN 275 284  
 FT TRANSMEM 285 308  
 FT DOMAIN 309 338  
 FT CYTOPLASMIC TAIL.  
 FT CARBOHYD 86 86  
 FT DISULFID 101 164  
 FT DISULFID 203 259  
 FT BY SIMILARITY.  
 SQ SEQUENCE 338 AA; 37804 MW; 33FB8134 CRC32;

Query Match 86.8%; Score 46; DB 1; Length 338;

Best Local Similarity 83.3%; Pred. No. 1.39e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 79 rllly 84

QY 1 rllly 6

QY 1 rllly 6  
 RESULT 10  
 ID PPI2\_TRYBB STANDARD; PRT; 346 AA.  
 AC P23734;  
 DT 01-NOV-1991 (REL. 20, CREATED)  
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
 DE SERINE/THREONINE PROTEIN PHOSPHATASE PPI(5.9) (EC 3.1.3.16).  
 OS TRYPAPOSOMA BRUCEI BRUCEI.  
 OC EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; MASTIGOPHORA; KINETOPLASTIDA;  
 CC TRYPAPOSOMATIDAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 90384806.  
 RA EVERS R., CORNELISSEN A.W.C.A.;  
 RL NUCLEIC ACIDS RES. 18:5089-5095(1990).  
 CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O -> A PROTEIN +  
 CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).  
 CC -!- TRYPAPOSOMA BRUCEI CONTAINS TWO PPI GENES WHICH ARE HIGHLY  
 CC SIMILAR.  
 CC -!- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-1  
 CC SUBFAMILY.  
 DR EMBL; X52746; G10509; -.  
 DR PROSITE; PS00125; SER\_THR\_PHOSPHATASE.  
 KW HYDROLASE; IRON; MANGANESE; MULTIGENE FAMILY.  
 FT METAL 102 102  
 FT METAL 104 104  
 FT METAL 130 130  
 FT METAL 162 162  
 FT ACT\_SITE 163 163  
 FT METAL 211 211  
 FT METAL 287 287  
 SQ SEQUENCE 346 AA; 39294 MW; 0276BED5 CRC32;  
 Query Match 86.8%; Score 46; DB 7; Length 346;  
 Best Local Similarity 83.3%; Pred. No. 1.39e+01;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 339 rllly 344

QY 1 rllly 6

RESULT 11  
 ID 1B14\_HUMAN STANDARD; PRT; 361 AA.  
 AC P03989;  
 DT 23-OCT-1986 (REL. 02, CREATED)  
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)  
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)  
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 ALPHA CHAIN PRECURSOR.  
 GN HLAB.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 86138405.  
 RA WEISS E.H., KUON W., DOERNER C., LANG M., RIETHMUELLER G.;  
 RL IMMUNOBIOLOGY 170:367-380(1985).  
 RN [2]  
 RP SEQUENCE OF 25-361 FROM N.A.  
 RX MEDLINE; 86149317.  
 RA SZOETS H., RIETHMUELLER G., WEISS E., MEO T.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 83:1428-1432(1986).  
 RN [3]  
 RP SEQUENCE OF 25-295.  
 RX MEDLINE; 85226361.  
 RA EZQUERRA A., BRAGADO R., VEGA M.A., STROMINGER J.L., WOODY J.,  
 RA LOPEZ DE CASTRO J.A.;  
 RL BIOCHEMISTRY 24:1733-1741(1985).  
 RN [4]

RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 25-300.  
 RX MEDLINE; 92405152.  
 RA MADDEN D.R., GORGA J.C., STROMINGER J.L., WILEY D.C.;  
 RL CELL 70:1035-1048(1992).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY.  
 RX MEDLINE; 92018187.  
 RA MADDEN D.R., GORGA J.C., STROMINGER J.L., WILEY D.C.;  
 RL NATURE 353:321-325(1991).  
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 CC -!- DISEASE: THIS PROTEIN CORRELATES WITH THE DEVELOPMENT OF  
 CC ANKYLOSING SPONDYLITIS.  
 DR EMBL; X03945; G32177; ALT\_TERM.  
 DR PIR; A25128; HLH02.  
 DR PIR; S07441; S07441.  
 DR PDB; 1HSA; 15-OCT-92.  
 DR PDB; 1HSA; 15-OCT-92.  
 DR PDB; 1HSA; 15-OCT-92.  
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.  
 FT SIGNAL 1 24  
 FT CHAIN 25 361 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 FT ALPHA CHAIN B-27.  
 FT DOMAIN 25 114  
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.  
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.  
 FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.  
 FT TRANSMEM 309 332 CONNECTING PEPTIDE.  
 FT DOMAIN 333 361 CYTOPLASMIC TAIL.  
 FT CARBOHYD 110 110  
 FT DISULFID 125 188  
 FT DISULFID 227 283  
 FT CONFLICT 206 206  
 FT CONFLICT 266 266  
 FT STRAND 27 38  
 FT TURN 39 41  
 FT STRAND 42 52  
 FT TURN 53 54  
 FT STRAND 55 61  
 FT TURN 62 63  
 FT STRAND 70 71  
 FT HELIX 74 76  
 FT TURN 77 78  
 FT TURN 81 108  
 FT TURN 109 110  
 FT TURN 113 114  
 FT STRAND 118 127  
 FT TURN 129 130  
 FT STRAND 133 142  
 FT TURN 143 144  
 FT STRAND 145 150  
 FT TURN 152 153  
 FT STRAND 157 159  
 FT HELIX 162 173  
 FT TURN 174 175  
 FT HELIX 176 185  
 FT TURN 186 186  
 FT TURN 187 187  
 FT TURN 189 199  
 FT HELIX 200 203  
 FT TURN 204 204  
 FT STRAND 207 207  
 FT STRAND 210 217  
 FT STRAND 222 233  
 FT STRAND 238 243  
 FT TURN 244 245  
 FT STRAND 246 247  
 FT HELIX 249 251  
 FT STRAND 253 254  
 FT STRAND 258 259  
 FT STRAND 265 274

FT TURN 275 276  
 FT HELIX 278 280  
 FT STRAND 281 286  
 FT TURN 288 289  
 FT STRAND 294 296  
 SQ SEQUENCE 361 AA; 40464 MW; 802130D5 CRC32;  
 Query Match 86.8%; Score 46; DB 1; Length 361;  
 Best Local Similarity 83.3%; Pred. No. 1.39e+01;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Db 103 rllly 108  
 QY 1 RLLRY 6  
 RESULT 12  
 ID HA13\_MOUSE STANDARD; PRT; 362 AA.  
 AC P14426;  
 DT 01-JAN-1990 (REL. 13, CREATED)  
 DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
 DE H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, D-K ALPHA CHAIN PRECURSOR.  
 GN H2-D.  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C3H;  
 RX MEDLINE; 88060499.  
 RA WATTS S., VOGEL J.M., HARRIMAN W.D., ITOH T., STAUSS H.J.,  
 RA GOODENOW R.S.;  
 RL J. IMMUNOL. 139:3878-3885(1987).  
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 CC EMBL; M18524; G387453; -.  
 DR HSP; P01901; 1VAA.  
 DR PROSITE; PS00290; IG\_MHC.  
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 24  
 FT CHAIN 25 362 H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 FT D-K ALPHA CHAIN.  
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.  
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.  
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.  
 FT TRANSMEM 307 333 CONNECTING PEPTIDE.  
 FT DOMAIN 334 362 CYTOPLASMIC TAIL.  
 FT DISULFID 125 188 BY SIMILARITY.  
 FT DISULFID 227 283 BY SIMILARITY.  
 FT CARBOHYD 110 110 POTENTIAL.  
 FT CARBOHYD 200 200 POTENTIAL.  
 FT CARBOHYD 280 280 POTENTIAL.  
 SQ SEQUENCE 362 AA; 40620 MW; 7A34877E CRC32;  
 Query Match 86.8%; Score 46; DB 4; Length 362;  
 Best Local Similarity 83.3%; Pred. No. 1.39e+01;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Db 103 rllly 108  
 QY 1 RLLRY 6  
 RESULT 13  
 ID 1B18 HUMAN STANDARD; PRT; 362 AA.  
 AC P10318;  
 DT 01-MAR-1989 (REL. 10, CREATED)  
 DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)

DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B\*2705 ALPHA CHAIN  
 DE PRECURSOR (B-27w) (B27.1).  
 GN HLAB.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 86220133.  
 RA SEMMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;  
 RL EMBO J. 5:547-552(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 86138405.  
 RA WEISS E.H., KUON W., DOERNER C., LANG M., RIETHMUELLER G.;  
 RL IMMUNOBIOLOGY 170:367-380(1985).  
 RN [3]  
 RP 3D-STRUCTURE MODELLING OF 115-206.  
 RA ROGNAN D., SCAPOZZA L., FOLKERS G., DASER A.;  
 RL SUBMITTED (JUL-1994) TO THE PDB DATA BANK.  
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 CC EMBL; X03665; G871297;  
 DR EMBL; X03666; G871297; JOINED.  
 DR EMBL; M12967; G187660;  
 DR PIR; A25092; HLHUBW.  
 DR PDB; 1ROG; 30-SEP-94.  
 DR PDB; 1ROH; 30-SEP-94.  
 DR PDB; 1ROI; 30-SEP-94.  
 DR PDB; 1ROJ; 30-SEP-94.  
 DR PDB; 1ROK; 30-SEP-94.  
 DR PDB; 1ROL; 30-SEP-94.  
 DR MIM; 142830;  
 DR PROSITE; PS00290; IG\_MHC.  
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.  
 FT SIGNAL 1 24  
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 FT DOMAIN 25 114 ALPHA CHAIN B-27 B\*2705.  
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.  
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.  
 FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.  
 FT TRANSMEM 309 332 CONNECTING PEPTIDE.  
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.  
 FT CARBOHYD 110 110 BY SIMILARITY.  
 FT DISULFID 125 188 BY SIMILARITY.  
 FT DISULFID 227 283 BY SIMILARITY.  
 SQ SEQUENCE 362 AA; 40428 MW; 73243566 CRC32;  
 Query Match 86.8%; Score 46; DB 1; Length 362;  
 Best Local Similarity 83.3%; Pred. No. 1.39e+01;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Db 103 rtfly 108  
 QY 1 RILLY 6  
 RESULT 14  
 ID 1B45\_HUMAN STANDARD; PRT; 362 AA.  
 AC P30485;  
 DT 01-APR-1993 (REL. 25, CREATED)  
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)  
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)  
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-47 B\*4701 ALPHA CHAIN  
 DE PRECURSOR.  
 GN HLAB.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE; 88152906.  
 RA ZEMMOUR J., ENNIS P.D., PARHAM P., DUPONT B.;  
 RL IMMUNOGENETICS 27:281-287(1988).  
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 CC EMBL; M19756; G386776;  
 DR HSSP; P03989; LISA.  
 DR MIM; 142830;  
 DR PROSITE; PS00290; IG\_MHC.  
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 24  
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 FT DOMAIN 25 114 ALPHA CHAIN BW-47 B\*4701.  
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.  
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.  
 FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.  
 FT TRANSMEM 310 333 CONNECTING PEPTIDE.  
 FT DOMAIN 334 362 CYTOPLASMIC TAIL.  
 FT CARBOHYD 110 110 BY SIMILARITY.  
 FT DISULFID 125 188 BY SIMILARITY.  
 FT DISULFID 227 283 BY SIMILARITY.  
 SQ SEQUENCE 362 AA; 40571 MW; 67734C1E CRC32;  
 Query Match 86.8%; Score 46; DB 1; Length 362;  
 Best Local Similarity 83.3%; Pred. No. 1.39e+01;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Db 103 rtfly 108  
 QY 1 RILLY 6  
 RESULT 15  
 ID 1B16\_HUMAN STANDARD; PRT; 362 AA.  
 AC P19373;  
 DT 01-NOV-1990 (REL. 16, CREATED)  
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B\*2703 ALPHA CHAIN  
 DE PRECURSOR (B-27D).  
 GN HLAB.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 88227491.  
 RA CHOO S.Y., ST JOHN T., ORR H.T., HANSEN J.A.;  
 RL HUM. IMMUNOL. 21:209-219(1988).  
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 CC EMBL; M54883; G187664;  
 DR HSSP; P03989; LISA.  
 DR MIM; 142830;  
 DR PROSITE; PS00290; IG\_MHC.  
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 24  
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 FT DOMAIN 25 114 ALPHA CHAIN B-27 B\*2703.  
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.  
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.  
 FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.  
 FT TRANSMEM 309 332 CONNECTING PEPTIDE.  
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.  
 FT CARBOHYD 110 110 BY SIMILARITY.  
 FT DISULFID 125 188 BY SIMILARITY.

FT DISULFID 227 283 BY SIMILARITY.  
SQ SEQUENCE 362 AA; 40402 MW; 7261C3AB CRC32;  
Query Match 86.8%; Score 46; DB 1; Length 362;  
Best Local Similarity 83.3%; Pred. No. 1.39e+01;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 103 rllry 108  
| | | | |  
QY 1 RLLRY 6

Search completed: Thu May 22 08:28:09 1997  
Job time : 11 secs.

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PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 CC I MHC HLA-B\*2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 79.2%; Score 42; DB 16; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 2.15e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 YRLAIR 6  
 ||| ||  
 QY 1 YRLAIR 6

RESULT 9  
 ID R92911 standard; peptide; 20 AA.  
 AC R92911;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B\*2702 CTL modulating peptide (B2702.84-75/84-75).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B\*2702.  
 OS Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI: 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B\*5-84 MHC antigen of the recipient  
 PT host

PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC  
 CC HLA-B\*2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 79.2%; Score 42; DB 16; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 2.15e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 YRLAIR 6  
 ||| ||  
 QY 1 YRLAIR 6

Search completed: Thu May 22 08:45:21 1997  
 Job time : 10 secs.

DR WPI; 95-194027/25.  
 CC Compens. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 12; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B2702 84-75-84 palindrome. These sequences can be used to isolate  
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
 CC protein associated with T-cell activation in mammalian T-cells, and is  
 CC also immunologically cross reactive with the heat shock protein Hsc70.  
 CC p74 is found in a limited number of cell types, but is particularly  
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
 CC cell with an amphoteric detergent, and then passed through an affinity  
 CC column containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B2702-60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 20 AA;

Query Match 79.2%; Score 42; DB 18; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 2.15e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 yrlair 6  
 ||| ||  
 QY 1 YRLAIR 6

RESULT 6  
 ID R95430 standard; peptide; 20 AA.  
 AC R95430;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B2702 84-75/75-84T palindrome.  
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytotoxic; antigen presenting cell.  
 OS Synthetic.  
 PN WO9513298-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI; 95-194027/25.

CC Compens. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 12; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B2702 84-75/75-84T palindrome. These sequences can be used to  
 CC isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface  
 CC membrane protein associated with T-cell activation in mammalian T-cells,  
 CC and is also immunologically cross reactive with the heat shock protein  
 CC Hsc70. p74 is found in a limited number of cell types, but is  
 CC particularly expressed on B and T cells. p74 can be isolated by lysis of  
 CC a suitable cell with an amphoteric detergent, and then passed through an  
 CC affinity column containing a covalently bound HLA-B2702 palindromic  
 CC peptide. Compositions comprising the extracellular fragment of p74  
 CC combined with HLA-B2702-60-84 (see R95416), induces calcium influx, and  
 CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity.  
 CC Candidate compounds can be screened for their effect on the cytolytic  
 CC activity of T-cells, by combining them with the extracellular portion of  
 CC p74 and determining the amount of binding between the candidate compound  
 CC and p74. Modulation of CTL activity can be inhibited in a cellular  
 CC composition containing T-cells and antigen presenting cells (APCs), by

CC adding to the mix the extracellular portion of p74, in an amount  
 CC sufficient to compete with p74 for the binding of the p74 ligand.  
 SQ Sequence 20 AA;

Query Match 79.2%; Score 42; DB 18; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 2.15e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 yrlair 6  
 ||| ||  
 QY 1 YRLAIR 6

RESULT 7  
 ID R92907 standard; peptide; 20 AA.  
 AC R92907;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW Class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN WO9526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 CC I MHC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 79.2%; Score 42; DB 16; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 2.15e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 yrlair 6  
 ||| ||  
 QY 1 YRLAIR 6

RESULT 8  
 ID R92909 standard; peptide; 20 AA.  
 AC R92909;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW Class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN WO9526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient

PA (DOHE-) DOHENY EYE INST.  
 PI Suzuki S;  
 DR WPI; 96-068873/07.  
 DR N-PSDB; T03617.  
 PT Polynucleotide(s) encoding human protocadherins pc3 and pc4 and rat  
 pc5 - involved in cell-cell adhesion and regulation activities  
 PS Example 2; Page 67-68; 146pp; English.  
 CC R87142-R87144 represent partial fragments of the drosophila protocadherin  
 CC sequence. The cDNAs encoding these sequences were isolated after  
 CC screening a drosophila whole body cDNA preparation with the primers shown  
 CC in R03575 and T03576. The primers were constructed from portions of the  
 CC amino acid sequences of the third and fourth extracellular domains of  
 CC published cadherin sequences. The cytoplasmic domain of cadherin  
 CC interacts with the cytoskeleton through catenins and other cytoskeleton  
 CC associated proteins. The cytoplasmic domain is not present in all  
 CC cadherins, but in those which possess it, it is essential for the  
 CC cadherins adhesive function. The cadherins which do not possess a  
 CC cytoplasmic domain appear to function via a different method from those  
 CC with a cytoplasmic domain. These protein sequences are involved in  
 CC cell-cell adhesion. These sequences may have regulatory functions in the  
 CC cell, as well as the cell-cell adhesive properties. Antibodies produced  
 CC against these sequences are useful for modulating the binding activity of  
 CC these protocadherins, and can be used therapeutically.  
 SQ Sequence 43 AA;

Query Match 86.8%; Score 46; DB 17; Length 43;  
 Best Local Similarity 83.3%; Pred. No. 7.66e+01;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 11 YRLVIR 16  
 |||||  
 QY 1 YRLLIIR 6

RESULT 3  
 ID R61548 standard; peptide; 10 AA.

DE Peptide fragment (1.0914) of HPV binds HLA-A2.1.  
 DE HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;  
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;  
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;  
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;  
 KW diagnostic; MHC class I molecule; major histocompatibility complex;  
 KW HLA-A2.1; Smer; 10mer; anchor; human leukocyte antigen.  
 OS Human papilloma virus strain 18.  
 PN W09420127-A.

PD 15-SEP-1994.

PF 04-MAR-1994; U02353.

PR 05-MAR-1993; US-027146.

PR 04-JUN-1993; US-073205.

PR 29-NOV-1993; US-159184.

PA (CYTEL) CYTEL CORP.

PI Grey HM, Kast WM, Sette A, Sidney J;

DR WPI; 94-302678/37.

PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used  
 PT for treatment or prophylaxis of cancer, virus infection or  
 PT autoimmune diseases.

PS Example 5; Page 109; 138pp; English.

CC R59496-R61666 are immunogenic 10mer peptides that contain a HLA-A2.1  
 CC binding motif. These peptides bind HLA-A2.1 and have a binding  
 CC affinity of at least 1% as compared to a reference peptide (R71293).  
 CC R61548 has an IC50 of 0.0036 and the sequence occurs at position 24  
 CC in the HPV E6 protein. The peptides of the invention can induce  
 CC cytotoxic T lymphocytes which can react with target cells. They can  
 CC be used for the treatment or prophylaxis of cancer, eg. prostate  
 CC cancer or lymphoma, etc.  
 SQ Sequence 10 AA;

Query Match 81.1%; Score 43; DB 11; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 1.66e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 3 YRLIIR 8  
 |||||  
 QY 1 YRLLIIR 6

RESULT 4

ID R95429 standard; peptide; 12 AA.

AC R95429;

DT 12-NOV-1996 (first entry)

DE HLA-B2702 84-79-84 palindromic.

KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.

PN W09513288-A1.

PD 18-MAY-1995.

PF 10-NOV-1994; U12985.

PR 10-NOV-1993; US-150493.

PI (STRD) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM;

DR WPI; 95-194027/25.

PT Compsns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.

PS Example; Page 12; 29pp; English.

CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the

CC HLA-B2702 84-79-84 palindromic. These sequences can be used to isolate  
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
 CC protein associated with T-cell activation in mammalian T-cells, and is  
 CC also immunologically cross reactive with the heat shock protein Hsc70.  
 CC p74 is found in a limited number of cell types, but is particularly  
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
 CC cell with an amphoteric detergent, and then passed through an affinity  
 CC column containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 12 AA;

Query Match 79.2%; Score 42; DB 18; Length 12;

Best Local Similarity 83.3%; Pred. No. 2.15e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 YRLIIR 6  
 |||||  
 QY 1 YRLLIIR 6

RESULT 5

ID R95428 standard; peptide; 20 AA.

AC R95428;

DT 12-NOV-1996 (first entry)

DE HLA-B2702 84-75-84 palindromic.

KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.

PN W09513288-A1.

PD 18-MAY-1995.

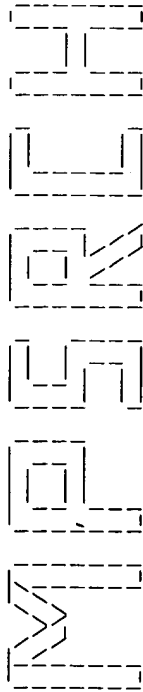
PF 10-NOV-1994; U12985.

PR 10-NOV-1993; US-150493.

PI (STRD) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM;

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:45:11 1997; MasPar time 1.73 Seconds  
Tabular output not generated. 37.783 Million cell updates/sec

Title: >US-08-653-294-6  
Description: (1-6) from US08653294.pep  
Perfect Score: 53  
Sequence: 1 YRLLR 6

Scoring table: GAP 150  
PAM 15  
Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Maximum DB seq length 60

Database: a-geneseq26  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19

Statistics: Mean 16.490; Variance 45.535; scale 0.362

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	46	86.8	43 11	R58902	Drosophila-12 cadher	7.66e+01
2	46	86.8	43 17	R87142	Protocadherin clone D	7.66e+01
3	43	81.1	10 11	R61548	Peptide fragment (1.0	1.66e+02
4	42	79.2	12 18	R95429	HLA-B*2702 84-79-84 pa	2.15e+02
5	42	79.2	20 18	R95428	HLA-B*2702 84-75-84 pa	2.15e+02
6	42	79.2	20 18	R95430	HLA-B*2702 84-75T/75-8	2.15e+02
7	42	79.2	20 16	R92907	HLA-B*2702 CTL modul	2.15e+02
8	42	79.2	20 16	R92909	HLA-B*2702 CTL modul	2.15e+02
9	42	79.2	20 16	R92911	HLA-B*2702 CTL modul	2.15e+02

Note: Post-processor removed 36 summaries from list due to search parameters chosen.

#### ALIGNMENTS

RESULT 1  
ID R58902 standard; Protein; 43 AA.  
AC R58902;  
DT 17-APR-1995 (first entry)

DE Drosophila-12 cadherin-related molecule.  
KW Cadherin; cell adhesion molecule.  
OS Drosophila.  
PN WO9414960-A.  
PD 07-JUL-1994.  
PF 23-DEC-1993; U12588.  
PR 29-DEC-1992; US-998003.  
PA (DOHE-) DOHENY EYE INST.  
PI Suzuki S.  
DR WPI; 94-293849/36.  
DR N-PSDB; Q68993.  
PT Polynucleotide sequences encoding new proto:cadherins - useful  
for modulating natural binding and regulating activities.  
PS Example; Page 63; 114pp; English.  
CC Two regions of conserved AA sequence, one from the middle of the  
third cadherin extracellular subdomain (EC-3) and the other from the  
C-terminus of the fourth extracellular subdomain (EC-4) were  
identified. The corresp. degenerate oligos (Q68949, Q68950) were  
designed for use as PCR primers. PCR was carried out on a rat brain  
cDNA prep. Two major bands of about 450 bps and 130 bps were found.  
CC The 450 bp band corresponded to the expected length between the two  
primer sites, but the 130 bp band could not be predicted from any  
of the previously identified cadherin sequences. The 450 bp and 130  
bp bands were extracted and sequenced. Nineteen novel partial CDNA  
clones were isolated. The DNA and deduced AA sequences of the  
clones (including sequences corresp. to the PCR primers) are given  
in Q68951-Q68959 and R58860-R58878. Various cDNA fragments  
structurally similar to the rat cDNAs were isolated from human,  
mouse and Xenopus brain cDNA preps. by PCR using the above primers.  
CC C. elegans whole body cDNA preps. by PCR using the above primers.  
CC The DNA and deduced AA sequences of the resulting PCR fragments  
(including sequences corresp. to the PCR primers) are given in  
Q68971, Q68972-Q68994 and R58882-R58905 and R49143. Comparison  
of the deduced AA sequences indicates a similarity, in particular,  
CC there are three sets of clones that appear to be cross-species  
homologues: RAT-218, MOUSE-322 and HUMAN-43; RAT-314, MOUSE-321 and  
CC HUMAN-11; and MOUSE-326 and HUMAN-42.  
CC Sequence 43 AA;  
SQ

Query Match 86.8%; Score 46; DB 11; Length 43;  
Best Local Similarity 83.3%; Pred. No. 7.66e+01;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 11 yr1vir 16  
| | | | |  
Qy 1 YRLLR 6

RESULT 2  
ID R87142 standard; Peptide; 43 AA.  
AC R87142;  
DT 29-AUG-1996 (first entry)  
DE Protocadherin clone DROSOPHILA-12.  
KW Protocadherin; pc3; pc4; pc5; human; rat; cadherin; cell adhesion; mouse;  
KW catenin; therapy; clone; frog; fruit fly.  
OS Drosophila melanogaster.  
FH Key Location/Qualifiers  
FT Misc\_difference 38  
FT /note= "encoded by CGA"  
FT Misc\_difference 39  
FT /note= "encoded by ATG"  
FT Misc\_difference 40  
FT /note= "encoded by ACA"  
FT Misc\_difference 41  
FT /note= "encoded by ATG"  
FT Misc\_difference 42  
FT /note= "encoded by CGC"  
FT Misc\_difference 43  
FT /note= "encoded by CGC"  
PN WO9600289-A1.  
PD 04-JAN-1996.  
PF 26-JUN-1995; U08071.  
PR 27-JUN-1994; US-268161.

\*\*\*\*\*

W O R L D

(TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:26:43 1997; MasPar time 2.78 Seconds  
Tabular output not generated. 61.517 Million cell updates/sec

Title: >US-08-653-294-4  
Description: (1-6) from US08653294.pep  
Perfect Score: 49  
Sequence: 1 RIALRY 6

Scoring table: PAM 150  
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir50  
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3  
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8  
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 21.604; Variance 27.804; scale 0.777

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description	Pred. No.
1	49	100.0	273 13	I38509 MHC class I histocompat	3.39e+00
2	49	100.0	274 2	HLHU32 MHC class I histocom	3.39e+00
3	49	100.0	274 13	I54463 MHC HLA-B*38 chain -	3.39e+00
4	49	100.0	354 13	I59308 class I histocompati	3.39e+00
5	49	100.0	354 13	I80168 class I histocompati	3.39e+00
6	49	100.0	354 13	I80167 class I histocompati	3.39e+00
7	49	100.0	355 13	I80171 class I histocompati	3.39e+00
8	49	100.0	355 13	I80169 class I histocompati	3.39e+00
9	49	100.0	359 2	HLHU12 MHC class I histocom	3.39e+00
10	49	100.0	362 13	I62045 gene HLA B-1517 prot	3.39e+00
11	49	100.0	362 13	I59633 MHC HLA-B transmembr	3.39e+00
12	49	100.0	362 13	I37521 HLA-B*57.2 antigen -	3.39e+00
13	49	100.0	362 13	I84486 transmembrane glycop	3.39e+00
14	49	100.0	362 13	I84490 lymphocyte antigen -	3.39e+00
15	49	100.0	362 6	A45834 MHC class I histocom	3.39e+00
16	49	100.0	362 2	HLHUB8 MHC class I histocom	3.39e+00
17	49	100.0	362 6	B30345 MHC class I histocom	3.39e+00
18	49	100.0	362 6	JH0541 class I histocompati	3.39e+00
19	49	100.0	362 6	JH0540 class I histocompati	3.39e+00
20	49	100.0	362 6	A30345 MHC class I histocom	3.39e+00
21	49	100.0	362 6	S24434 class I histocompati	3.39e+00

22	49	100.0	362 6	JH0539 class I histocompati	3.39e+00
23	49	100.0	362 13	I37120 MHC class I HLA-B*51	3.39e+00
24	49	100.0	363 16	S07113 class I histocompati	3.39e+00
25	49	100.0	363 13	I36957 MHC CH1A chain - chi	3.39e+00
26	49	100.0	363 6	S03537 class I histocompati	3.39e+00
27	49	100.0	364 6	D35997 MHC class I histocom	3.39e+00
28	49	100.0	364 6	A35997 MHC class I histocom	3.39e+00
29	49	100.0	365 13	I54493 HLA-A protein - huma	3.39e+00
30	49	100.0	365 6	JH0537 class I histocompati	3.39e+00
31	49	100.0	365 13	I54416 HLA-AW24 protein - h	3.39e+00
32	46	93.9	161 14	I48932 adenosine receptor s	1.34e+01
33	46	93.9	409 14	I48095 A2 adenosine recepto	1.34e+01
34	46	93.9	410 14	A48974 adenosine receptor A	1.34e+01
35	46	93.9	412 13	A48978 adenosine A2 recepto	1.34e+01
36	46	93.9	412 16	JC4844 adenosine receptor A	1.34e+01
37	46	93.9	412 13	S37160 adenosine receptor A	1.34e+01
38	46	93.9	412 13	D30341 G protein-coupled re	1.34e+01
39	46	93.9	505 16	S61307 membrane-bound nitr	1.34e+01
40	46	93.9	652 11	S52683 probable membrane pr	1.34e+01
41	46	93.9	1220 12	S64916 apolipoprotein(a) (E	1.34e+01
42	46	93.9	1420 5	A32869 COX10 protein precu	2.09e+01
43	45	91.8	482 2	COBY10 DNA-directed RNA pol	2.09e+01
44	45	91.8	880 5	S04717 pyrimidine synthesis	2.09e+01
45	45	91.8	2225 2	A23443	

ALIGNMENTS

RESULT 1  
ENTRY I38509 #type fragment  
TITLE MHC class I histocompatibility antigen - human (fragment)  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 06-Sep-1996  
ACCESSIONS I38509  
REFERENCE I38509  
#authors Cereb, N.; Choi, J.W.; Riu, K.Z.; Yang, S.Y.  
#journal Tissue Antigens (1994) 44:271-273  
#title HLA-B\*5105: a newly identified B51 IEF variant.  
#cross-references MIM:95176331  
#accession I38509  
#status preliminary; translated from GB/EMBL/DBBJ  
#molecule\_type mRNA  
#residues 1-273 #label RES  
#cross-references EMBL:U06697; NID:g469544; CDS\_PID:g469545  
GENETICS  
#note gene name HLA-B  
SUMMARY #length 273 #checksum 6533

Query Match 100.0%; Score 49; DB 13; Length 273;  
Best Local Similarity 100.0%; Pred. No. 3.39e+00;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 78 rialry 83  
Qy 1 RIALRY 6

RESULT 2  
ENTRY HLHU32 #type fragment  
TITLE MHC class I histocompatibility antigen HLA-A32 alpha chain - human (fragment)  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 06-Sep-1996  
ACCESSIONS A26088  
REFERENCE A26088  
#authors Wan, A.M.; Ennis, P.; Parham, P.; Holmes, N.  
#journal J. Immunol. (1986) 137:3671-3674  
#title The primary structure of HLA-A32 suggests a region involved in formation of the Bw4/Bw6 epitopes.  
#cross-references MIM:87058961  
#accession A26088

SUMMARY	#length 354 #checksum 3211
Query Match	100.0%; Score 49; DB 13; Length 354;
Best Local Similarity	100.0%; Pred. No. 3.39e+00;
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	95 rialry 100 
QY	1 RIALRY 6
RESULT	5
ENTRY	I80168      #type fragment
TITLE	class I histocompatibility antigen - chimpanzee (fragment)
ORGANISM	#formal_name Pan troglodytes #common_name chimpanzee
DATE	24-May-1996 #sequence_revision 24-May-1996 #text_change
ACCESSIONS	24-May-1996
REFERENCE	I80168
#authors	McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkins, D.I.
#journal	Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title	A uniquely high level of recombination at the HLA-B locus.
#cross-references	EMBL:U05578
#accession	I80168
#status	preliminary; translated from GB/EMBL/DDBBJ
#molecule_type	mRNA
#residues	1-354 ##label RES
#cross-references	EMBL:U05579; NID:g454775; CDS_PID:g454776
SUMMARY	#length 354 #checksum 5087
Query Match	100.0%; Score 49; DB 13; Length 354;
Best Local Similarity	100.0%; Pred. No. 3.39e+00;
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	95 rialry 100 
QY	1 RIALRY 6
RESULT	6
ENTRY	I80167      #type fragment
TITLE	class I histocompatibility antigen - pygmy chimpanzee (fragment)
ORGANISM	#formal_name Pan paniscus #common_name pygmy chimpanzee,
DATE	Bonobo
ACCESSIONS	24-May-1996 #sequence_revision 24-May-1996 #text_change
REFERENCE	I80167
#authors	McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkins, D.I.
#journal	Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title	A uniquely high level of recombination at the HLA-B locus.
#cross-references	EMBL:U05578; NID:g454773; CDS_PID:g454774
#accession	I80167
#status	Preliminary; translated from GB/EMBL/DDBBJ
#molecule_type	mRNA
#residues	1-354 ##label RES
#cross-references	EMBL:U05578; NID:g454773; CDS_PID:g454774
SUMMARY	#length 354 #checksum 3983
Query Match	100.0%; Score 49; DB 13; Length 354;
Best Local Similarity	100.0%; Pred. No. 3.39e+00;
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	95 rialry 100 
QY	1 RIALRY 6
RESULT	7
ENTRY	I80171      #type fragment

```

TITLE      class I histocompatibility antigen - chimpanzee (fragment)
ORGANISM   #formal_name Pan troglodytes #common_name chimpanzee
DATE       24-May-1996 #sequence_revision 24-May-1996 #text_change
24-May-1996

ACCESSIONS I80171
REFERENCE   159308
AUTHORS    McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
            A.L.; Bontrop, R.E.; Watkins, D.I.
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
TITLE      A uniquely high level of recombination at the HLA-B locus.
CROSS-REFERENCES MUID:9428654
ACCESSION  I80171
STATUS     preliminary; translated from GB/EMBL/DBDJ
MOLECULE   1-355 #label RES
RESIDUES   #cross-references EMBL:U05582; NID:9454781; CDS_PID:9454782
SUMMARY    #length 355 #checksum 6021

Query Match 100.0%; Score 49; DB 13; Length 355;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 95 rialry 100
    |||||
QY 1 RIALRY 6

RESULT 8
ENTRY   class I histocompatibility antigen - chimpanzee (fragment)
TITLE   #formal_name Pan troglodytes #common_name chimpanzee
ORGANISM
DATE    24-May-1996 #sequence_revision 24-May-1996 #text_change
24-May-1996

ACCESSIONS I80169
REFERENCE   159308
AUTHORS    McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
            A.L.; Bontrop, R.E.; Watkins, D.I.
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
TITLE      A uniquely high level of recombination at the HLA-B locus.
CROSS-REFERENCES MUID:9428654
ACCESSION  I80169
STATUS     preliminary; translated from GB/EMBL/DBDJ
MOLECULE   1-355 #label RES
RESIDUES   #cross-references EMBL:U05580; NID:9454777; CDS_PID:9454778
SUMMARY    #length 355 #checksum 4603

Query Match 100.0%; Score 49; DB 13; Length 355;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 95 rialry 100
    |||||
QY 1 RIALRY 6

RESULT 9
ENTRY   MHC class I histocompatibility antigen HLA alpha chain
TITLE   precursor (clone pHLA 12.4) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change
15-Jun-1996

ACCESSIONS A02189
REFERENCE   A02189
AUTHORS    Malissen, M.; Malissen, B.; Jordan, B.R.
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. (1982) 79:893-897
TITLE      Exon/intron organization and complete nucleotide sequence of
            an HLA gene.
CROSS-REFERENCES MUID:82151002
ACCESSION  A02189
MOLECULE   1-359 #label MAL
RESIDUES

```

```

COMMENT    The seven exons correspond approximately to the domain structure of
            this chain.

GENETICS   #map-position 6p21.3
            #introns 22/1; 112/1; 204/1; 296/1; 335/1; 346/1
CLASSIFICATION
            #superfamily class I histocompatibility antigen;
            immunoglobulin homology
KEYWORDS    duplication; glycoprotein; heterodimer; transmembrane
            protein; transplantation antigen
FEATURE     #domain signal sequence #status predicted #label SIG\
            #product class I histocompatibility antigen HLA alpha
            chain #status predicted #label MAT\
            #domain extracellular #status predicted #label EXT\
            #domain alpha-1 #label EX1\
            #domain alpha-2 #label EX2\
            #domain immunoglobulin homology #label IMM\
            #domain transmembrane #status predicted #label TMM\
            #domain intracellular #status predicted #label INT\
            #binding site carbohydrate (Asn) (covalent) #status
            predicted\
            #disulfide_bonds #status predicted
            #length 359 #molecular_weight 40548 #checksum 2195
SUMMARY

Query Match 100.0%; Score 49; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 100 rialry 105
    |||||
QY 1 RIALRY 6

RESULT 10
ENTRY   gene HLA B-1517 protein - human
TITLE   #formal_name Homo sapiens #common_name man
ORGANISM
DATE    02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
13-Sep-1996

ACCESSIONS I62045
REFERENCE   I38421
AUTHORS    Hildebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.;
            Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
            Bias, W.B.; Parham, P.
JOURNAL    Tissue Antigens (1994) 43:209-218
TITLE      HLA-B*51: a widespread and diverse family of HLA-B alleles.
CROSS-REFERENCES MUID:94367483
ACCESSION  I62045
STATUS     preliminary; translated from GB/EMBL/DBDJ
MOLECULE   1-362 #label RES
RESIDUES   #cross-references EMBL:U01848; NID:9402676; CDS_PID:9402677
GENETICS
NOTE      gene name HLA B-1517
SUMMARY    #length 362 #molecular_weight 40417 #checksum 7730

Query Match 100.0%; Score 49; DB 13; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108
    |||||
QY 1 RIALRY 6

RESULT 11
ENTRY   MHC HLA-B transmembrane glycoprotein - human
TITLE   #formal_name Homo sapiens #common_name man
ORGANISM
DATE    02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996

ACCESSIONS I59633
REFERENCE   I59633

```

#authors Hildebrand, W.H.; Domena, J.D.; Parham, P.  
 #journal Tissue Antigens (1993) 41:190-195  
 #title Primary structure shows HLA-B59 to be a hybrid of HLA-B55 and HLA-B51, and not a subtype of HLA-B8.  
 #cross-references MUID:193369833

#accession I59633  
 #molecule\_type mRNA  
 #status preliminary; translated from GB/EMBL/DBJ  
 #residues 1-362 #label RES  
 #cross-references GB:L07743; NID:g388314; CDS\_PID:g388315

## GENETICS

#note

SUMMARY  
 gene name HLA-B  
 #length 362 #molecular-weight 40584 #checksum 8821

Query Match 100.0%; Score 49; DB 13; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 3.39e+00;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108  
 |||||  
 Qy 1 RIALRY 6

## RESULT 12

ENTRY I37521 #type complete  
 TITLE HLA-Bw57.2 antigen - human  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 02-Jul-1996  
 ACCESSIONS I37521  
 REFERENCE I37476  
 #authors Madrigal, J.A.; Belich, M.P.; Hildebrand, W.H.; Benjamin, R.J.; Little, A.M.; Zemmour, J.; Ennis, P.D.; Ward, F.E.; Petzl-Erler, M.L.; Du Toit, E.D.; Parham, P.  
 #journal J. Immunol. (1992) 149:3411-3415  
 #title Distinctive HLA-A,B antigens of black populations formed by interallelic conversion.  
 #cross-references MUID:93056508

#accession I37521  
 #status preliminary; translated from GB/EMBL/DBJ  
 #molecule\_type mRNA  
 #residues 1-362 #label RES  
 #cross-references EMBL:X61707; NID:g32186; CDS\_PID:g32187  
 #length 362 #molecular-weight 40342 #checksum 7369

SUMMARY  
 gene name HLA-B  
 #length 362 #molecular-weight 40342 #checksum 7369

Query Match 100.0%; Score 49; DB 13; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 3.39e+00;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108  
 |||||  
 Qy 1 RIALRY 6

## RESULT 13

ENTRY I84486 #type complete  
 TITLE transmembrane glycoprotein - human  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 02-Aug-1996  
 ACCESSIONS I84486  
 REFERENCE I38421  
 #authors Hildebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.; Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.; Blas, W.B.; Parham, P.

#journal Tissue Antigens (1994) 43:209-218  
 #title HLA-B15: a widespread and diverse family of HLA-B alleles.  
 #cross-references MUID:94367483  
 #accession I84486  
 #status preliminary; translated from GB/EMBL/DBJ  
 #molecule\_type mRNA  
 #residues 1-362 #label RES  
 #cross-references GB:L15005; NID:g493154; CDS\_PID:g493155

## GENETICS

#note

SUMMARY  
 gene name HLA-B\*1513  
 #length 362 #molecular-weight 40378 #checksum 9453

Query Match 100.0%; Score 49; DB 13; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 3.39e+00;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108  
 |||||  
 Qy 1 RIALRY 6

## RESULT 14

ENTRY I84490 #type complete  
 TITLE lymphocyte antigen - human  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 02-Aug-1996  
 ACCESSIONS I84490  
 REFERENCE I38518  
 #authors Browning, M.J.; Madrigal, J.A.; Krausa, P.; Kowalski, H.; Allsopp, C.E.; Little, A.M.; Turner, S.; Adams, E.J.; Arnett, K.L.; Bodmer, W.F.; Bodmer, J.G.; Parham, P.  
 #journal Tissue Antigens (1995) 45:177-187  
 #title The HLA-A,B,C genotype of the class I negative cell line Daudi reveals novel HLA-A and -B alleles.  
 #cross-references MUID:95282145

#accession I84490  
 #status preliminary; translated from GB/EMBL/DBJ  
 #molecule\_type mRNA  
 #residues 1-362 #label RES  
 #cross-references GB:L33923; NID:g520836; CDS\_PID:g520837

## GENETICS

#note

SUMMARY  
 gene name HLA-A10-B38  
 #length 362 #molecular-weight 40355 #checksum 8277

Query Match 100.0%; Score 49; DB 13; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 3.39e+00;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108  
 |||||  
 Qy 1 RIALRY 6

## RESULT 15

ENTRY A45834 #type complete  
 TITLE MHC class I histocompatibility antigen HLA-B53 alpha chain precursor - human  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 06-Sep-1996  
 ACCESSIONS A45834  
 REFERENCE A45834  
 #authors Hayashi, H.; Ooba, T.; Nakayama, S.; Sekimata, M.; Kano, K.; Takiguchi, M.

#journal Immunogenetics (1990) 32:195-199  
 #title Allospecificities between HLA-Bw53 and HLA-B35 are generated by substitution of the residues associated with HLA-Bw4/Bw6 public epitopes.  
 #accession A45834  
 #molecule\_type DNA  
 #residues 1-362 #label HAY  
 #cross-references GB:M58636; GB:M33574  
 #note this allele is designated B\*5301

## GENETICS

#gene

GDB:HLA-B  
 #cross-references GDB:120048  
 #map\_position gp21.3-6p21.3  
 CLASSIFICATION #superfamily class I histocompatibility antigen; immunoglobulin homology  
 KEYWORDS heterodimer; transmembrane protein



```

FEATURE
1-24      #domain signal sequence #status predicted #label SIG\
220-285   #domain immunoglobulin homology #label IMM\
110       #binding_site carbohydrate (Asn) (covalent) #status
          predicted
SUMMARY   #length 362 #molecular-weight 40495 #checksum 9558

Query Match      100.0%; Score 49; DB 6; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.39e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108
    |||||
QY 1 RIALRY 6

```

Search completed: Thu May 22 08:27:07 1997  
Job time : 24 secs.

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\*\*\*\*\*  
 W P S R E H  
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 (TM)

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 \*\*\*\*\*

MPSrch.pp protein - protein database search, using Smith-Waterman algorithm  
 Run on: Thu May 22 08:27:25 1997; MasPar time 1.93 Seconds  
 Tabular output not generated. 33.906 Million cell updates/sec

Title: >US-08-653-294-4  
 Description: (1-6) from US08633294.pep  
 Perfect Score: 49  
 Sequence: 1 RIALRY 6

Scoring table: PAM 150  
 Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: a-geneseq26  
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
 14:part14 15:part15 16:part16 17:part17 18:part18  
 19:part19

Statistics: Mean 15.639; Variance 39.027; scale 0.401

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	49	100.0	10 18	R95413	Alphal-helix of HLA-B	1.25e+01
2	49	100.0	10 18	R95425	HLA-B2702.75-84 (P)	1.25e+01
3	49	100.0	10 8	R41208	Peptide fragment of C	1.25e+01
4	49	100.0	10 16	R33062	HLA-B2702 CTL modul	1.25e+01
5	49	100.0	10 16	R33094	HLA-B2702 CTL modul	1.25e+01
6	49	100.0	12 18	R95429	HLA-B2702 84-79-84 pa	1.25e+01
7	49	100.0	15 16	R32912	HLA-B2702 CTL modul	1.25e+01
8	49	100.0	20 18	R95428	HLA-B2702 84-75-84 pa	1.25e+01
9	49	100.0	20 16	R32907	HLA-B2702 CTL modul	1.25e+01
10	49	100.0	20 16	R32908	HLA-B2702 CTL modul	1.25e+01
11	49	100.0	25 18	R95416	HLA-B2702.60-84.	1.25e+01
12	49	100.0	25 18	R95422	HLAB38.6084	1.25e+01
13	49	100.0	25 16	R33090	HLA-B2702 CTL modul	1.25e+01
14	49	100.0	25 8	R41205	Peptide fragment of C	1.25e+01
15	49	100.0	25 16	R33093	HLAB38 CTL modul	1.25e+01
16	49	100.0	25 8	R48286	Peptide fragment of H	1.25e+01
17	49	100.0	362 3	R12463	HLA-Bw53 exon.	1.25e+01
18	49	100.0	362 2	R33142	Sequence of HLA-Bw52	1.25e+01
19	49	100.0	362 2	R33144	Sequence of HLA-B51 a	1.25e+01
20	47	95.9	939 1	R04104	pJH1 gene product - b	2.26e+01

21	46	93.9	349 19	W02658	G-protein coupled dog	3.03e+01
22	46	93.9	349 16	R48686	G-protein coupled dog	3.03e+01
23	46	93.9	412 9	R47387	Human A2a adenosine r	3.03e+01
24	46	93.9	412 15	R84193	Human A2a adenosine r	3.03e+01
25	46	93.9	412 18	R33990	Human ventricle A2a a	3.03e+01
26	46	93.9	412 8	R41525	Human A2a adenosine r	3.03e+01
27	46	93.9	412 16	R87656	Human adenosine recep	3.03e+01
28	45	91.8	43 18	R92804	PB145 serpin enzyme c	4.07e+01
29	45	91.8	959 14	R76066	Yeast MSH1 protein.	4.07e+01
30	45	91.8	971 14	R76070	Yeast MSH1 protein wi	4.07e+01
31	42	85.7	10 18	R95426	HLA-B2702.75-84 (P)	9.64e+01
32	42	85.7	10 16	R33096	HLA-B2702 CTL modul	9.64e+01
33	42	85.7	10 16	R83095	HLA-B2702 CTL modul	9.64e+01
34	42	85.7	20 16	R92910	HLA-B2702 CTL modul	9.64e+01
35	42	85.7	20 16	R92909	HLA-B2702 CTL modul	9.64e+01
36	42	85.7	1165 7	R37309	Cardiac adenylyl cycl	9.64e+01
37	42	85.7	3567 8	R44431	eryA region polypepti	9.64e+01
38	41	83.7	314 19	W02659	G-protein coupled dog	1.28e+02
39	41	83.7	326 9	R45744	Human A1 adenosine re	1.28e+02
40	41	83.7	326 8	R41524	Human A1 adenosine re	1.28e+02
41	41	83.7	326 9	R47386	Human A1 adenosine re	1.28e+02
42	41	83.7	326 4	R22007	A1 adenosine receptor	1.28e+02
43	41	83.7	326 18	R93989	Human ventricle A1 ad	1.28e+02
44	41	83.7	335 1	P80386	DNA polymerase beta 1	1.28e+02
45	41	83.7	593 5	R05874	Hsp70 antigen of Myco	1.28e+02

## ALIGNMENTS

RESULT 1  
 ID R95413 standard; peptide; 10 AA.

AC R95413;  
 DT 12-NOV-1996 (first entry)  
 DE Alphal-helix of HLA-B2702  
 KW HLA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN W09513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI; 95-194027/25.  
 PT Compens. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 11; 29pp; English.  
 PS This sequence represents the alphal-helix of the  
 CC human-leucocyte-associated antigen B2702 (HLA-B2702). This sequence,  
 CC epitopes, and palindromes of it (such as R95428) can be used to isolate  
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
 CC protein associated with T-cell activation in mammalian T-cells, and is  
 CC also immunologically cross reactive with the heat shock protein Hsc70.  
 CC p74 is found in a limited number of cell types, but is particularly  
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
 CC cell with an amphoteric detergent, and then passed through an affinity  
 CC column containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 18; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 rialry 10  
 |||||  
 QY 1 RIALRY 6

## RESULT 2

ID R95425 standard; peptide; 10 AA.  
 AC R95425;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B\*2702.75-84(D).  
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Misc difference 3  
 FT /note- "N3D mutation"  
 PN W09513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DI WPI; 95-194027/25.  
 PT Compsns. comprising lymphoid surface membrane proteins - which may exhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 11; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the HLA-B\*2702.75-84(D). These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B\*2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with HLA-B\*2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 18; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 rialry 10  
 |||||  
 QY 1 RIALRY 6

## RESULT 3

ID R41208 standard; peptide; 10 AA.  
 AC R41208;  
 DT 15-MAR-1994 (first entry)  
 DE Peptide fragment of Class I HLA peptide.  
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;  
 KW parasitic disease; cytotoxic T lymphocyte; modulation.  
 OS Synthetic.  
 PN W09317699-A.  
 PD 16-SEP-1993.  
 PF 25-FEB-1993; U01758.  
 PR 02-MAR-1992; US-844716.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger CA, Krensky AM;  
 DR WPI; 93-303134/38.  
 PT New peptides(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets  
 PS Claim 11; Page 54; 61pp; English.  
 CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition.  
 CC This peptide sequence is more commonly found within larger peptide compounds of not more than 30 amino acids in length.  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 rialry 10  
 |||||  
 QY 1 RIALRY 6

## RESULT 4

ID R83062 standard; peptide; 10 AA.  
 AC R83062;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B\*2702 CTL modulating peptide (B2702.75-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW Class I MHC; HLA-B\*2702.  
 OS Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995;  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358382/46.  
 PT Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient host  
 PS Claim 15; Page 9; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R82907-R82913 represent fragments of Class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HLA-B\*2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 16; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 rialry 10  
 |||||  
 QY 1 RIALRY 6

## RESULT 5

ID R83094 standard; peptide; 10 AA.  
 AC R83094;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B\*2702 CTL modulating peptide (B2702.75-84(D)).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN WO9526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 14; Page 34; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC  
 CC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with  
 CC a subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 CC Sequence 10 AA;  
 SQ  
 Query Match 100.0%; Score 49; DB 16; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 5 rialry 10  
 QY 1 RIALRY 6  
 RESULT 6  
 ID R95429 standard; peptide; 12 AA.  
 AC R95429;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B2702 84-79-84 palindromic.  
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN WO9513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI; 95-194027/25.  
 FT Compns. comprising lymphoid surface membrane proteins - which may  
 FT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 12; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B2702 84-79-84 palindromic. These sequences can be used to isolate  
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
 CC protein associated with T-cell activation in mammalian T-cells, and is  
 CC also immunologically cross reactive with the heat shock protein Hsc70.  
 CC p74 is found in a limited number of cell types, but is particularly  
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
 CC cell with an amphoteric detergent, and then passed through an affinity  
 CC column containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B2702 60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition

CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 12 AA;  
 Query Match 100.0%; Score 49; DB 18; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 7 rialry 12  
 QY 1 RIALRY 6  
 RESULT 7  
 ID R92912 standard; peptide; 15 AA.  
 AC R92912;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.70-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN WO9526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC corresponds to residues 70-84 of the alpha-1 domain of the class I MHC  
 CC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 CC Sequence 15 AA;  
 SQ  
 Query Match 100.0%; Score 49; DB 16; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 10 rialry 15  
 QY 1 RIALRY 6  
 RESULT 8  
 ID R95428 standard; peptide; 20 AA.  
 AC R95428;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B2702 84-75-84 palindromic.  
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN WO9513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI; 95-194027/25.

PT Compens. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 12; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).  
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
 CC also immunologically cross reactive with the heat shock protein Hsc70.  
 CC p74 is found in a limited number of cell types, but is particularly  
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
 CC cell with an amphoteric detergent, and then passed through an affinity  
 CC column containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxic. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 18; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 r1aly 20  
 |||||  
 QY 1 RIALRY 6

RESULT 9  
 ID R92907 standard; peptide; 20 AA.  
 AC R92907;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN WO9526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 WPI: 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host

PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 CC I MHC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 16; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 r1aly 20  
 |||||

QY 1 RIALRY 6  
 RESULT 10  
 ID R92908 standard; peptide; 20 AA.  
 AC R92908;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN WO9526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 WPI: 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host

PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 CC I MHC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 16; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 r1aly 20  
 |||||  
 QY 1 RIALRY 6

RESULT 11  
 ID R95416 standard; peptide; 25 AA.  
 AC R95416;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B2702.60-84.  
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytotoxicity; antigen presenting cell.  
 OS Synthetic.  
 PN WO9513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PI (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 WPI: 95-194027/25.  
 PT Compens. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 9; 29pp; English.

CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents  
 CC HLA-B2702.60-84. These sequences can be used to isolate the protein p74  
 CC from a T-cell lysate. p74 is a T-cell surface membrane protein  
 CC associated with T-cell activation in mammalian T-cells, and is also  
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is  
 CC found in a limited number of cell types, but is particularly expressed on  
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an

CC amphoteric detergent, and then passed through an affinity column  
 CC containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC this sequence, induces calcium influx, and inhibits cytotoxic T  
 CC lymphocyte (CTL) differentiation or cytotoxicity. Candidate compounds can  
 CC be screened for their effect on the cytolytic activity of T-cells, by  
 CC combining them with the extracellular portion of p74 and determining the  
 CC amount of binding between the candidate compound and p74. Modulation of  
 CC CTL activity can be inhibited in a cellular composition containing  
 CC T-cells and antigen presenting cells (APCs), by adding to the mix the  
 CC extracellular portion of p74, in an amount sufficient to compete with p74  
 CC for the binding of the p74 ligand.  
 SQ Sequence 25 AA;

Query Match 100.0%; Score 49; DB 18; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 r1alry 25  
 QY 1 R1ALRY 6  
 |||||

RESULT 12  
 ID R95422 standard; peptide; 25 AA.  
 AC R95422;  
 DT 12-NOV-1996 (first entry)  
 DE HL338.6084.  
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytotoxicity; antigen presenting cell.  
 OS Synthetic.  
 PN WO9513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI: 95-194027/25.  
 CC Compsns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 9; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA338.6084. These sequences can be used to isolate the protein p74 from  
 CC a T-cell lysate. p74 is a T-cell surface membrane protein associated  
 CC with T-cell activation in mammalian T-cells, and is also immunologically  
 CC cross reactive with the heat shock protein Hsc70. p74 is found in a  
 CC limited number of cell types, but is particularly expressed on B and T  
 CC cells. p74 can be isolated by lysis of a suitable cell with an  
 CC amphoteric detergent, and then passed through an affinity column  
 CC containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 25 AA;

Query Match 100.0%; Score 49; DB 18; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 r1alry 25  
 QY 1 R1ALRY 6  
 |||||

RESULT 13  
 ID R83090 standard; peptide; 25 AA.  
 AC R83090;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.60-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN WO9526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI: 95-358582/46.  
 CC Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 13; Page 32; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC  
 CC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with  
 CC a subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 25 AA;

Query Match 100.0%; Score 49; DB 16; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 r1alry 25  
 QY 1 R1ALRY 6  
 |||||

RESULT 14  
 ID R41205 standard; peptide; 25 AA.  
 AC R41205;  
 DT 15-MAR-1994 (first entry)  
 DE Peptide fragment of Class I HLA peptide.  
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;  
 KW parasitic disease; cytotoxic T lymphocyte; modulation.  
 OS Synthetic.  
 PN WO9317599-A.  
 PD 16-SEP-1993.  
 PF 25-FEB-1993; U01758.  
 PR 02-MAR-1992; US-844716.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger CA, Krensky AM;  
 DR WPI: 93-303134/38.  
 CC New peptide(s) based on Class I HLA antigen domains - used for  
 CC modulating cytotoxic T-lymphocyte activity towards targets  
 CC Claim 8; Page 53; 61pp; English.  
 CC The peptide (or a fragment of at least 10 amino acids, joined at at  
 CC least one terminus to a sequence other than that of wild type HLA  
 CC antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity,  
 CC either by inhibition or stimulation. It can be used for  
 CC inhibiting CTL toxicity in transplantations, for inducing CTL  
 CC activity in parasitic diseases and neoplasia and in studies on viral  
 CC infection. The peptide can also be used for identifying CTLs which  
 CC bind to it and removing subsets of CTLs from a T-cell composition.  
 SQ Sequence 25 AA;

Query Match 100.0%; Score 49; DB 8; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 rialry 25  
|||||  
QY 1 RIALRY 6

RESULT 15  
ID R83093 standard; peptide; 25 AA.  
AC R83093;  
DT 16-MAY-1996 (first entry)  
DE HLAB38 CTL modulating peptide (B38.6084).  
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
KW class I MHC; HLAB38.  
OS Synthetic.  
PN WO9526979-A1.  
PD 12-OCT-1995.  
PF 05-APR-1995; U04349.  
PR 05-APR-1994; US-222851.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PI Clayberger C, Krensky AM, Parham P;  
DR WPI; 95-358382/46.  
PT Extension of acceptance period of transplants from MHC unmatched  
PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
PT host  
PS Example 13: Page 32: 80pp; English.  
CC R83061-R83085, R83090-R83096 and R82907-R82913 represent fragments of  
CC class I major histocompatibility complex (MHC) antigens. This sequence  
CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC  
CC HLAB38. These sequences can be used to extend the period of acceptance  
CC by a recipient of a transplant from an MHC unmatched donor. The peptides  
CC are administered to a patient in conjunction with a subtherapeutic amount  
CC of an immunosuppressant. This is administered to the patient for a  
CC limited period of time (compared to the lifetime administration for  
CC current treatments). The peptides particularly modulate (or inhibit) the  
CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.  
SQ Sequence 25 AA;

Query Match 100.0%; Score 49; DB 16; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 rialry 25  
|||||  
QY 1 RIALRY 6

Search completed: Thu May 22 08:27:40 1997  
Job time : 15 secs.



\*\*\*\*\*  
MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu May 22 08:28:27 1997; MasPar time 2.70 seconds  
Tabular output not generated. 63.421 Million cell updates/sec  
Title: >US-08-653-294-5  
Description: (1-6) from US08653294.pep  
Perfect Score: 53  
Sequence: 1 RILLRY 6  
Scoring table: PAM 150  
Gap 15  
Searched: 89912 seqs, 28507787 residues  
Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Database: pir50  
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3  
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8  
13:unann9 14:unann10 15:unenc 16:unrev  
Statistics: Mean 22.859; Variance 32.635; scale 0.700  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.  
SUMMARIES  
Result No. Score Query Match Length DB ID Description Pred. No.  
-----  
1 51 96.2 616 10 JC4084 prolyl endopeptidase 6.99e+00  
2 48 90.6 830 11 S25198 vacuolar membrane pr 2.39e+01  
3 48 90.6 832 11 S19418 probable membrane pr 2.39e+01  
4 47 88.7 139 13 S00258 VpreB protein - huma 3.57e+01  
5 47 88.7 142 14 A28344 VpreB protein precu 3.57e+01  
6 47 88.7 142 14 B28344 VpreB protein precu 3.57e+01  
7 47 88.7 145 13 I57832 VPre-B protein - hum 3.57e+01  
8 47 88.7 497 5 B42902 methylmalonate-semia 3.57e+01  
9 46 86.8 137 13 I80174 class I histocompati 5.29e+01  
10 46 86.8 168 5 S43337 protein-lysine 6-oxi 5.29e+01  
11 46 86.8 217 9 A42644 neuE protein - Esche 5.29e+01  
12 46 86.8 218 13 I72808 MHC class I HLA-J an 5.29e+01  
13 46 86.8 274 13 I55965 HLA-B27 M2+ - human 5.29e+01  
14 46 86.8 284 6 A45840 MHC class I histocom 5.29e+01  
15 46 86.8 328 14 I54414 MHC H-2K transplanta 5.29e+01  
16 46 86.8 338 13 I56116 MHC HLA-B27-HS - hum 5.29e+01  
17 46 86.8 346 5 S12599 phosphoprotein phosph 5.29e+01  
18 46 86.8 346 5 B45640 phosphoprotein phosph 5.29e+01  
19 46 86.8 349 14 JC4221 transcription enhanc 5.29e+01  
20 46 86.8 362 14 I71998 MHC H-2D-K protein - 5.29e+01  
21 46 86.8 362 13 I68724 MHC HLA-Bw47 precurs 5.29e+01

22 46 86.8 362 6 C35997 MHC class I histocom 5.29e+01  
23 46 86.8 362 2 HLHUB2 MHC class I histocom 5.29e+01  
24 46 86.8 362 13 I54289 MHC HLA-B27d - human 5.29e+01  
25 46 86.8 362 13 I37485 human lymphocyte ant 5.29e+01  
26 46 86.8 365 13 A39481 serum response facto 5.29e+01  
27 46 86.8 367 6 S31651 MHC class I histocom 5.29e+01  
28 46 86.8 368 14 I68705 MHC H-2K-w28 protein 5.29e+01  
29 46 86.8 411 1 OXRTL protein-lysine 6-oxi 5.29e+01  
30 46 86.8 411 1 OXMSL protein-lysine 6-oxi 5.29e+01  
31 46 86.8 417 1 OXHUL protein-lysine 6-oxi 5.29e+01  
32 46 86.8 420 13 A45166 protein-lysine 6-oxi 5.29e+01  
33 46 86.8 574 5 A48501 lysyl oxidase homolo 5.29e+01  
34 46 86.8 1612 16 S59969 DNA topoisomerase (A 5.29e+01  
35 46 86.8 1612 6 S54154 DNA topoisomerase (A 5.29e+01  
36 46 86.8 1626 6 A39242 DNA topoisomerase (A 5.29e+01  
37 46 86.8 3712 16 S28399 laminin chain A - fr 5.29e+01  
38 45 84.9 218 8 S30287 regulatory protein t 7.79e+01  
39 45 84.9 218 8 S07359 regulatory protein t 7.79e+01  
40 45 84.9 298 12 S53849 ribosomal protein S3 7.79e+01  
41 45 84.9 1203 12 A33165 finger protein sdc-1 7.79e+01  
42 44 83.0 147 16 S60894 Invi protein - Salmo 1.14e+02  
43 44 83.0 351 16 S62783 UDPglucose 4-epimera 1.14e+02  
44 44 83.0 733 13 A57459 growth factor-stimul 1.14e+02  
45 44 83.0 735 14 A53300 S6 protein kinase - 1.14e+02

ALIGNMENTS

RESULT 1  
ENTRY JC4084 #type complete  
TITLE prolyl endopeptidase (EC 3.4.-.-) - Pyrococcus furiosus  
ALTERNATE\_NAMES mlr-2 protein  
ORGANISM #formal\_name Pyrococcus furiosus  
DATE 12-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 21-Mar-1996  
ACCESSIONS JC4084  
REFERENCE JC4084  
#authors Robinson, K.A.; Bartley, D.A.; Robb, F.T.; Schreier, H.J.  
#journal Gene (1995) 152:103-106  
#title A gene from the hyperthermophile Pyrococcus furiosus whose deduced product is homologous to members of the prolyl oligopeptidase family of proteases.  
#accession JC4084  
#molecule\_type DNA  
#residues 1-616 #label ROB  
#cross-references GB:U08343  
KEYWORDS hydrolase; oligopeptidase  
FEATURE  
477,561,592 #active\_site Ser, Asp, His #status predicted  
SUMMARY #length 616 #molecular-weight 70867 #checksum 9939

Query Match 96.2%; Score 51; DB 10; Length 616;  
Best Local Similarity 83.3%; Pred. No. 6.99e+00;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db 334 rvllry 339  
l:||||  
QY 1 RILLRY 6

RESULT 2  
ENTRY S25198 #type complete  
TITLE vacuolar membrane protein HMT1 - fission yeast  
ALTERNATE\_NAMES (Schizosaccharomyces pombe)  
ORGANISM #formal\_name Schizosaccharomyces pombe  
DATE 28-May-1993 #sequence\_revision 28-May-1993 #text\_change 20-Jan-1995  
ACCESSIONS S25198  
REFERENCE S25198  
#authors Ortiz, D.F.; Kreppel, L.; Speiser, D.M.; Scheel, G.; McDonald, G.; Ow, D.W.  
#journal EMBO J. (1992) 11:3491-3499  
#title Heavy metal tolerance in the fission yeast requires an

```
#accession S25198
#molecule_type mRNA
##residues 1-830 ##label ORT
##cross-references EMBL:Z14055

GENETICS
#gene html
#map_position III
CLASSIFICATION #superfamily malk protein homology
KEYWORDS ATP binding; transmembrane protein
FEATURE
10-31 #domain transmembrane #status predicted #label TM1\
52-71 #domain transmembrane #status predicted #label TM2\
88-108 #domain transmembrane #status predicted #label TM3\
126-146 #domain transmembrane #status predicted #label TM4\
403-423 #domain transmembrane #status predicted #label TM5\
490-511 #domain transmembrane #status predicted #label TM6\
600-794 #domain malk protein homology #label MK1
SUMMARY
#length 830 #molecular-weight 94007 #checksum 7697

Query Match 90.6%; Score 48; DB 11; Length 830;
Best Local Similarity 83.3%; Pred. No. 2.39e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 628 rllrf 633
|||||
QY 1 RILRY 6

RESULT 3
ENTRY S19418 #type complete
TITLE probable membrane protein YCR106w - yeast (Saccharomycetes cerevisiae)
ORGANISM #formal_name Saccharomycetes cerevisiae
DATE 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 12-May-1995
ACCESSIONS S19418; S19747
REFERENCE van der Linden, C.G.; Maurer, C.T.C.; Planta, R.J.; van Vliet-Reedijk, J.C.; Vreken, P. The Protein Sequence Database, March 1992
#authors submitted to the Protein Sequence Database, March 1992
#submission S19418
#accession S19747
##molecule_type DNA
##residues 1-517 ##label LIN
##cross-references EMBL:X59720
REFERENCE Grenson, M.; Jauniaux, J.C.; Urrestarazu, L.A.
#authors submitted to the Protein Sequence Database, March 1992
#submission S19747
#accession S19747
##molecule_type DNA
##residues 130-832 ##label GRE
##cross-references EMBL:X59720

GENETICS
#map_position 3R
CLASSIFICATION #superfamily GAL4 zinc binuclear cluster homology
KEYWORDS transmembrane protein
FEATURE
10-47 #domain GAL4 zinc binuclear cluster homology #label GAL4\
104-121 #domain transmembrane #status predicted #label TM1\
275-292 #domain transmembrane #status predicted #label TM2\
398-414 #domain transmembrane #status predicted #label TM3\
542-558 #domain transmembrane #status predicted #label TM4\
616-632 #domain transmembrane #status predicted #label TM5\
699-715 #domain transmembrane #status predicted #label TM6\
767-783 #domain transmembrane #status predicted #label TM7
SUMMARY
#length 832 #molecular-weight 95689 #checksum 36

Query Match 90.6%; Score 48; DB 11; Length 832;
Best Local Similarity 83.3%; Pred. No. 2.39e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 629 rllrf 634
```

```
QY 1 RILRY 6
|||||
RESULT 4
ENTRY S00258 #type complete
TITLE VpreB protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 06-Sep-1996
ACCESSIONS S00258
REFERENCE Bauer, S.R.; Kudo, A.; Melchers, F.
#authors EMBO J. (1988) 7:111-116
#journal Structure and pre-B lymphocyte restricted expression of the
#title VpreB gene in humans and conservation of its structure in
other mammalian species.
#cross-references MUID:88196069
#accession S00258
##molecule_type DNA
##residues_type 1-139 ##label BAU
##cross-references EMBL:M34927
GENETICS
#gene GDB:VPREB1
#map_position 22q11.2-22q11.2
#introns 16/1
SUMMARY #length 139 #molecular-weight 15948 #checksum 2257

Query Match 88.7%; Score 47; DB 13; Length 139;
Best Local Similarity 83.3%; Pred. No. 3.57e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 66 rllry 71
|||||
QY 1 RILRY 6

RESULT 5
ENTRY A28344 #type complete
TITLE VpreB protein precursor - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 19-May-1989 #sequence_revision 19-May-1989 #text_change 23-Mar-1993
ACCESSIONS A28344
REFERENCE A91077
#authors Kudo, A.; Melchers, F.
#journal EMBO J. (1987) 6:2267-2272
#title A second gene, VpreB in the lambda-5 locus of the mouse,
which appears to be selectively expressed in pre-B
lymphocytes
#cross-references MUID:88029315
#accession A28344
##molecule_type DNA
##residues 1-142 ##label KUD
##note the authors translated the codon GAG for residue 110 as
Gln

FEATURE
20-142 #product VpreB protein #status predicted #label MAT
SUMMARY #length 142 #molecular-weight 16125 #checksum 8179

Query Match 88.7%; Score 47; DB 14; Length 142;
Best Local Similarity 83.3%; Pred. No. 3.57e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 66 rllry 71
|||||
QY 1 RILRY 6

RESULT 6
ENTRY B28344 #type complete
TITLE VpreB protein precursor - mouse
```

```

ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 19-May-1989 #sequence_revision 19-May-1989 #text_change
23-Mar-1993
ACCESSIONS B28344
REFERENCE A91077
#authors Kudo, A.; Melchers, F.
#journal EMBO J. (1987) 6:2267-2272
#title A second gene, VpreB in the lambda-5 locus of the mouse,
which appears to be selectively expressed in pre-B
lymphocytes.
#cross-references MUID:88029315
#accession B28344
#molecule_type DNA
#residues 1-142 #label KUD
#note the authors translated the codon GAG for residue 110 as
Gln
FEATURE
20-142 #product VpreB protein #status predicted #label MAT
SUMMARY #length 142 #molecular-weight 16052 #checksum 7379
Query Match 88.7%; Score 47; DB 14; Length 142;
Best Local Similarity 83.3%; Pred. No. 3.57e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 66 rfillry 71
QY 1 RILLRY 6
RESULT 7
ENTRY #type complete
TITLE Vpre-B protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
157832
ACCESSIONS 157832
REFERENCE Fougereau, M.; Schiff, C.
#authors Guelpa-Fonlupt, V.; Bossy, D.; Alzari, P.; Fumoux, F.;
#journal Mol. Immunol. (1994) 31:1099-1108
#title The human pre-B cell receptor: structural constraints for a
tentative model of the pseudo-light (psi L) chain.
#cross-references MUID:95021318
#accession 157832
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-145 #label RES
#cross-references GB:S74019; NID:9693810; CDS_PID:9693811
GENETICS
#introns 16/1
#note gene name Vpre-B
SUMMARY #length 145 #molecular-weight 16605 #checksum 5991
Query Match 88.7%; Score 47; DB 13; Length 145;
Best Local Similarity 83.3%; Pred. No. 3.57e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 66 rfillry 71
QY 1 RILLRY 6
RESULT 8
ENTRY #type complete
TITLE methylmalonate-semialdehyde dehydrogenase (acylating) (EC
1.2.1.27) - Pseudomonas aeruginosa (ATCC 15692)
ORGANISM #formal_name Pseudomonas aeruginosa
DATE 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change
25-Aug-1995
ACCESSIONS B42902; S27602
REFERENCE A42902
#authors Steele, M.I.; Lorenz, D.; Hatter, K.; Park, A.; Sokatch, J.R.
#journal J. Biol. Chem. (1992) 267:13585-13592

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#title Characterization of the mmsAB operon of pseudomonas
aeruginosa PAO encoding methylmalonate-semialdehyde
dehydrogenase and 3-hydroxyisobutyrate dehydrogenase.
#cross-references MUID:92317087
#accession B42902
#status preliminary
#molecule_type DNA
#residues 1-497 #label STE
#cross-references EMBL:M84911; NCBI:P107707
GENETICS
#gene mmsA
#superfamily aldehyde dehydrogenase (NAD+)
#CLASSIFICATION oxidoreductase
KEYWORDS #length 497 #molecular-weight 53663 #checksum 4590
SUMMARY
Query Match 88.7%; Score 47; DB 5; Length 497;
Best Local Similarity 66.7%; Pred. No. 3.57e+01;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 68 rvmlyry 73
QY 1 RILLRY 6
RESULT 9
ENTRY #type fragment
TITLE class I histocompatibility antigen - chimpanzee (fragment)
ORGANISM #formal_name Pan troglodytes #common_name chimpanzee
DATE 24-May-1996 #sequence_revision 24-May-1996 #text_change
180174
ACCESSIONS 180174
REFERENCE McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
#authors A.L.; Bontryp, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession 180174
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-137 #label RES
#cross-references EMBL:005585; NID:9454787; CDS_PID:9454788
SUMMARY #length 137 #checksum 5064
Query Match 86.8%; Score 46; DB 13; Length 137;
Best Local Similarity 83.3%; Pred. No. 5.29e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 44 rlllyry 49
QY 1 RILLRY 6
RESULT 10
ENTRY #type fragments
TITLE protein-lysine 6-oxidase (EC 1.4.3.13) - pig (fragments)
ALTERNATE_NAMES lysyl oxidase
ORGANISM #formal_name Sus scrofa domestica #common_name domestic pig
DATE 27-Oct-1995 #sequence_revision 06-Sep-1996 #text_change
06-Sep-1996
ACCESSIONS S54337
REFERENCE S54337
#authors Crouchaw, A.D.; Fothergill-Gilmore, L.A.; Hulmes, D.J.S.
#journal Biochem. J. (1995) 306:279-284
#title The proteolytic processing site of the precursor of lysyl
oxidase.
#accession S54337
#molecule_type protein
#residues 1-168 #label CRO
#note the amino end of the mature protein was determined after
unblocking; the nature of the blocking group was not
determined
FUNCTION

```

#description using molecular oxygen catalyzes the oxidative deamination of peptidyl-lysine to peptidyl-allysine, ammonium and hydrogen peroxide

#pathway collagen biosynthesis; elastin biosynthesis

CLASSIFICATION superfamily protein-lysine 6-oxidase

KEYWORDS blocked amino end; copper; extracellular protein; glycoprotein; oxidoreductase; quinoprotein

FEATURE #modified\_site blocked amino end (Asp) #status

1 experimental

SUMMARY #length 168 #checksum 7344

Query Match 86.8%; Score 46; DB 5; Length 168;

Best Local Similarity 66.7%; Pred. No. 5.29e+01;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 85 rvllrf 90

QY 1 RILLY 6

RESULT 11

ENTRY A42644 #type fragment

TITLE neuE protein - Escherichia coli (fragment)

ORGANISM #formal\_name Escherichia coli

DATE 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change

ACCESSIONS A42644; S21890

REFERENCE A42644

#authors Steenbergen, S.M.; Wrona, T.J.; Vimr, E.R.

#journal J. Bacteriol. (1992) 174:1099-1108

#title Functional analysis of the sialyltransferase complexes in

Escherichia coli K1 and K92.

#cross-references MUID:92138601

#accession A42644

##status preliminary

##molecule\_type DNA

##residues 1-217 #label STE

##cross-references NCBI:79370; NCBI:79375

##experimental\_source K1, strain EV1

##note sequence inconsistent with the nucleotide translation

##note sequence extracted from NCBI backbone

REFERENCE S21890

#authors Weisgerber, C.

#submission submitted to the EMBL Data Library, July 1991

#accession S21890

##status preliminary

##molecule\_type DNA

##residues 35-217 #label WEI

##cross-references EMBL:X60598

GENETICS

#gene neuE

SUMMARY #length 217 #checksum 1066

Query Match 86.8%; Score 46; DB 9; Length 217;

Best Local Similarity 66.7%; Pred. No. 5.29e+01;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 207 kvllry 212

QY 1 RILLY 6

RESULT 12

ENTRY I72808 #type complete

TITLE MHC class I HLA-J antigen - human

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change

ACCESSIONS I72808

REFERENCE I56139

#authors Messer, G.; Zemmour, J.; Orr, H.T.; Parham, P.; Weiss, E.H.;

Girdlestone, J.

#journal J. Immunol. (1992) 148:4043-4053

#title HLA-J, a second inactivated class I HLA gene related to HLA-G

and HLA-A. Implications for the evolution of the

HLA-A-related genes.

#cross-references MUID:92291530

#accession I72808

##status preliminary; translated from GB/EMBL/DBJ

##molecule\_type DNA

##residues 1-218 #label RES

##cross-references GB:M80470; NID:9808907; CDS\_PID:g553586

SUMMARY #length 218 #molecular\_weight 24840 #checksum 7887

Query Match 86.8%; Score 46; DB 13; Length 218;

Best Local Similarity 83.3%; Pred. No. 5.29e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 102 rllly 107

QY 1 RILLY 6

RESULT 13

ENTRY I55965 #type fragment

TITLE HLA-B\*27 M2+ - human (fragment)

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change

ACCESSIONS I55965

REFERENCE I55965

#authors Coppin, H.L.; McDevitt, H.O.

#journal J. Immunol. (1986) 137:2168-2172

#title Absence of polymorphism between HLA-B\*27 genomic exon

sequences isolated from normal donors and ankylosing

spondylitis patients.

#cross-references MUID:87009855

#accession I55965

##status preliminary; translated from GB/EMBL/DBJ

##molecule\_type DNA

##residues 1-274 #label RES

##cross-references GB:M14013; NID:9187743; CDS\_PID:g187744

SUMMARY #length 274 #checksum 8911

Query Match 86.8%; Score 46; DB 13; Length 274;

Best Local Similarity 83.3%; Pred. No. 5.29e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 79 rllly 84

QY 1 RILLY 6

RESULT 14

ENTRY A45840 #type fragment

TITLE MHC class I histocompatibility antigen RT-BM1 alpha chain -

rat (fragment)

ORGANISM #formal\_name Rattus norvegicus #common\_name Norway rat

DATE 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change

ACCESSIONS A45840

REFERENCE A45840

#authors Parker, K.E.; Carter, C.A.; Fabre, J.W.

#journal Immunogenetics (1990) 31:211-214

#title A rat class I cDNA clone with an Alu-like sequence and

mapping to two genes in Rtl.C/E.

#accession A45840

##status preliminary

##molecule\_type mRNA

##residues 1-284 #label PAR

##cross-references GB:X16979

CLASSIFICATION #superfamily class I histocompatibility antigen;

immunoglobulin homology

FEATURE #domain immunoglobulin homology #label IMM

137-202

```

SUMMARY      #length 284  #checksum 7381
Query Match   86.8%; Score 46; DB 6; Length 284;
Best Local Similarity 83.3%; Pred.No. 5.29e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 20 rllry 25
  | | | |
QY 1 RLLRY 6

RESULT 15
ENTRY
TITLE      #type fragment
ORGANISM   MHC H-2K transplantation antigen - mouse (fragment)
DATE       #formal_name Mus musculus #common_name house mouse
           02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
           02-Aug-1996
ACCESSIONS I54414
REFERENCE  I54414
#authors   Morita, T.; Delarbre, C.; Kress, M.; Kourilsky, P.; Gachelin,
           G.
#journal   Immunogenetics (1985) 21:367-383
#title     An H-2K gene of the t-w32 mutant at the T/t complex is a
           close parent of an H-2K-q gene.
#cross-references MUID:85206119
#accession  I54414
#status     preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues   1-328 #label RES
#cross-references GB:M14827; NID:g199550; CDS_PID:g387471
#length 328 #checksum 6118
SUMMARY

Query Match   86.8%; Score 46; DB 14; Length 328;
Best Local Similarity 83.3%; Pred.No. 5.29e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 60 rllry 65
  | | | |
QY 1 RLLRY 6

```

Search completed: Thu May 22 08:28:46 1997  
 Job time : 19 secs.

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M P S R E H  
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:29:04 1997; MasPar time 1.90 Seconds  
Tabular output not generated. 34,326 Million cell updates/sec

Title: >US-08-653-294-5  
Description: (1-6) from US08653294.pep  
Perfect Score: 53  
Sequence: 1 RILLRY 6

Scoring table: PAM 150  
Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq26  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19

Statistics: Mean 16.452; Variance 46.284; scale 0.355

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description Pred. No.
1	53	100.0	10 16	R83096 HLA-B2702 CTL modulat 1.30e+01
2	47	88.7	125 1	P80289 Human Vpre-B protein. 6.38e+01
3	47	88.7	142 1	P83001 V preB-2 protein. 6.38e+01
4	47	88.7	142 1	P80288 V preB-1 protein. 6.38e+01
5	46	86.8	10 18	R95423 HLA-B2705.75-84. 8.26e+01
6	46	86.8	10 8	R41212 Peptide fragment of C 8.26e+01
7	46	86.8	10 16	R83075 HLA-B2702 CTL modulat 8.26e+01
8	46	86.8	17 13	R71425 Human MHC 1 alpha 1 d 8.26e+01
9	46	86.8	17 13	R71442 Human HLA-B27-(62-85) 8.26e+01
10	46	86.8	17 13	R71443 Human (Phe74)-HLA-B27 8.26e+01
11	46	86.8	17 13	R71440 Human MHC 1 and HLA f 8.26e+01
12	46	86.8	17 13	R71436 Human MHC 1 alpha 1 d 8.26e+01
13	46	86.8	17 13	R71426 Human MHC 1 alpha 1 d 8.26e+01
14	46	86.8	17 13	R71428 Human MHC 1 alpha 1 d 8.26e+01
15	46	86.8	24 13	R71424 Human MHC 1 alpha 1 d 8.26e+01
16	46	86.8	24 13	R71434 Human MHC 1 alpha 1 d 8.26e+01
17	46	86.8	24 13	R71436 Human MHC 1 alpha 1 d 8.26e+01
18	46	86.8	24 13	R71427 Human MHC 1 alpha 1 d 8.26e+01
19	46	86.8	24 13	R71435 Human MHC 1 alpha 1 d 8.26e+01
20	46	86.8	25 18	R95417 HLA-B2705.60-84. 8.26e+01

21	46	86.8	25 13	R71420 Human MHC 1 alpha 1 d 8.26e+01
22	46	86.8	25 3	R20116 MHC Class I-derived p 8.26e+01
23	46	86.8	25 8	R41221 Peptide fragment of H 8.26e+01
24	46	86.8	25 13	R69619 MHC-1 peptide DK-(61- 8.26e+01
25	46	86.8	25 16	R83091 HLA-B2702 CTL modulat 8.26e+01
26	46	86.8	337 2	P70590 Sequence of the human 8.26e+01
27	46	86.8	362 2	P70155 Sequence encoded by g 8.26e+01
28	46	86.8	365 9	R50040 xMEF2. 8.26e+01
29	45	84.9	24 13	R71438 Human MHC 1 alpha 1 d 1.07e+02
30	44	83.0	306 12	R63791 Aspergillus aculeatus 1.38e+02
31	44	83.0	740 18	R95911 Mutant insulin-stimul 1.38e+02
32	44	83.0	740 18	R95911 Insulin-stimulated pr 1.38e+02
33	43	81.1	415 3	R20104 ERK2. 1.77e+02
34	43	81.1	534 13	R69720 Cyclic-GMP stimulated 1.77e+02
35	43	81.1	534 5	R28404 63 kD Cam PDE from cl 1.77e+02
36	42	79.2	10 18	R95425 HLA-B2702.75-84(D). 2.28e+02
37	42	79.2	10 16	R95413 Alpha1-helix of HLA-B 2.28e+02
38	42	79.2	12 18	R83062 HLA-B2702 CTL modulat 2.28e+02
39	42	79.2	12 18	R95429 HLA-B2702 84-79-84 pa 2.28e+02
40	42	79.2	20 18	R95428 HLA-B2702 84-75-84 pa 2.28e+02
41	42	79.2	20 16	R92908 HLA-B2702 CTL modulat 2.28e+02
42	42	79.2	25 18	R95416 HLA-B2702.60-84. 2.28e+02
43	42	79.2	25 18	R95422 HLAB38.6084. 2.28e+02
44	42	79.2	108 18	R93159 Murine monoclonal ant 2.28e+02
45	42	79.2	595 8	R41359 Tumour associated 90K 2.28e+02

ALIGNMENTS

RESULT 1  
ID R83096 standard; peptide; 10 AA.  
AC R83096:  
DT 16-MAY-1996 (first entry)  
DE HLA-B2702 CTL modulating peptide (B2702.75-84(L)).  
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
KW Immunosuppressant; graft versus host disorder; transplantation; therapy;  
KW Class I MHC; HLA-B2702.  
OS Synthetic.  
PN W09526979-A1.  
PD 12-OCT-1995.  
PF 05-APR-1995; U04349.  
PR 05-APR-1994; US-222851.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PI Clayberger C, Krensky AM, Parham P;  
DR WPI; 95-359582/46.  
PT Extension of acceptance period of transplants from MHC unmatched  
PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
PT host  
PS Example 14; Page 34; 80pp; English.  
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
CC class I major histocompatibility complex (MHC) antigens. This sequence  
CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC  
CC HLA-B2702. These sequences can be used to extend the period of  
CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
CC The peptides are administered to a patient in conjunction with  
CC a subtherapeutic amount of an immunosuppressant. This is administered to  
CC the patient for a limited period of time (compared to the lifetime  
CC administration for current treatments). The peptides particularly  
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
CC of the patient.  
SQ Sequence 10 AA;

Query Match 100.0%; Score 53; DB 16; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.30e+01;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 5 rillyr 10  
QY 1 RILLRY 6  
RESULT 2  
ID P80289 standard; protein; 125 AA.

AC P80289;  
 DT 07-DEC-1990 (first entry)  
 DE Human Vpre-B protein.  
 KW Pre-B cells; non-T acute lymphoblast leukaemia.  
 PN EP-269127-A.  
 PD 01-JUN-1988.  
 PF 27-NOV-1987; 117619.  
 PR 27-NOV-1986; GB-028433.  
 PR 14-JUL-1987; GB-016497.  
 PR 14-OCT-1987; GB-024100.  
 PA (HOFF) HOFFMANN-LA ROCHE AG.  
 PI Bauer SR, Kudo A, Melchers GF, Sakaguchi N;  
 DR WPI; 88-148947/22.  
 DR N-PSDB; N80476.  
 PT Nucleotide sequence selectively expressed in pre-B cells - used  
 PT in probes for determining non-T acute lymphoblast leukaemia and  
 PT for prepn. of polypeptide(s)  
 PS Disclosure; pp; English.  
 CC This is encoded by the human pre-B gene which differs from the  
 CC mouse pre-B-2 gene (of N82441) at several posns. The gene is also  
 CC selectively expressed in pre-B cell lines. Its pattern of expres-  
 CC ion follows that of Vpre-B1 and lambda-5 in the mouse.  
 CC See also N80470-75, N80475 and N82441-42.  
 SQ Sequence 125 AA;  
 Query Match 88.7%; Score 47; DB 1; Length 125;  
 Best Local Similarity 83.3%; Pred. No. 6.38e+01;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Db 52 rllly 57  
 I:||||  
 QY 1 RILLY 6  
 RESULT 3  
 ID P83001 standard; protein; 142 AA.  
 AC P83001;  
 DT 07-DEC-1990 (first entry)  
 DE V pre-B-2 protein.  
 KW Pre-B cells; non-T acute lymphoblast leukaemia.  
 PN EP-269127-A.  
 PD 01-JUN-1988.  
 PF 27-NOV-1987; 117619.  
 PR 27-NOV-1986; GB-028433.  
 PR 14-JUL-1987; GB-016497.  
 PR 14-OCT-1987; GB-024100.  
 PA (HOFF) HOFFMANN-LA ROCHE AG.  
 PI Bauer SR, Kudo A, Melchers GF, Sakaguchi N;  
 DR WPI; 88-148947/22.  
 DR N-PSDB; N82441.  
 PT Nucleotide sequence selectively expressed in pre-B cells - used  
 PT in probes for determining non-T acute lymphoblast leukaemia and  
 PT for prepn. of polypeptide(s)  
 PS Disclosure; pp; English.  
 CC This is encoded by the genomic form of the variable region pre-B-2  
 CC sequence. The gene is not rearranged during pre-B cell development.  
 CC This protein may associate with itself or with heavy chain V domains  
 CC expressed in pre-B cells. The gene is expressed only in pre-B cell lines.  
 CC See also N80470-75, N80476-77 and N82442.  
 SQ Sequence 142 AA;  
 Query Match 88.7%; Score 47; DB 1; Length 142;  
 Best Local Similarity 83.3%; Pred. No. 6.38e+01;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Db 66 rllly 71  
 I:||||  
 QY 1 RILLY 6  
 RESULT 4  
 ID P80288 standard; protein; 142 AA.  
 AC P80288;

DT 07-DEC-1990 (first entry)  
 DE V pre-B-1 protein.  
 KW Pre-B cells; non-T acute lymphoblast leukaemia; ss;  
 PN EP-269127-A.  
 PD 01-JUN-1988.  
 PF 27-NOV-1987; 117619.  
 PR 27-NOV-1986; GB-028433.  
 PR 14-JUL-1987; GB-016497.  
 PR 14-OCT-1987; GB-024100.  
 PA (HOFF) HOFFMANN-LA ROCHE AG.  
 PI Bauer SR, Kudo A, Melchers GF, Sakaguchi N;  
 DR WPI; 88-148947/22.  
 DR N-PSDB; N80475.  
 PT Nucleotide sequence selectively expressed in pre-B cells - used  
 PT in probes for determining non-T acute lymphoblast leukaemia and  
 PT for prepn. of polypeptide(s)  
 PS Disclosure; pp; English.  
 CC This is encoded by the genomic form of the variable region pre-B-1  
 CC sequence. The gene is not rearranged during pre-B cell development  
 CC and is 4.6 kb upstream of the lambda-5 gene. This protein can  
 CC associate with itself or with heavy chain V domains expressed in  
 CC pre-B cells. Vpre-B-1 and lambda-5 form a complete V domain via  
 CC non-covalent bonds. The gene is expressed only in pre-B cell lines.  
 CC See also N80470-74, N80476-77 and N82441-42.  
 SQ Sequence 142 AA;  
 Query Match 88.7%; Score 47; DB 1; Length 142;  
 Best Local Similarity 83.3%; Pred. No. 6.38e+01;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Db 66 rllly 71  
 I:||||  
 QY 1 RILLY 6  
 RESULT 5  
 ID R95423 standard; peptide; 10 AA.  
 AC R95423;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B2705.75-84.  
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN W09513288-21.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI; 95-194027/25.  
 PT Compens. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 11; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B2705.75-84. These sequences can be used to isolate the protein p74  
 CC from a T-cell lysate. p74 is a T-cell surface membrane protein  
 CC associated with T-cell activation in mammalian T-cells, and is also  
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is  
 CC found in a limited number of cell types, but is particularly expressed on  
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an  
 CC amphoteric detergent, and then passed through an affinity column  
 CC containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs), by adding to the



CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 10 AA;

Query Match 86.8%; Score 46; DB 18; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 8.26e+01;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 5 rtllry 10  
 | ||||

QY 1 RILLY 6

#### RESULT 6

ID R41212 standard; peptide; 10 AA.  
 AC R41212;  
 DT 15-MAR-1994 (first entry)  
 DE Peptide fragment of Class I HLA peptide.  
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;  
 KW parasitic disease; cytotoxic T lymphocyte; modulation.  
 OS Synthetic.  
 PN W09317699-A.  
 PD 16-SEP-1993.  
 PF 25-FEB-1993; U01758.  
 PR 02-MAR-1992; US-844716.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger CA, Krensky AM;  
 DR WPI: 93-303134/38.  
 PT New peptide(s) based on Class I HLA antigen domains - used for  
 PT modulating cytotoxic T-lymphocyte activity towards targets  
 PS Claim 11; Page 54; 61pp; English.  
 CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)  
 CC activity, either by inhibition or stimulation. It can be used  
 CC for inhibiting CTL toxicity in transplantations, for inducing CTL  
 CC activity in parasitic diseases and neoplasia and in studies on viral  
 CC infection. The peptide can also be used for identifying CTLs which  
 CC bind to it and removing subsets of CTLs from a T-cell composition.  
 CC This peptide sequence is more commonly found within larger peptide  
 CC compounds of not more than 30 amino acids in length.  
 SQ Sequence 10 AA;

Query Match 86.8%; Score 46; DB 8; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 8.26e+01;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 5 rtllry 10  
 | ||||

QY 1 RILLY 6

#### RESULT 7

ID R83075 standard; peptide; 10 AA.  
 AC R83075;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.75-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW Class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI: 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 14; Page 34; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R82907-R82913 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC corresponds to residues 75-84 of the alpha-1 domain of the class

CC I MHC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 10 AA;

Query Match 86.8%; Score 46; DB 16; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 8.26e+01;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 5 rtllry 10  
 | ||||

QY 1 RILLY 6

#### RESULT 8

ID R71425 standard; peptide; 17 AA.  
 AC R71425;  
 DT 12-OCT-1995 (first entry)  
 DE Human MHC 1 alpha 1 domain peptide Dk-(69-85).  
 KW Major histocompatibility complex class 1; MHC 1; cell receptor;  
 KW alpha 1 domain; peptide Dk-(62-85); interaction modulation;  
 KW arthritis; neoplasias; lupus erythematosus.  
 OS Homo sapiens.  
 PN W09505189-A.  
 PD 23-FEB-1995.  
 PF 12-AUG-1994; U09189.  
 PR 12-AUG-1993; US-105416.  
 PA (RECC ) UNIV CALIFORNIA.  
 PI Goldstein A, Goodenow RS, Olsson L;  
 DR WPI: 95-098577/13.  
 PT Regulating cell surface receptor response - by modulating  
 PT interaction between MHC class I antigen and the cell surface  
 PT receptor  
 PS Example 4; Page 45; 103pp; English.  
 CC R71424-R71438 are human major histocompatibility complex class 1  
 CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they  
 CC were used to modulate interactions between MHC 1 and cell surface  
 CC receptors. Via competitive inhibition the peptides diminish the  
 CC receptors response, this feature may be useful for the treatment  
 CC of neoplasias, lupus erythematosus and arthritis.  
 SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;  
 Best Local Similarity 83.3%; Pred. No. 8.26e+01;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rtllry 16  
 | ||||

QY 1 RILLY 6

#### RESULT 9

ID R71442 standard; peptide; 17 AA.  
 AC R71442;  
 DT 12-OCT-1995 (first entry)  
 DE Human HLA-B27-(62-85) antigen derived peptide.  
 KW Human HLA-B27-(62-85) antigen derived peptide; cell receptor;  
 KW interaction modulation; arthritis; neoplasias; lupus erythematosus.  
 OS Homo sapiens.  
 PN W09505189-A.  
 PD 23-FEB-1995.  
 PF 12-AUG-1994; U09189.  
 PR 12-AUG-1993; US-105416.  
 PA (RECC ) UNIV CALIFORNIA.  
 PI Goldstein A, Goodenow RS, Olsson L;  
 DR WPI: 95-098577/13.  
 PT Regulating cell surface receptor response - by modulating  
 PT interaction between MHC class I antigen and the cell surface

PT receptor  
 PS Example 4; Page 45; 103pp; English.  
 CC R71439-R71443 are human major histocompatibility complex class 1  
 CC (MHC 1) alpha 1 domain and HLA derived peptides and fusion peptides.  
 CC They were used to modulate interactions between MHC 1/HLA and cell  
 CC surface receptors. Via competitive inhibition the peptides diminish  
 CC the receptors response, this feature may be useful for the treatment  
 CC of neoplasias, lupus erythematosus and arthritis.  
 SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;  
 Best Local Similarity 83.3%; Pred. No. 8.26e+01;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rtllry 16  
 | | | | |  
 QY 1 RILLY 6

RESULT 10  
 ID R71443 standard; peptide; 17 AA.  
 AC R71443;  
 DT 12-OCT-1995 (first entry)  
 DE Human [Phe74]-HLA-B27-(62-85) antigen derived peptide.  
 KW Human [Phe74]-HLA-B27-(62-85) antigen derived peptide; cell receptor;  
 KW interaction modulation; arthritis; neoplasias; lupus erythematosus.  
 OS Homo sapiens.  
 PN WO9505189-A.  
 PD 23-FEB-1995.  
 PF 12-AUG-1994; U09189.  
 PR 12-AUG-1993; US-105416.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Goldstein A. Goodenow RS, Olsson L;  
 DR WPI; 95-098577/13.  
 PT Regulating cell surface receptor response - by modulating  
 PT interaction between MHC class I antigen and the cell surface  
 PT receptor  
 PS Example 4; Page 45; 103pp; English.  
 CC R71439-R71443 are human major histocompatibility complex class 1  
 CC (MHC 1) alpha 1 domain and HLA derived peptides and fusion peptides.  
 CC They were used to modulate interactions between MHC 1/HLA and cell  
 CC surface receptors. Via competitive inhibition the peptides diminish  
 CC the receptors response, this feature may be useful for the treatment  
 CC of neoplasias, lupus erythematosus and arthritis.  
 SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;  
 Best Local Similarity 83.3%; Pred. No. 8.26e+01;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rtllry 16  
 | | | | |  
 QY 1 RILLY 6

RESULT 11  
 ID R71440 standard; peptide; 17 AA.  
 AC R71440;  
 DT 12-OCT-1995 (first entry)  
 DE Human MHC 1 and HLA fusion peptide HLA-A2-(69-76)Dk-(77-85).  
 KW Major histocompatibility complex class 1; MHC 1; cell receptor;  
 KW alpha 1 domain; fusion peptide HLA-A2-(69-76)Dk-(77-85);  
 KW interaction modulation; arthritis; neoplasias; lupus erythematosus.  
 OS Homo sapiens.  
 PN WO9505189-A.  
 PD 23-FEB-1995.  
 PF 12-AUG-1994; U09189.  
 PR 12-AUG-1993; US-105416.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Goldstein A. Goodenow RS, Olsson L;  
 DR WPI; 95-098577/13.  
 PT Regulating cell surface receptor response - by modulating  
 PT interaction between MHC class I antigen and the cell surface

PT receptor  
 PS Example 4; Page 45; 103pp; English.  
 CC R71439-R71443 are human major histocompatibility complex class 1  
 CC (MHC 1) alpha 1 domain and HLA derived peptides and fusion peptides.  
 CC They were used to modulate interactions between MHC 1/HLA and cell  
 CC surface receptors. Via competitive inhibition the peptides diminish  
 CC the receptors response, this feature may be useful for the treatment  
 CC of neoplasias, lupus erythematosus and arthritis.  
 SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;  
 Best Local Similarity 83.3%; Pred. No. 8.26e+01;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rtllry 16  
 | | | | |  
 QY 1 RILLY 6

RESULT 12  
 ID R71433 standard; peptide; 17 AA.  
 AC R71433;  
 DT 12-OCT-1995 (first entry)  
 DE Human MHC 1 alpha 1 domain peptide [Ala85]-Dk-(69-85).  
 KW Major histocompatibility complex class 1; MHC 1; cell receptor;  
 KW alpha 1 domain; peptide [Ala85]-Dk-(69-85); interaction modulation;  
 KW arthritis; neoplasias; lupus erythematosus.  
 OS Homo sapiens.  
 PN WO9505189-A.  
 PD 23-FEB-1995.  
 PF 12-AUG-1994; U09189.  
 PR 12-AUG-1993; US-105416.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Goldstein A. Goodenow RS, Olsson L;  
 DR WPI; 95-098577/13.  
 PT Regulating cell surface receptor response - by modulating  
 PT interaction between MHC class I antigen and the cell surface  
 PT receptor  
 PS Example 4; Page 45; 103pp; English.  
 CC R71439-R71443 are human major histocompatibility complex class 1  
 CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they  
 CC were used to modulate interactions between MHC 1 and cell surface  
 CC receptors. Via competitive inhibition the peptides diminish the  
 CC receptors response, this feature may be useful for the treatment  
 CC of neoplasias, lupus erythematosus and arthritis.  
 SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;  
 Best Local Similarity 83.3%; Pred. No. 8.26e+01;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rtllry 16  
 | | | | |  
 QY 1 RILLY 6

RESULT 13  
 ID R71426 standard; peptide; 17 AA.  
 AC R71426;  
 DT 12-OCT-1995 (first entry)  
 DE Human MHC 1 alpha 1 domain peptide [Ala71]-Dk-(69-85).  
 KW Major histocompatibility complex class 1; MHC 1; cell receptor;  
 KW alpha 1 domain; peptide [Ala71]-Dk-(69-85); interaction modulation;  
 KW arthritis; neoplasias; lupus erythematosus.  
 OS Homo sapiens.  
 PN WO9505189-A.  
 PD 23-FEB-1995.  
 PF 12-AUG-1994; U09189.  
 PR 12-AUG-1993; US-105416.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Goldstein A. Goodenow RS, Olsson L;  
 DR WPI; 95-098577/13.  
 PT Regulating cell surface receptor response - by modulating

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PT interaction between MHC class I antigen and the cell surface
PT receptor
PS Example 4; Page 45; 103pp; English.
CC R71424-R71438 are human major histocompatibility complex class I
CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they
CC were used to modulate interactions between MHC 1 and cell surface
CC receptors. Via competitive inhibition the peptides diminish the
CC receptors response, this feature may be useful for the treatment
CC of neoplasias, lupus erythematosus and arthritis.
SQ Sequence 17 AA;

Query Match      86.8%; Score 46; DB 13; Length 17;
Best Local Similarity 83.3%; Pred. No. 8.26e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rllly 16
QY 1 RILLY 6

RESULT 14
ID R71428 standard; peptide; 17 AA.
AC R71428.
DE Human MHC 1 alpha 1 domain peptide [Ala78]-Dk-(69-85).
KW Major histocompatibility complex class I; MHC 1; cell receptor;
KW alpha 1 domain; peptide [Ala78]-Dk-(69-85); interaction modulation;
KW arthritis; neoplasias; lupus erythematosus.
OS Homo sapiens.
PN WO9505189-A.
PD 23-FEB-1995.
PR 12-AUG-1994; U09189.
PR 12-AUG-1993; US-105416.
PA (REGC ) UNIV CALIFORNIA.
PI Goldstein A, Goodenow RS, Olsson L;
DR WPI; 95-098577/13.
PT Regulating cell surface receptor response - by modulating
PT interaction between MHC class I antigen and the cell surface
PT receptor
PS Example 4; Page 45; 103pp; English.
CC R71424-R71438 are human major histocompatibility complex class I
CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they
CC were used to modulate interactions between MHC 1 and cell surface
CC receptors. Via competitive inhibition the peptides diminish the
CC receptors response, this feature may be useful for the treatment
CC of neoplasias, lupus erythematosus and arthritis.
SQ Sequence 17 AA;

Query Match      86.8%; Score 46; DB 13; Length 17;
Best Local Similarity 83.3%; Pred. No. 8.26e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rllly 16
QY 1 RILLY 6

RESULT 15
ID R71424 standard; peptide; 24 AA.
AC R71424;
DE Human MHC 1 alpha 1 domain peptide Dk-(62-85).
KW Major histocompatibility complex class I; MHC 1; cell receptor;
KW alpha 1 domain; peptide Dk-(62-85); interaction modulation;
KW arthritis; neoplasias; lupus erythematosus.
OS Homo sapiens.
PN WO9505189-A.
PD 23-FEB-1995.
PR 12-AUG-1994; U09189.
PR 12-AUG-1993; US-105416.
PA (REGC ) UNIV CALIFORNIA.
PI Goldstein A, Goodenow RS, Olsson L;
DR WPI; 95-098577/13.

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PT Regulating cell surface receptor response - by modulating
PT interaction between MHC class I antigen and the cell surface
PT receptor
PS Example 4; Page 45; 103pp; English.
CC R71424-R71438 are human major histocompatibility complex class I
CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they
CC were used to modulate interactions between MHC 1 and cell surface
CC receptors. Via competitive inhibition the peptides diminish the
CC receptors response, this feature may be useful for the treatment
CC of neoplasias, lupus erythematosus and arthritis.
SQ Sequence 24 AA;

Query Match      86.8%; Score 46; DB 13; Length 24;
Best Local Similarity 83.3%; Pred. No. 8.26e+01;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 18 rllly 23
QY 1 RILLY 6

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Search completed: Thu May 22 08:29:12 1997  
 Job time : 8 secs.

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(TM)  
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu May 22 08:43:51 1997; MasPar time 1.74 Seconds  
37.653 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-653-294-5  
Description: (1-6) from US08653294.pep  
Perfect score: 53  
Sequence: 1 RILLY 6

Scoring table: PAM 150  
Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Maximum DB seq length 60

Database: a-geneseq26  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19

Statistics: Mean 16.452; Variance 46.284; scale 0.355

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	53	100.0	10 16	R83096	HLA-B2702 CTL modul	1.30e+01
2	46	86.8	10 18	R95423	HLA-B2705.75-84.	8.26e+01
3	46	86.8	10 18	R41212	Peptide fragment of C	8.26e+01
4	46	86.8	10 16	R83075	HLA-B2702 CTL modul	8.26e+01
5	46	86.8	17 13	R71425	Human MHC 1 alpha 1 d	8.26e+01
6	46	86.8	17 13	R71442	Human HLA-B27-(62-85)	8.26e+01
7	46	86.8	17 13	R71443	Human (Phe74)-HLA-B27	8.26e+01
8	46	86.8	17 13	R71440	Human MHC 1 and HLA f	8.26e+01
9	46	86.8	17 13	R71433	Human MHC 1 alpha 1 d	8.26e+01
10	46	86.8	17 13	R71426	Human MHC 1 alpha 1 d	8.26e+01
11	46	86.8	17 13	R71428	Human MHC 1 alpha 1 d	8.26e+01
12	46	86.8	24 13	R71424	Human MHC 1 alpha 1 d	8.26e+01
13	46	86.8	24 13	R71434	Human MHC 1 alpha 1 d	8.26e+01
14	46	86.8	24 13	R71436	Human MHC 1 alpha 1 d	8.26e+01
15	46	86.8	24 13	R71427	Human MHC 1 alpha 1 d	8.26e+01
16	46	86.8	24 13	R71435	Human MHC 1 alpha 1 d	8.26e+01
17	46	86.8	25 18	R95417	HLA-B2705.60-84.	8.26e+01
18	46	86.8	25 13	R71420	Human MHC 1 alpha 1 d	8.26e+01
19	46	86.8	25 3	R20116	MHC Class I-derived p	8.26e+01

20	46	86.8	25 8	R41221	Peptide fragment of H	8.26e+01
21	46	86.8	25 13	R95619	MHC-I peptide Dk-(61-	8.26e+01
22	46	86.8	25 16	R83091	HLA-B2702 CTL modul	8.26e+01
23	45	84.9	24 13	R71438	Human MHC 1 alpha 1 d	1.07e+02
24	42	79.2	10 18	R95425	HLA-B2702.75-84(D).	2.28e+02
25	42	79.2	10 18	R95413	Alphal-helix of HLA-B	2.28e+02
26	42	79.2	10 16	R83062	HLA-B2702 CTL modul	2.28e+02
27	42	79.2	12 18	R95429	HLA-B2702 84-79-84 pa	2.28e+02
28	42	79.2	20 18	R95428	HLA-B2702 84-75-84 pa	2.28e+02
29	42	79.2	20 16	R92908	HLA-B2702 CTL modul	2.28e+02
30	42	79.2	25 18	R95416	HLA-B2702.60-84.	2.28e+02
31	42	79.2	25 18	R95422	HLA-B2702.60-84.	2.28e+02

Note: Post-processor removed 14 summaries from list due to search parameters chosen.

ALIGNMENTS

RESULT 1  
ID R83096 standard; peptide; 10 AA.  
AC R83096;  
DT 16-MAY-1996 (first entry)  
DE HLA-B2702 CTL modulating peptide (B2702.75-84(L)).  
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
KW class I MHC; HLA-B2702.  
OS Synthetic.  
PN WO9526979-A1.  
PD 12-OCT-1995.  
PF 05-APR-1995; U04349.  
PR 05-APR-1994; US-222851.  
PA (STRD) UNIV LELAND STANFORD JUNIOR.  
PI Clayberger C, Krensky AM, Parham P;  
DR WPI; 95-358582/46.  
PT Extension of acceptance period of transplants from MHC unmatched  
PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
PT host  
PS Example 14; Page 34; 80pp; English.  
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
CC class I major histocompatibility complex (MHC) antigens. This sequence  
CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC  
CC HLA-B2702. These sequences can be used to extend the period of  
CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
CC The peptides are administered to a patient in conjunction with  
CC a subtherapeutic amount of an immunosuppressant. This is administered to  
CC the patient for a limited period of time (compared to the lifetime  
CC administration for current treatments). The peptides particularly  
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
CC of the patient.  
SQ Sequence 10 AA;

Query Match 100.0%; Score 53; DB 16; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.30e+01;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 RILLY 10  
QY 1 RILLY 6

RESULT 2  
ID R95423 standard; peptide; 10 AA.  
AC R95423;  
DT 12-NOV-1996 (first entry)  
DE HLA-B2705.75-84.  
KW HLA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;  
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
KW cytolysis; antigen presenting cell.  
OS Synthetic.  
PN WO9513288-A1.  
PD 18-MAY-1995.  
PF 10-NOV-1994; U12985.

PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI; 95-194027/25.  
 PT Compens. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 11; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B2705.75-84. These sequences can be used to isolate the protein p74  
 CC from a T-cell lysate. p74 is a T-cell surface membrane protein  
 CC associated with T-cell activation in mammalian T-cells, and is also  
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is  
 CC found in a limited number of cell types, but is particularly expressed on  
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an  
 CC amphoteric detergent, and then passed through an affinity column  
 CC containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 10 AA;

Query Match 86.8%; Score 46; DB 18; Length 10;

Best Local Similarity 83.3%; Pred. No. 8.26e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 5 rtllry 10  
 | | | | |  
 QY 1 RILLY 6

### RESULT 3

ID R41212 standard; peptide; 10 AA.

AC R41212;

DT 15-MAR-1994 (first entry)

DE Peptide fragment of Class I HLA peptide.

KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;

KW parasitic disease; cytotoxic T lymphocyte; modulation.

OS Synthetic.

PN W09317699-A.

PD 16-SEP-1993.

PF 25-FEB-1993; U01758.

PR 02-MAR-1992; US-844716.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

PI Clayberger CA, Krensky AM;

DR WPI; 93-303134/38.

PT New peptide(s) based on Class I HLA antigen domains - used for

PT modulating cytotoxic T-lymphocyte activity towards targets

PS Claim 11; Page 54; 61pp; English.

CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)

CC activity, either by inhibition or stimulation. It can be used

CC for inhibiting CTL toxicity in transplantations, for inducing CTL

CC activity in parasitic diseases and neoplasia and in studies on viral

CC infection. The peptide can also be used for identifying CTLs which

CC bind to it and removing subsets of CTLs from a T-cell composition.

CC This peptide sequence is more commonly found within larger peptide

CC compounds of not more than 30 amino acids in length.

SQ Sequence 10 AA;

Query Match 86.8%; Score 46; DB 8; Length 10;

Best Local Similarity 83.3%; Pred. No. 8.26e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 5 rtllry 10  
 | | | | |  
 QY 1 RILLY 6

### RESULT 4

ID R83075 standard; peptide; 10 AA.

AC R83075;

DT 16-MAY-1996 (first entry)

DE HLA-B2702 CTL modulating peptide (B2702.75-84).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW immunosuppressant; graft versus host disorder; transplantation; therapy;

KW class I MHC; HLA-B2702.

OS Synthetic.

PN W09526979-A1.

PD 12-OCT-1995.

PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM, Parham P;

DR WPI; 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient

PT host

PS Example 14; Page 34; 80pp; English.

CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of

CC class I major histocompatibility complex (MHC) antigens. This sequence

CC corresponds to residues 75-84 of the alpha-1 domain of the class

CC I MHC HLA-B2702. These sequences can be used to extend the period of

CC acceptance by a recipient of a transplant from an MHC unmatched donor.

CC The peptides are administered to a patient in conjunction with a

CC subtherapeutic amount of an immunosuppressant. This is administered to

CC the patient for a limited period of time (compared to the lifetime

CC administration for current treatments). The peptides particularly

CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)

CC of the patient.

SQ Sequence 10 AA;

Query Match 86.8%; Score 46; DB 16; Length 10;

Best Local Similarity 83.3%; Pred. No. 8.26e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 5 rtllry 10  
 | | | | |  
 QY 1 RILLY 6

### RESULT 5

ID R71425 standard; peptide; 17 AA.

AC R71425;

DT 12-OCT-1995 (first entry)

DE Human MHC 1 alpha 1 domain peptide Dk-(69-85).

KW Major histocompatibility complex class 1; MHC 1; cell receptor;

KW alpha 1 domain; peptide Dk-(62-85); interaction modulation;

KW arthritis; neoplasias; lupus erythematosus.

OS Homo sapiens.

PN W09505189-A.

PD 23-FEB-1995.

PF 12-AUG-1994; U09189.

PR 12-AUG-1993; US-105416.

PA (REGC ) UNIV CALIFORNIA.

PI Goldstein A, Goodenow RS, Olsson L;

DR WPI; 95-098577/13.

PT Regulating cell surface receptor response - by modulating

PT interaction between MHC class I antigen and the cell surface

PT receptor

PS Example 4; Page 45; 103pp; English.

CC R71424-R71438 are human major histocompatibility complex class 1

CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they

CC were used to modulate interactions between MHC 1 and cell surface

CC receptors. Via competitive inhibition the peptides diminish the

CC receptors response, this feature may be useful for the treatment

CC of neoplasias, lupus erythematosus and arthritis.

SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;

Best Local Similarity 83.3%; Pred. No. 8.26e+01;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rllly 16  
1 | | | |  
Qy 1 RILLRY 6

RESULT 6  
ID R71442 standard; peptide; 17 AA.  
AC R71442;  
DT 12-OCT-1995 (first entry)  
DE Human HLA-B27-(62-85) antigen derived peptide.  
KW Human HLA-B27-(62-85) antigen derived peptide; cell receptor;  
KW interaction modulation; arthritis; neoplasias; lupus erythematosus.  
OS Homo sapiens.  
PN WO9505189-A.  
PD 23-FEB-1995.  
PF 12-AUG-1994; U09189.  
PR 12-AUG-1993; US-105416.  
PA (REGC ) UNIV CALIFORNIA.  
PI Goldstein A, Goodenow RS, Olsson L;  
DR WPI; 95-098577/13.  
PT Regulating cell surface receptor response - by modulating  
PT interaction between MHC class I antigen and the cell surface  
PT receptor  
PS Example 4; Page 45; 103pp; English.  
CC R71439-R71443 are human major histocompatibility complex class 1  
CC (MHC 1) alpha 1 domain and HLA derived peptides and fusion peptides.  
CC They were used to modulate interactions between MHC 1/HLA and cell  
CC surface receptors. Via competitive inhibition the peptides diminish  
CC the receptors response. This feature may be useful for the treatment  
CC of neoplasias, lupus erythematosus and arthritis.  
SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;  
Best Local Similarity 83.3%; Pred. No. 8.26e+01;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rllly 16  
1 | | | |  
Qy 1 RILLRY 6

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rllly 16  
1 | | | |  
Qy 1 RILLRY 6

RESULT 8  
ID R71440 standard; peptide; 17 AA.  
AC R71440;  
DT 12-OCT-1995 (first entry)  
DE Human MHC 1 and HLA fusion peptide HLA-A2-(69-76)Dk-(77-85).  
KW Major histocompatibility complex class 1; MHC 1; cell receptor;  
KW alpha 1 domain; fusion peptide HLA-A2-(69-76)Dk-(77-85);  
KW interaction modulation; arthritis; neoplasias; lupus erythematosus.  
OS Homo sapiens.  
PN WO9505189-A.  
PD 23-FEB-1995.  
PF 12-AUG-1994; U09189.  
PR 12-AUG-1993; US-105416.  
PA (REGC ) UNIV CALIFORNIA.  
PI Goldstein A, Goodenow RS, Olsson L;  
DR WPI; 95-098577/13.  
PT Regulating cell surface receptor response - by modulating  
PT interaction between MHC class I antigen and the cell surface  
PT receptor  
PS Example 4; Page 45; 103pp; English.  
CC R71439-R71443 are human major histocompatibility complex class 1  
CC (MHC 1) alpha 1 domain and HLA derived peptides and fusion peptides.  
CC They were used to modulate interactions between MHC 1/HLA and cell  
CC surface receptors. Via competitive inhibition the peptides diminish  
CC the receptors response. This feature may be useful for the treatment  
CC of neoplasias, lupus erythematosus and arthritis.  
SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;  
Best Local Similarity 83.3%; Pred. No. 8.26e+01;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rllly 16  
1 | | | |  
Qy 1 RILLRY 6

RESULT 7  
ID R71443 standard; peptide; 17 AA.  
AC R71443;  
DT 12-OCT-1995 (first entry)  
DE Human [Phe74]-HLA-B27-(62-85) antigen derived peptide.  
KW Human [Phe74]-HLA-B27-(62-85) antigen derived peptide; cell receptor;  
KW interaction modulation; arthritis; neoplasias; lupus erythematosus.  
OS Homo sapiens.  
PN WO9505189-A.  
PD 23-FEB-1995.  
PF 12-AUG-1994; U09189.  
PR 12-AUG-1993; US-105416.  
PA (REGC ) UNIV CALIFORNIA.  
PI Goldstein A, Goodenow RS, Olsson L;  
DR WPI; 95-098577/13.  
PT Regulating cell surface receptor response - by modulating  
PT interaction between MHC class I antigen and the cell surface  
PT receptor  
PS Example 4; Page 45; 103pp; English.  
CC R71439-R71443 are human major histocompatibility complex class 1  
CC (MHC 1) alpha 1 domain and HLA derived peptides and fusion peptides.  
CC They were used to modulate interactions between MHC 1/HLA and cell  
CC surface receptors. Via competitive inhibition the peptides diminish  
CC the receptors response. This feature may be useful for the treatment  
CC of neoplasias, lupus erythematosus and arthritis.  
SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;  
Best Local Similarity 83.3%; Pred. No. 8.26e+01;

Db 11 rllly 16  
1 | | | |  
Qy 1 RILLRY 6

RESULT 9  
ID R71433 standard; peptide; 17 AA.  
AC R71433;  
DT 12-OCT-1995 (first entry)  
DE Human MHC 1 alpha 1 domain peptide [Ala85]-Dk-(69-85).  
KW Major histocompatibility complex class 1; MHC 1; cell receptor;  
KW alpha 1 domain; peptide [Ala85]-Dk-(69-85); interaction modulation;  
KW arthritis; neoplasias; lupus erythematosus.  
OS Homo sapiens.  
PN WO9505189-A.  
PD 23-FEB-1995.  
PF 12-AUG-1994; U09189.  
PR 12-AUG-1993; US-105416.  
PA (REGC ) UNIV CALIFORNIA.  
PI Goldstein A, Goodenow RS, Olsson L;  
DR WPI; 95-098577/13.  
PT Regulating cell surface receptor response - by modulating  
PT interaction between MHC class I antigen and the cell surface  
PT receptor  
PS Example 4; Page 45; 103pp; English.  
CC R71424-R71438 are human major histocompatibility complex class 1  
CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they  
CC were used to modulate interactions between MHC 1 and cell surface  
CC receptors. Via competitive inhibition the peptides diminish the  
CC receptors response, this feature may be useful for the treatment  
CC of neoplasias, lupus erythematosus and arthritis.  
SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;

Db 11 rllly 16  
1 | | | |  
Qy 1 RILLRY 6

Best Local Similarity 83.3%; Pred. No. 8.26e+01;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rllry 16  
| | | |  
QY 1 RILLY 6

## RESULT 10

ID R71426 standard; peptide; 17 AA.  
AC R71426;  
DE 12-OCT-1995 (first entry)  
DE Human MHC 1 alpha 1 domain peptide [Ala71]-Dk-(69-85).  
KW Major histocompatibility complex class 1; MHC 1; cell receptor;  
KW alpha 1 domain; peptide [Ala71]-Dk-(69-85); interaction modulation;  
KW arthritis; neoplasias; lupus erythematosus.  
OS Homo sapiens.  
PN WO9505189-A.  
PD 23-FEB-1995.  
PF 12-AUG-1994; U09189.  
PR 12-AUG-1993; US-105416.  
PA (REGC ) UNIV CALIFORNIA.  
PI Goldstein A, Goodenow RS, Olsson L;  
DR WPI; 95-098577/13.  
PT Regulating cell surface receptor response - by modulating  
PT interaction between MHC class I antigen and the cell surface  
PT receptor  
PS Example 4; Page 45; 103pp; English.  
CC R71424-R71438 are human major histocompatibility complex class 1  
CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they  
CC were used to modulate interactions between MHC 1 and cell surface  
CC receptors. Via competitive inhibition the peptides diminish the  
CC receptors response, this feature may be useful for the treatment  
CC of neoplasias, lupus erythematosus and arthritis.  
SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;  
Best Local Similarity 83.3%; Pred. No. 8.26e+01;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rllry 16  
| | | |  
QY 1 RILLY 6

## RESULT 11

ID R71428 standard; peptide; 17 AA.  
AC R71428;  
DE 12-OCT-1995 (first entry)  
DE Human MHC 1 alpha 1 domain peptide [Ala78]-Dk-(69-85).  
KW Major histocompatibility complex class 1; MHC 1; cell receptor;  
KW alpha 1 domain; peptide [Ala78]-Dk-(69-85); interaction modulation;  
KW arthritis; neoplasias; lupus erythematosus.  
OS Homo sapiens.  
PN WO9505189-A.  
PD 23-FEB-1995.  
PF 12-AUG-1994; U09189.  
PR 12-AUG-1993; US-105416.  
PA (REGC ) UNIV CALIFORNIA.  
PI Goldstein A, Goodenow RS, Olsson L;  
DR WPI; 95-098577/13.  
PT Regulating cell surface receptor response - by modulating  
PT interaction between MHC class I antigen and the cell surface  
PT receptor  
PS Example 4; Page 45; 103pp; English.  
CC R71424-R71438 are human major histocompatibility complex class 1  
CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they  
CC were used to modulate interactions between MHC 1 and cell surface  
CC receptors. Via competitive inhibition the peptides diminish the  
CC receptors response, this feature may be useful for the treatment  
CC of neoplasias, lupus erythematosus and arthritis.  
SQ Sequence 17 AA;

Query Match 86.8%; Score 46; DB 13; Length 17;  
Best Local Similarity 83.3%; Pred. No. 8.26e+01;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 rllry 16  
| | | |  
QY 1 RILLY 6

## RESULT 12

ID R71424 standard; peptide; 24 AA.  
AC R71424;  
DE 12-OCT-1995 (first entry)  
DE Human MHC 1 alpha 1 domain peptide Dk-(62-85).  
KW Major histocompatibility complex class 1; MHC 1; cell receptor;  
KW alpha 1 domain; peptide Dk-(62-85); interaction modulation;  
KW arthritis; neoplasias; lupus erythematosus.  
OS Homo sapiens.  
PN WO9505189-A.  
PD 23-FEB-1995.  
PF 12-AUG-1994; U09189.  
PR 12-AUG-1993; US-105416.  
PA (REGC ) UNIV CALIFORNIA.  
PI Goldstein A, Goodenow RS, Olsson L;  
DR WPI; 95-098577/13.  
PT Regulating cell surface receptor response - by modulating  
PT interaction between MHC class I antigen and the cell surface  
PT receptor  
PS Example 4; Page 45; 103pp; English.  
CC R71424-R71438 are human major histocompatibility complex class 1  
CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they  
CC were used to modulate interactions between MHC 1 and cell surface  
CC receptors. Via competitive inhibition the peptides diminish the  
CC receptors response, this feature may be useful for the treatment  
CC of neoplasias, lupus erythematosus and arthritis.  
SQ Sequence 24 AA;

Query Match 86.8%; Score 46; DB 13; Length 24;  
Best Local Similarity 83.3%; Pred. No. 8.26e+01;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 18 rllry 23  
| | | |  
QY 1 RILLY 6

## RESULT 13

ID R71434 standard; peptide; 24 AA.  
AC R71434;  
DE 12-OCT-1995 (first entry)  
DE Human MHC 1 alpha 1 domain peptide [Ala68, 75]-Dk-(62-85).  
KW Major histocompatibility complex class 1; MHC 1; cell receptor;  
KW alpha 1 domain; peptide [Ala68, 75]-Dk-(62-85); interaction modulation;  
KW arthritis; neoplasias; lupus erythematosus.  
OS Homo sapiens.  
PN WO9505189-A.  
PD 23-FEB-1995.  
PF 12-AUG-1994; U09189.  
PR 12-AUG-1993; US-105416.  
PA (REGC ) UNIV CALIFORNIA.  
PI Goldstein A, Goodenow RS, Olsson L;  
DR WPI; 95-098577/13.  
PT Regulating cell surface receptor response - by modulating  
PT interaction between MHC class I antigen and the cell surface  
PT receptor  
PS Example 4; Page 45; 103pp; English.  
CC R71424-R71438 are human major histocompatibility complex class 1  
CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they  
CC were used to modulate interactions between MHC 1 and cell surface  
CC receptors. Via competitive inhibition the peptides diminish the  
CC receptors response, this feature may be useful for the treatment  
CC of neoplasias, lupus erythematosus and arthritis.  
SQ Sequence 24 AA;



Query Match 86.8%; Score 46; DB 13; Length 24;  
 Best Local Similarity 83.3%; Pred. No. 8.26e+01;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 18 rtllry 23  
 | | | |  
 QY 1 RILLY 6

SQ Sequence 24 AA;  
 Query Match 86.8%; Score 46; DB 13; Length 24;  
 Best Local Similarity 83.3%; Pred. No. 8.26e+01;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 18 rtllry 23  
 | | | |  
 QY 1 RILLY 6

Search completed: Thu May 22 08:44:00 1997  
 Job time : 9 secs.

RESULT 14  
 ID R71436 standard; peptide; 24 AA.  
 AC R71436;  
 DE 12-OCT-1995 (first entry)  
 DT Human MHC 1 alpha 1 domain peptide [Ala70, 77]-DK-(62-85).  
 KW Major histocompatibility complex class 1; MHC 1; cell receptor;  
 KW alpha 1 domain; peptide [Ala70, 77]-DK-(62-85); interaction modulation;  
 KW arthritis; neoplasias; lupus erythematosus.  
 OS Homo sapiens.  
 PN WO9505189-A.  
 PD 23-FEB-1995.  
 PF 12-AUG-1994; U09189.  
 PR 12-AUG-1993; US-105416.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Goldstein A, Goodenow RS, Olsson L;  
 DR WPI; 95-098577/13.  
 PT Regulating cell surface receptor response - by modulating  
 PT interaction between MHC class I antigen and the cell surface  
 PT receptor  
 PS Example 4; Page 45; 103pp; English.  
 CC R71424-R71438 are human major histocompatibility complex class 1  
 CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they  
 CC were used to modulate interactions between MHC 1 and cell surface  
 CC receptors. Via competitive inhibition the peptides diminish the  
 CC receptors response, this feature may be useful for the treatment  
 CC of neoplasias, lupus erythematosus and arthritis.  
 SQ Sequence 24 AA;

Query Match 86.8%; Score 46; DB 13; Length 24;  
 Best Local Similarity 83.3%; Pred. No. 8.26e+01;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 18 rtllry 23  
 | | | |  
 QY 1 RILLY 6

RESULT 15  
 ID R71427 standard; peptide; 24 AA.  
 AC R71427;  
 DE 12-OCT-1995 (first entry)  
 DT Human MHC 1 alpha 1 domain peptide [Ala74]-DK-(62-85).  
 KW Major histocompatibility complex class 1; MHC 1; cell receptor;  
 KW alpha 1 domain; peptide [Ala74]-DK-(62-85); interaction modulation;  
 KW arthritis; neoplasias; lupus erythematosus.  
 OS Homo sapiens.  
 PN WO9505189-A.  
 PD 23-FEB-1995.  
 PF 12-AUG-1994; U09189.  
 PR 12-AUG-1993; US-105416.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Goldstein A, Goodenow RS, Olsson L;  
 DR WPI; 95-098577/13.  
 PT Regulating cell surface receptor response - by modulating  
 PT interaction between MHC class I antigen and the cell surface  
 PT receptor  
 PS Example 4; Page 45; 103pp; English.  
 CC R71424-R71438 are human major histocompatibility complex class 1  
 CC (MHC 1) alpha 1 domain derived peptides and peptide mutants, they  
 CC were used to modulate interactions between MHC 1 and cell surface  
 CC receptors. Via competitive inhibition the peptides diminish the  
 CC receptors response, this feature may be useful for the treatment  
 CC of neoplasias, lupus erythematosus and arthritis.

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MPSRCH (TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:42:00 1997; MasPar time 2.57 Seconds  
66.443 Million cell updates/sec

Tabular output not generated.

Title: >US-08-653-294-4  
Description: (1-6) from US08653294.pep  
Perfect Score: 49  
Sequence: 1 RIALRY 6

Scoring table: PAM 150  
Gap 15

Searched: 89912 seqs, 2850787 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Maximum DB seq length 60

Database: pir50  
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3  
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8  
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 21.604; Variance 27.804; scale 0.777

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	No. Score	Match Length	ID	Description	Pred. No.
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No matches found.

Search completed: Thu May 22 08:42:12 1997  
Job time : 12 secs.

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MPERCH (TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:41:35 1997; MasPar time 1.89 Seconds  
Tabular output not generated. 67.442 Million cell updates/sec

Title: >US-08-653-294-4  
Description: (1-6) from US08653294.pep  
Perfect Score: 49  
Sequence: 1 RIALRY 6

Scoring table: PAM 150  
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Maximum DB seq length 60

Database: swiss-prot34  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 22.521; Variance 22.707; scale 0.992

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

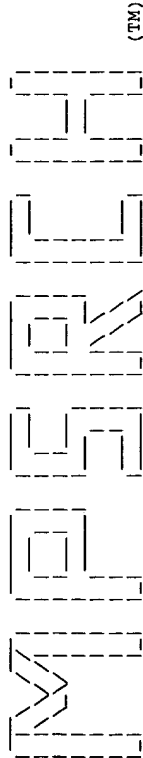
Result No.	Query Match	Score	Length	ID	Description	Pred. No.
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No matches found.

Search completed: Thu May 22 08:41:43 1997  
Job time : 8 secs.

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:42:30 1997; MasPar time 1.75 Seconds  
Tabular output not generated. 37.295 Million cell updates/sec

Title: >US-08-653-294-4  
Description: (1-6) from US08653294.pep  
Perfect Score: 49  
Sequence: 1 RIALRY 6

Scoring table: PAM 150  
Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Maximum DB seq length 60

Database: a-geneseq26  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19

Statistics: Mean 15.638; Variance 39.027; scale 0.401

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	49	100.0	10 18	R95413	Alpha-helix of HLA-B	1.25e+01
2	49	100.0	10 18	R95425	HLA-B2702.75-84(D)	1.25e+01
3	49	100.0	10 18	R41208	Peptide fragment of C	1.25e+01
4	49	100.0	10 16	R83062	HLA-B2702 CTL modul	1.25e+01
5	49	100.0	10 16	R83094	HLA-B2702 CTL modul	1.25e+01
6	49	100.0	12 18	R95429	HLA-B2702 84-79-84 pa	1.25e+01
7	49	100.0	15 16	R92912	HLA-B2702 CTL modul	1.25e+01
8	49	100.0	20 18	R95428	HLA-B2702 84-75-84 pa	1.25e+01
9	49	100.0	20 16	R92907	HLA-B2702 CTL modul	1.25e+01
10	49	100.0	20 16	R92908	HLA-B2702 CTL modul	1.25e+01
11	49	100.0	25 18	R95416	HLA-B2702.60-84	1.25e+01
12	49	100.0	25 18	R95422	HLAB38.6084	1.25e+01
13	49	100.0	25 16	R83090	HLA-B2702 CTL modul	1.25e+01
14	49	100.0	25 8	R41205	Peptide fragment of C	1.25e+01
15	49	100.0	25 16	R83093	HLAB38 CTL modul	1.25e+01
16	49	100.0	25 8	R48286	Peptide fragment of H	1.25e+01
17	45	91.8	43 18	R92804	PB145 serpin enzyme c	4.07e+01
18	42	85.7	10 18	R95426	HLA-B2702.75-84(T)	9.64e+01
19	42	85.7	10 16	R83096	HLA-B2702 CTL modul	9.64e+01

20 42 85.7 10 16 R83095 HLA-B2702 CTL modul 9.64e+01  
21 42 85.7 20 16 R92910 HLA-B2702 CTL modul 9.64e+01  
22 42 85.7 20 16 R92909 HLA-B2702 CTL modul 9.64e+01

Note: Post-processor removed 23 summaries from list due to search parameters chosen.

ALIGNMENTS

RESULT 1

ID R95413 standard; peptide; 10 AA.  
AC R95413;  
DT 12-NOV-1996 (first entry)  
DE Alpha-helix of HLA-B2702.  
KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;  
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
KW cytolysis; antigen presenting cell.  
OS Synthetic.  
PN WO9513288-A1.  
PD 18-MAY-1995.  
PF 10-NOV-1994; U12985.  
PR 10-NOV-1993; US-150493.  
PI (STRD) UNIV LELAND STANFORD JUNIOR.  
PA Clayberger C, Krensky AM;  
DR WPI; 95-194027/25.  
PT Compsns. comprising lymphoid surface membrane proteins - which may  
PT inhibit cytolytic activity and differentiation of CTLs.  
PS Example: Page 11; 29pp; English.  
CC This sequence represents the alpha-helix of the  
CC human-leucocyte-associated antigen B2702 (HLA-B2702). This sequence,  
CC epitopes, and palindromes of it (such as R95428) can be used to isolate  
CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
CC protein associated with T-cell activation in mammalian T-cells, and is  
CC also immunologically cross reactive with the heat shock protein Hsc70.  
CC p74 is found in a limited number of cell types, but is particularly  
CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
CC cell with an amphoteric detergent, and then passed through an affinity  
CC column containing a covalently bound HLA-B2702 palindromic peptide.  
CC Compositions comprising the extracellular fragment of p74 combined with  
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate  
CC compounds can be screened for their effect on the cytolytic activity of  
CC T-cells, by combining them with the extracellular portion of p74 and  
CC determining the amount of binding between the candidate compound and p74.  
CC Modulation of CTL activity can be inhibited in a cellular composition the  
CC containing T-cells and antigen presenting cells (APCs), by adding to the  
CC mix the extracellular portion of p74, in an amount sufficient to compete  
CC with p74 for the binding of the p74 ligand.  
SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 18; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.25e+01; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0;

Db 5 rialry 10  
QY 1 RIALRY 6

RESULT 2

ID R95425 standard; peptide; 10 AA.  
AC R95425;  
DT 12-NOV-1996 (first entry)  
DE HLA-B2702.75-84(D).  
KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;  
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
KW cytolysis; antigen presenting cell.  
OS Synthetic.  
PN Key Location/Qualifiers  
FH Misc-difference 3  
FT /note= "N3D mutation"

PN W09513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI; 95-194027/25.  
 PT compns. comprising lymphoid surface membrane proteins - which may  
 PS inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 11; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B2702.75-84(D). These sequences can be used to isolate the protein  
 CC p74 from a T-cell lysate. p74 is a T-cell surface membrane protein  
 CC associated with T-cell activation in mammalian T-cells, and is also  
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is  
 CC found in a limited number of cell types, but is particularly expressed on  
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an  
 CC amphoteric detergent, and then passed through an affinity column  
 CC containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs) by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 CC Sequence 10 AA;

Query Match 100.0%; Score 49; DB 18; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.25e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 rialry 10  
 |||||  
 QY 1 RIALRY 6

RESULT 3

ID R41208 standard; peptide; 10 AA.

AC R41208;

DE 15-MAR-1994 (first entry)

DE Peptide fragment of Class I HLA peptide.

KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;

KW parasitic disease; cytotoxic T lymphocyte; modulation.

OS Synthetic.

PN W09317699-A.

PD 16-SEP-1993.

PF 23-FEB-1993; U01758.

PR 02-MAR-1992; US-844716.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

PI Clayberger CA, Krensky AM;

DR WPI; 93-303134/38.

PT New peptide(s) based on Class I HLA antigen domains - used for

PT modulating cytotoxic T-lymphocyte activity towards targets

PS Claim 11; Page 54; 61pp; English.

CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)

CC activity, either by inhibition or stimulation. It can be used

CC for inhibiting CTL toxicity in transplantations, for inducing CTL

CC activity in parasitic diseases and neoplasia and in studies on viral

CC infection. The peptide can also be used for identifying CTLs which

CC bind to it and removing subsets of CTLs from a T-cell composition.

CC This peptide sequence is more commonly found within larger peptide

CC compounds of not more than 30 amino acids in length.

CC Sequence 10 AA;

Query Match 100.0%; Score 49; DB 8; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.25e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 rialry 10  
 |||||  
 QY 1 RIALRY 6

RESULT 4

ID R83062 standard; peptide; 10 AA.

AC R83062;

DE 16-MAY-1996 (first entry)

DE HLA-B2702 CTL modulating peptide (B2702.75-84).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW immunosuppressant; CTL; major histocompatibility complex; therapy;

KW class I MHC; HLA-B2702.

OS Synthetic.

PN W09526979-A1.

PD 12-OCT-1995.

PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM, Parham P;

DR WPI; 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient

PT host

PS Claim 15; Page 9; 80pp; English.

CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of

CC class I major histocompatibility complex (MHC) antigens. This sequence

CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC

CC HLA-B2702. These sequences can be used to extend the period of

CC acceptance by a recipient of a transplant from an MHC unmatched donor.

CC The peptides are administered to a patient in conjunction with a

CC subtherapeutic amount of an immunosuppressant. This is administered to

CC the patient for a limited period of time (compared to the lifetime

CC administration for current treatments). The peptides particularly

CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)

CC of the patient.

CC Sequence 10 AA;

Query Match 100.0%; Score 49; DB 16; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.25e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 rialry 10  
 |||||  
 QY 1 RIALRY 6

RESULT 5

ID R83094 standard; peptide; 10 AA.

AC R83094;

DE 16-MAY-1996 (first entry)

DE HLA-B2702 CTL modulating peptide (B2702.75-84(D)).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW immunosuppressant; graft versus host disorder; transplantation; therapy;

KW class I MHC; HLA-B2702.

OS Synthetic.

PN W09526979-A1.

PD 12-OCT-1995.

PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM, Parham P;

DR WPI; 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient

PT host

PS Example 14; Page 34; 80pp; English.

CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of

CC class I major histocompatibility complex (MHC) antigens. This sequence

CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC

CC HLA-B2702. These sequences can be used to extend the period of

CC acceptance by a recipient of a transplant from an MHC unmatched donor.

CC The peptides are administered to a patient in conjunction with



CC a subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 49; DB 16; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 r1alry 10  
 |||||  
 QY 1 R1ALRY 6

RESULT 6  
 ID R95429 standard; peptide: 12 AA.

AC R95429;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B\*2702 84-79-84 palindromic.  
 KW HLA: p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN W09513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI: 95-194027/25.

PT Compsns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.

PS Example; Page 12; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B\*2702 84-79-84 palindromic. These sequences can be used to isolate  
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
 CC protein associated with T-cell activation in mammalian T-cells, and is  
 CC also immunologically cross reactive with the heat shock protein Hsc70.  
 CC p74 is found in a limited number of cell types, but is particularly  
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
 CC cell with an amphoteric detergent, and then passed through an affinity  
 CC column containing a covalently bound HLA-B\*2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B\*2702.60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs). By adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 12 AA;

Query Match 100.0%; Score 49; DB 18; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 r1alry 12  
 |||||  
 QY 1 R1ALRY 6

RESULT 7

ID R92912 standard; peptide: 15 AA.  
 AC R92912;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B\*2702 CTL modulating peptide (B2702.70-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B\*2702.  
 OS Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI: 95-358582/45.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B\*5-84 MHC antigen of the recipient  
 PT host

PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC corresponds to residues 70-84 of the alpha-1 domain of the class I MHC  
 CC HLA-B\*2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 49; DB 16; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 r1alry 15  
 |||||  
 QY 1 R1ALRY 6

RESULT 8

ID R95428 standard; peptide: 20 AA.  
 AC R95428;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B\*2702 84-75-84 palindromic.  
 KW HLA: p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN W09513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI: 95-194027/25.

PT Compsns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 12; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B\*2702 84-75-84 palindromic. These sequences can be used to isolate  
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
 CC protein associated with T-cell activation in mammalian T-cells, and is  
 CC also immunologically cross reactive with the heat shock protein Hsc70.  
 CC p74 is found in a limited number of cell types, but is particularly  
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
 CC cell with an amphoteric detergent, and then passed through an affinity  
 CC column containing a covalently bound HLA-B\*2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B\*2702.60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition

CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 18; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 15 rialry 20  
 QY 1 RIALRY 6  
 |||||

## RESULT 9

ID R92907 standard; peptide; 20 AA.  
 AC R92907;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN WO9526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 CC I MHC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 16; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 15 rialry 20  
 QY 1 RIALRY 6  
 |||||

## RESULT 10

ID R92908 standard; peptide; 20 AA.  
 AC R92908;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN WO9526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 CC I MHC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 16; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 15 rialry 20  
 QY 1 RIALRY 6  
 |||||

## RESULT 11

ID R95416 standard; peptide; 25 AA.  
 AC R95416;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B2702.60-84.  
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN WO9513288-A1.  
 PD 18-MAY-1995.  
 PR 10-NOV-1994; US-150493.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI; 95-194027/25.  
 PT Compsns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 9; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents  
 CC HLA-B2702.60-84. These sequences can be used to isolate the protein p74  
 CC from a T-cell lysate. p74 is a T-cell surface membrane protein  
 CC associated with T-cell activation in mammalian T-cells, and is also  
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is  
 CC found in a limited number of cell types, but is particularly expressed on  
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an  
 CC amphoteric detergent, and then passed through an affinity column  
 CC containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC this sequence, induces calcium influx, and inhibits cytotoxic T  
 CC lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can  
 CC be screened for their effect on the cytolytic activity of T-cells, by  
 CC combining them with the extracellular portion of p74 and determining the  
 CC amount of binding between the candidate compound and p74. Modulation of  
 CC CTL activity can be inhibited in a cellular composition containing  
 CC T-cells and antigen presenting cells (APCs), by adding to the mix the  
 CC extracellular portion of p74, in an amount sufficient to compete with p74  
 CC for the binding of the p74 ligand.  
 SQ Sequence 25 AA;

Query Match 100.0%; Score 49; DB 18; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 20 rialry 25  
 |||||

QY 1 RIALRY 6

RESULT 12  
ID R95422 standard; peptide; 25 AA.

AC R95422;

DT 12-NOV-1996 (first entry)

DE HLAB38.6084.

KW HLA: p74: alpha1-helix; human-leucocyte-associated antigen; inhibitor;

KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;

KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;

KW Cytolysis; antigen presenting cell.

OS Synthetic.

PN W09513288-A1.

PD 18-MAY-1995.

PF 10-NOV-1994; U12985

PR 10-NOV-1993; US-150493.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM;

DR WPI; 95-194027/25.

PT Compsns. comprising lymphoid surface membrane proteins - which may

PT inhibit cytolytic activity and differentiation of CTLs.

PS Example; Page 9; 25pp; English.

CC R95413, and R95415-R95431 represent palindromes and fragments of

CC human-leucocyte-associated antigens. This sequence represents the

CC a T-cell lysate. p74 is a T-cell surface membrane protein associated

CC with T-cell activation in mammalian T-cells, and is also immunologically

CC cross reactive with the heat shock protein Hsc70. p74 is found in a

CC limited number of cell types, but is particularly expressed on B and T

CC cells. p74 can be isolated by lysis of a suitable cell with an

CC amphoteric detergent, and then passed through an affinity column

CC containing a covalently bound HLA-B2702 palindromic peptide.

CC Compositions comprising the extracellular fragment of p74 combined with

CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits

CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate

CC compounds can be screened for their effect on the cytolytic activity of

CC T-cells, by combining them with the extracellular portion of p74 and

CC determining the amount of binding between the candidate compound and p74.

CC Modulation of CTL activity can be inhibited in a cellular composition

CC containing T-cells and antigen presenting cells (APCs), by adding to the

CC mix the extracellular portion of p74, in an amount sufficient to compete

CC with p74 for the binding of the p74 ligand.

SQ Sequence 25 AA;

Query Match 100.0%; Score 49; DB 18; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.25e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 rialry 25

QY 1 RIALRY 6

RESULT 13

ID R83090 standard; peptide; 25 AA.

AC R83090;

DT 16-MAY-1996 (first entry)

DE HLA-B2702 CTL modulating peptide (B2702.60-84).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW Immunosuppressant; graft versus host disorder; transplantation; therapy;

KW Class I MHC; HLA-B2702.

OS Synthetic.

PN W09526979-A1.

PD 12-OCT-1995.

PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM, Farham P;

DR WPI; 95-358562/46.

PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient

PT host

PS Example 13; Page 32; 80pp; English.  
CC R83061-R83085, R83090-R83096 and R82907-R82913 represent fragments of  
CC Class I major histocompatibility complex (MHC) antigens. This sequence  
CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC  
CC HLA-B2702. These sequences can be used to extend the period of  
CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
CC The peptides are administered to a patient in conjunction with  
CC a subtherapeutic amount of an immunosuppressant. This is administered to  
CC the patient for a limited period of time (compared to the lifetime  
CC administration for current treatments). The peptides particularly  
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
CC of the patient.  
SQ Sequence 25 AA;

Query Match 100.0%; Score 49; DB 16; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.25e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 rialry 25

QY 1 RIALRY 6

RESULT 14

ID R41205 standard; peptide; 25 AA.

AC R41205;

DT 15-MAR-1994 (first entry)

DE Peptide fragment of Class I HLA peptide.

KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;

KW parasitic disease; cytotoxic T lymphocyte; modulation.

OS Synthetic.

PN W09317695-A.

PD 16-SEP-1993.

PF 25-FEB-1993; U01758.

PR 02-MAR-1992; US-844716.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

PI Clayberger CA, Krensky AM;

DR WPI; 93-303134/38.

PT New peptide(s) based on Class I HLA antigen domains - used for

PT modulating cytotoxic T-lymphocyte activity towards targets

PS Claim 8; Page 53; 61pp; English.

CC The peptide (or a fragment of at least 10 amino acids, joined at at

CC least one terminus to a sequence other than that of wild type HLA

CC antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity,

CC either by inhibition or stimulation. It can be used for

CC inhibiting CTL toxicity in transplantations, for inducing CTL

CC activity in parasitic diseases and neoplasia and in studies on viral

CC infection. The peptide can also be used for identifying CTLs which

CC bind to it and removing subsets of CTLs from a T-cell composition.

SQ Sequence 25 AA;

Query Match 100.0%; Score 49; DB 8; Length 25;

Best Local Similarity 100.0%; Pred. No. 1.25e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 rialry 25

QY 1 RIALRY 6

RESULT 15

ID R83093 standard; peptide; 25 AA.

AC R83093;

DT 16-MAY-1996 (first entry)

DE HLAB38 CTL modulating peptide (B38.6084).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW Immunosuppressant; graft versus host disorder; transplantation; therapy;

KW Class I MHC; HLAB38.

OS Synthetic.

PN W09526979-A1.

PD 12-OCT-1995.

PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI: 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 13; Page 32; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC  
 CC HLAB38. These sequences can be used to extend the period of acceptance  
 CC by a recipient of a transplant from an MHC unmatched donor. The peptides  
 CC are administered to a patient in conjunction with a subtherapeutic amount  
 CC of an immunosuppressant. This is administered to the patient for a  
 CC limited period of time (compared to the lifetime administration for  
 CC current treatments). The peptides particularly modulate (or inhibit) the  
 CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.  
 SQ Sequence 25 AA;

Query Match 100.0%; Score 49; DB 16; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.25e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 r1alry 25  
 |||||  
 QY 1 RIALRY 6

Search completed: Thu May 22 08:42:40 1997  
 Job time : 10 secs.

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MPERCH (TM)

\*\*\*\*\*

Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MPERCH protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:44:44 1997; MasPar time 2.46 Seconds  
69.444 Million cell updates/sec

Tabular output not generated.

Title: >US-08-653-294-6  
Description: (1-6) from US08653294.pep  
Perfect Score: 53  
Sequence: 1 YRLLIR 6

Scoring table: PAM 150  
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Maximum DB seq length 60

Database: pir50  
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3  
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8  
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 22.841; Variance 31.665; scale 0.721

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description	Pred. No.
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No matches found.

Search completed: Thu May 22 08:44:53 1997  
Job time : 9 secs.

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Db 232 yslirrkplfy 243  
| | | | |  
QY 1 YRLAIRIALRY 12

RESULT 13  
ID RUB2\_BRANA STANDARD; PRT; 583 AA.  
AC P34794;  
DT 01-FEB-1994 (REL. 28, CREATED)  
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)  
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
DE RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD  
CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA).  
OS BRASSICA NAPUS (RAPE).  
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;  
OC CAPPARALE; CRUCIFERAE.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE-SEED;  
RA COLE K.P., BLAKELEY S.D., DENNIS D.T.;  
RL PLANT PHYSIOL. 105:453-453(1994).  
CC -!- FUNCTION: THIS PROTEIN BINDS RUBISCO SMALL AND LARGE SUBUNITS AND  
IS IMPLICATED IN THE ASSEMBLY OF THE ENZYME OLIGOMER.  
CC -!- SUBUNIT: OLIGOMER OF PROBABLY SIX ALPHA AND SIX BETA SUBUNITS.  
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.  
CC -!- THIS PROTEIN SHOWS ATPASE ACTIVITY.  
CC -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.  
DR EMBL: 227222; G415925;  
DR PIR: S38642; S38642.  
DR PROSITE; PS00296; CHAPERONINS\_CPN60.  
DR CHAPERONE; ATP-BINDING; CHLOROPLAST; TRANSIT PEPTIDE.  
KW CHAPERONE; ATP-BINDING; CHLOROPLAST (BY SIMILARITY).  
FT TRANSIT 1 45 CHLOROPLAST  
FT CHAIN 46 583 RUBISCO SUBUNIT BINDING-PROTEIN ALPHA.  
SQ SEQUENCE 583 AA; 61605 MW; 44188FDD CRC32;

Query Match 56.1%; Score 55; DB 9; Length 583;  
Best Local Similarity 63.6%; Pred. No. 1.17e+01;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 34 yrkanrfrslr 44  
| | | | |  
QY 1 YRLAIRIALRY 11

RESULT 14  
ID DNL4\_HUMAN STANDARD; PRT; 844 AA.  
AC P49917;  
DT 01-OCT-1996 (REL. 34, CREATED)  
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
DE DNA LIGASE IV (EC 6.5.1.1) (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)).  
GN LIG4.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX TISSUE-PROSTATE;  
RA WEI Y.-F., ROBINS P., CARTER K., CALDECOTT K., PAPPIN D.J.C.,  
RA YU G.-L., WANG R.-P., SHELL B.K., NASH R.A., SCHAR P., BARNES D.E.,  
RA HASELTINE W.A., LINDAHL T.;  
RL MOL. CELL. BIOL. 15:3206-3216(1995).  
CC -!- CATALYTIC ACTIVITY: ATP + (DEOXYRIBONUCLEOTIDE)(N) +  
(DEOXYRIBONUCLEOTIDE)(M) -> AMP + PYROPHOSPHATE +  
(DEOXYRIBONUCLEOTIDE)(N+M).  
CC -!- SUBCELLULAR LOCATION: NUCLEAR.  
CC -!- TISSUE SPECIFICITY: TESTIS, THYMUS, PROSTATE AND HEART.  
CC -!- SIMILARITY: HIGH TO OTHER EUKARYOTIC AND VIRUSES DNA LIGASES, LOW  
TO PHAGES LIGASES.  
DR EMBL: X83441; G860937;  
KW DNA REPAIR; DNA REPLICATION; DNA RECOMBINATION; CELL DIVISION; LIGASE;

KW ATP-BINDING; NUCLEAR PROTEIN.  
FT BINDING 206 206 AMP (BY SIMILARITY).  
SQ SEQUENCE 844 AA; 96154 MW; A4C8599F CRC32;

Query Match 56.1%; Score 55; DB 3; Length 844;  
Best Local Similarity 54.3%; Pred. No. 1.17e+01;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 770 rlaikalelrf 780  
| | | | |  
QY 2 RLAIIRIALRY 12

RESULT 15  
ID APOA\_MACMU STANDARD; PRT; 1420 AA.  
AC P14417;  
DT 01-JAN-1990 (REL. 13, CREATED)  
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)  
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
DE APOLIPOPROTEIN(A) (EC 3.4.21.-) (APO(A)) (LP(A)) (FRAGMENT).  
GN LPA.  
OS MACACA MULATTA (RHESUS MACAQUE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 89174660.  
RA TOMLINSON J.E., MCLEAN J.W., LAWN R.M.;  
RL J. BIOL. CHEM. 264:5957-5965(1989).  
CC -!- FUNCTION: APO(A) IS THE MAIN CONSTITUENT OF LIPOPROTEIN(A). APO(A)  
CAN BIND TO FIBRONECTIN AND HAS SERINE PROTEINASE ACTIVITY CAPABLE  
OF CLEAVING IT.  
CC -!- SUBUNIT: APO(A) IS DISULFIDE LINKED TO APO-B100.  
CC -!- DISEASE: CONCENTRATION OF LP(A) IN PLASMA IS CORRELATED WITH  
ATHEROSCLEROSIS.  
CC -!- SIMILARITY: CONTAINS FOUR KRINGLE REGIONS.  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
TRYPSIN FAMILY. BELONGS TO THE PLASMINOGEN SUBFAMILY.  
DR EMBL: J04635; G342073;  
DR PIR: A30848; A30848.  
DR PIR: A32869; A32869.  
DR HSP; P00766; 1CHG.  
DR PROSITE; PS00021; KRINGLE.  
DR PROSITE; PS00134; TRYPSIN\_HIS.  
DR PROSITE; PS00135; TRYPSIN\_SER.  
KW HYDROLASE; SERINE PROTEASE; LIPID TRANSPORT; PLASMA; GLYCOPROTEIN;  
KW KRINGLE; DUPLICATION; REPEAT; ATHEROSCLEROSIS.  
FT NON\_TER 1 1  
SQ SEQUENCE 1420 AA; 158367 MW; 03F1D517 CRC32;

Query Match 56.1%; Score 55; DB 1; Length 1420;  
Best Local Similarity 85.7%; Pred. No. 1.17e+01;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

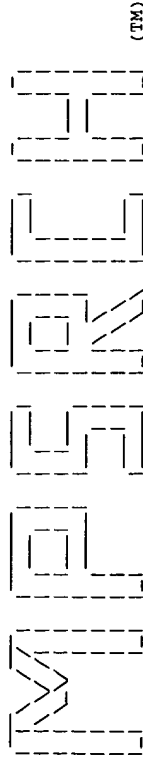
Db 873 rrlply 879  
| | | | |  
QY 6 RLAIIRY 12

Search completed: Thu May 22 08:36:00 1997  
Job time : 8 secs.





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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:44:16 1997; MasPar time 1.84 Seconds  
69.215 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-653-294-6  
Description: (1-6) from US08653294.pep  
Perfect Score: 53  
Sequence: 1 YRLIIR 6

Scoring table: PAM 150  
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Maximum DB seq length 60

Database: swiss-prot34  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 23.777; Variance 26.124; scale 0.910

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	%
No.	Score	Match Length DB ID Description Pred. No.

No matches found.

Search completed: Thu May 22 08:44:25 1997  
Job time : 9 secs.

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W P S R L H (TW)

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu May 22 08:46:31 1997; MasPar time 1.77 Seconds  
Tabular output not generated. 36.872 Million cell updates/sec

Title: >US-08-653-294-7  
Description: (1-6) from US08653294.pep  
Perfect Score: 49  
Sequence: 1 YRLAIR 6

Scoring table: PAM 150  
Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Maximum DB seq length 60

Database: a-geneseq26  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19

Statistics: Mean 15.681; Variance 40.195; scale 0.390

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	49	100.0	12 18	R95429	HLA-B2702 84-79-84 pa	1.52e+01
2	49	100.0	20 18	R95430	HLA-B2702 84-75T/75-8	1.52e+01
3	49	100.0	20 18	R95428	HLA-B2702 84-75-84 pa	1.52e+01
4	49	100.0	20 16	R92909	HLA-B2702 CTL modul	1.52e+01
5	49	100.0	20 16	R92911	HLA-B2702 CTL modul	1.52e+01
6	49	100.0	20 16	R92907	HLA-B2702 CTL modul	1.52e+01
7	45	91.8	43 11	R58902	Drosophila-12 cadher	4.80e+01
8	45	91.8	43 17	R87142	Protocadherin clone D	4.80e+01
9	42	85.7	20 16	R92910	HLA-B2702 CTL modul	1.11e+02
10	42	85.7	20 16	R92908	HLA-B2702 CTL modul	1.11e+02

Note: Post-processor removed 35 summaries from list due to search parameters chosen.

ALIGNMENTS

RESULT 1  
ID R95429 standard; peptide; 12 AA.  
AC R95429;

DT 12-NOV-1996 (first entry)  
DE HLA-B2702 84-79-84 palindrome.  
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
KW cytolysis; antigen presenting cell.  
PS Synthetic.  
PN W09513288-A1.  
PD 18-MAY-1995.  
PF 10-NOV-1994; U12985.  
PR 10-NOV-1993; US-150493.  
PT (STRD ) UNIV LELAND STANFORD JUNIOR.  
PI Clayberger C, Krensky AM;  
DR WPI; 95-194027/25.  
PT Compsns. comprising lymphoid surface membrane proteins - which may  
PT inhibit cytolytic activity and differentiation of CTLs.  
PS Example; Page 12; 29pp; English.  
CC R95413, and R95415-R95431 represent palindromes and fragments of  
CC human-leucocyte-associated antigens. This sequence represents the  
CC HLA-B2702 84-79-84 palindrome. These sequences can be used to isolate  
CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
CC protein associated with T-cell activation in mammalian T-cells, and is  
CC also immunologically cross reactive with the heat shock protein Hsc70.  
CC p74 is found in a limited number of cell types, but is particularly  
CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
CC cell with an amphoteric detergent, and then passed through an affinity  
CC column containing a covalently bound HLA-B2702 palindromic peptide.  
CC Compositions comprising the extracellular fragment of p74 combined with  
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate  
CC compounds can be screened for their effect on the cytolytic activity of  
CC T-cells, by combining them with the extracellular portion of p74 and  
CC determining the amount of binding between the candidate compound and p74.  
CC Modulation of CTL activity can be inhibited in a cellular composition  
CC containing T-cells and antigen presenting cells (APCs), by adding to the  
CC mix the extracellular portion of p74, in an amount sufficient to compete  
CC with p74 for the binding of the p74 ligand.  
SQ Sequence 12 AA;  
  
Query Match 100.0%; Score 49; DB 18; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.52e+01;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 1 yrlair 6  
QY 1 YRLAIR 6  
  
RESULT 2  
ID R95430 standard; peptide; 20 AA.  
AC R95430;  
DT 12-NOV-1996 (first entry)  
DE HLA-B2702 84-75T/75-84T palindrome.  
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
KW cytolysis; antigen presenting cell.  
PS Synthetic.  
PN W09513288-A1.  
PD 18-MAY-1995.  
PF 10-NOV-1994; U12985.  
PR 10-NOV-1993; US-150493.  
PT (STRD ) UNIV LELAND STANFORD JUNIOR.  
PI Clayberger C, Krensky AM;  
DR WPI; 95-194027/25.  
PT Compsns. comprising lymphoid surface membrane proteins - which may  
PT inhibit cytolytic activity and differentiation of CTLs.  
PS Example; Page 12; 29pp; English.  
CC R95413, and R95415-R95431 represent palindromes and fragments of  
CC human-leucocyte-associated antigens. This sequence represents the  
CC HLA-B2702 84-75T/75-84T palindrome. These sequences can be used to  
CC isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface  
CC membrane protein associated with T-cell activation in mammalian T-cells,

CC and is also immunologically cross reactive with the heat shock protein  
 CC Hsc70. p74 is found in a limited number of cell types, but is  
 CC particularly expressed on B and T cells. p74 can be isolated by lysis of  
 CC a suitable cell with an amphoteric detergent, and then passed through an  
 CC affinity column containing a covalently bound HLA-B2702 palindromic  
 CC peptide. Compositions comprising the extracellular fragment of p74  
 CC combined with HLA-B2702 60-84 (see R95416), induces calcium influx, and  
 CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity.  
 CC Candidate compounds can be screened for their effect on the cytolytic  
 CC activity of T-cells, by combining them with the extracellular portion of  
 CC p74 and determining the amount of binding between the candidate compound  
 CC and p74. Modulation of CTL activity can be inhibited in a cellular  
 CC composition containing T-cells and antigen presenting cells (APCs), by  
 CC adding to the mix the extracellular portion of p74, in an amount  
 CC sufficient to compete with p74 for the binding of the p74 ligand.  
 CC Sequence 20 AA;

Query Match 100.0%; Score 49; DB 18; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.52e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6  
 |||||  
 QY 1 YRLAIR 6

## RESULT 3

ID R95428 standard; peptide; 20 AA.  
 AC R95428;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B2702 84-75-84 palindromic.  
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN WO9513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI; 95-194027/25.  
 PT Compsns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 12; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B2702 84-75-84 palindromic. These sequences can be used to isolate  
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
 CC protein associated with T-cell activation in mammalian T-cells, and is  
 CC also immunologically cross reactive with the heat shock protein Hsc70.  
 CC p74 is found in a limited number of cell types, but is particularly  
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
 CC cell with an amphoteric detergent, and then passed through an affinity  
 CC column containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B2702 60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 CC Sequence 20 AA;

Query Match 100.0%; Score 49; DB 18; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.52e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6

QY 1 yrlair 6  
 |||||

## RESULT 4

ID R92909 standard; peptide; 20 AA.  
 AC R92909;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN WO9526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 CC I MHC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 CC Sequence 20 AA;

Query Match 100.0%; Score 49; DB 16; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.52e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6  
 |||||  
 QY 1 YRLAIR 6

## RESULT 5

ID R92911 standard; peptide; 20 AA.  
 AC R92911;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN WO9526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC  
 CC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to

CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 16; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.52e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6  
 |||||  
 QY 1 YRLAIR 6

## RESULT 6

ID R92907 standard; peptide; 20 AA.  
 AC R92907;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B\*2702 CTL modulating peptide (B2702.84-75/75-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW Class I MHC; HLA-B\*2702.  
 OS Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B\*75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R83097-R83098 represent fragments of  
 CC Class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 CC I MHC HLA-B\*2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 16; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.52e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6  
 |||||  
 QY 1 YRLAIR 6

## RESULT 7

ID R58902 standard; Protein; 43 AA.  
 AC R58902;  
 DT 17-APR-1995 (first entry)  
 DE Drosophila-12 cadherin-related molecule.  
 KW Cadherin; cell adhesion molecule.  
 OS Drosophila.  
 PN W09414960-A.  
 PD 07-JUL-1994.  
 PF 23-DEC-1993; U12588.  
 PR 29-DEC-1992; US-998003.  
 PA (DOHE-) DOHENY EYE INST.  
 PI Suzuki S;  
 DR WPI; 94-293849/36.  
 DR N-PSDB; Q68993.  
 PT Polynucleotide sequences encoding new proto:cadherins - useful  
 for modulating natural binding and regulating activities.  
 Example; Page 63; 114pp; English.  
 CC Two regions of conserved AA sequence, one from the middle of the  
 CC third cadherin extracellular subdomain (EC-3) and the other from the  
 CC C-terminus of the fourth extracellular subdomain (EC-4) were  
 CC identified. The corresp. degenerate oligos (Q68949, Q68950) were  
 CC designed for use as PCR primers. PCR was carried out on a rat brain  
 CC cDNA prep. Two major bands of about 450 bps and 130 bps were found.  
 CC The 450 bp band corresponded to the expected length between the two  
 CC primer sites, but the 130 bp band could not be predicted from any  
 CC of the previously identified cadherin sequences. The 450 bp and 130  
 CC bp bands were extracted and sequenced. Nineteen novel partial cDNA  
 CC clones were isolated. The DNA and deduced AA sequences of the  
 CC in Q68951-Q68969 and R58860-R58878. Various cDNA fragments  
 CC structurally similar to the rat cDNAs were isolated from human,  
 CC mouse and Xenopus brain cDNA preps. and from Drosophila and  
 CC C. elegans whole body cDNA preps. by PCR using the above primers.  
 CC The DNA and deduced AA sequences of the resulting PCR fragments  
 CC (including sequences corresp. to the PCR primers) are given in  
 CC Q68971, Q68972-Q68994 and R58882-R58905 and R49143. Comparison  
 CC of the deduced AA sequences indicates a similarity, in particular,  
 CC there are three sets of clones that appear to be cross-species  
 CC homologues: RAT-218, MOUSE-322 and HUMAN-43; RAT-314, MOUSE-321 and  
 CC HUMAN-11; and MOUSE-326 and HUMAN-42.  
 SQ Sequence 43 AA;

Query Match 91.8%; Score 45; DB 11; Length 43;

Best Local Similarity 83.3%; Pred. No. 4.80e+01;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 yrlvir 16  
 |||||  
 QY 1 YRLAIR 6

## RESULT 8

ID R87142 standard; Peptide; 43 AA.  
 AC R87142;  
 DT 29-AUG-1996 (first entry)  
 DE Protocadherin clone DROSOPHILA-12.  
 KW Protocadherin; pc3; pc4; pc5; human; rat; cadherin; cell adhesion; mouse;  
 KW catenin; therapy; clone; frog; fruit fly.  
 OS Drosophila melanogaster.  
 FH Key Location/Qualifiers  
 FT Misc\_difference 38  
 FT /note= "encoded by CGA"  
 FT Misc\_difference 39  
 FT /note= "encoded by ATG"  
 FT Misc\_difference 40  
 FT /note= "encoded by ACA"  
 FT Misc\_difference 41  
 FT /note= "encoded by ATG"  
 FT Misc\_difference 42  
 FT /note= "encoded by CGC"  
 FT Misc\_difference 43  
 FT /note= "encoded by CGC"  
 PN W09600289-A1.  
 PD 04-JAN-1996.  
 PR 26-JUN-1995; U08071.  
 PR 27-JUN-1994; US-268161.  
 PA (DOHE-) DOHENY EYE INST.  
 PI Suzuki S;  
 DR WPI; 96-068873/07.  
 DR N-PSDB; T03617.  
 PT Polynucleotide(s) encoding human protocadherins pc3 and pc4 and rat  
 PT pc5 - involved in cell-cell adhesion and regulation activities  
 PS Example 2; Page 67-68; 146pp; English.  
 CC R87142-R87144 represent partial fragments of the drosophila protocadherin  
 CC sequence. The cDNAs encoding these sequences were isolated after  
 CC screening a drosophila whole body cDNA preparation with the primers shown  
 CC in T03575 and T03576. The primers were constructed from portions of the  
 CC amino acid sequences of the third and fourth extracellular domains of

CC published cadherin sequences. The cytoplasmic domain of cadherin  
 CC interacts with the cytoskeleton through catenins and other cytoskeleton  
 CC associated proteins. The cytoplasmic domain is not present in all  
 CC cadherins, but in those which possess it, it is essential for the  
 CC cadherins adhesive function. The cadherins which do not possess a  
 CC cytoplasmic domain appear to function via a different method from those  
 CC with a cytoplasmic domain. These protein sequences are involved in  
 CC cell-cell adhesion. These sequences may have regulatory functions in the  
 CC cell, as well as the cell-cell adhesive properties. Antibodies produced  
 CC against these sequences are useful for modulating the binding activity of  
 CC these protocadherins, and can be used therapeutically.  
 SQ Sequence 43 AA;

Query Match 91.8%; Score 45; DB 17; Length 43;

Best Local Similarity 83.3%; Pred. No. 4.80e+01;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 yrlvir 16

QY 1 YRLAIR 6

#### RESULT 9

ID R92910 standard; peptide; 20 AA.

AC R92910;

DT 16-MAY-1996 (first entry)

DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW Immunosuppressant; graft versus host disorder; transplantation; therapy;

KW Class I MHC; HLA-B2702.

OS Synthetic.

PN W09526979-A1.

PD 12-OCT-1995.

PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.

PI (STRD ) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM, Parham P;

DR WPI: 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient

PT host

PS Example 15; Page 36; 80pp; English.

CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 CC I MHC HLA-B2702. These sequences can be used to extend the period of

CC acceptance by a recipient of a transplant from an MHC unmatched donor.

CC The peptides are administered to a patient in conjunction with a

CC subtherapeutic amount of an immunosuppressant. This is administered to

CC the patient for a limited period of time (compared to the lifetime

CC administration for current treatments). The peptides particularly

CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)

CC of the patient.

SQ Sequence 20 AA;

Query Match 85.7%; Score 42; DB 16; Length 20;

Best Local Similarity 83.3%; Pred. No. 1.11e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 yrlvir 6

QY 1 YRLAIR 6

#### RESULT 10

ID R92908 standard; peptide; 20 AA.

AC R92908;

DT 16-MAY-1996 (first entry)

DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW Immunosuppressant; graft versus host disorder; transplantation; therapy;

KW Class I MHC; HLA-B2702.

OS Synthetic.

PN W09526979-A1.

PD 12-OCT-1995.

PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.

PI (STRD ) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM, Parham P;

DR WPI: 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient

PT host

PS Example 15; Page 36; 80pp; English.

CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 CC I MHC HLA-B2702. These sequences can be used to extend the period of

CC acceptance by a recipient of a transplant from an MHC unmatched donor.

CC The peptides are administered to a patient in conjunction with a

CC subtherapeutic amount of an immunosuppressant. This is administered to

CC the patient for a limited period of time (compared to the lifetime

CC administration for current treatments). The peptides particularly

CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)

CC of the patient.

SQ Sequence 20 AA;

Query Match 85.7%; Score 42; DB 16; Length 20;

Best Local Similarity 83.3%; Pred. No. 1.11e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 yrlvir 6

QY 1 YRLAIR 6

Search completed: Thu May 22 08:46:40 1997

Job time : 9 secs.

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MPSEARCH (TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:46:03 1997; MasPar time 2.50 Seconds  
Tabular output not generated. 68.363 Million cell updates/sec

Title: >US-08-653-294-7  
Description: (1-6) from US08653294.pep  
Perfect Score: 49  
Sequence: 1 YRLAIR 6

Scoring table: PAM 150  
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Maximum DB seq length 60

Database: pir50  
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3  
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8  
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 21.577; Variance 27.148; scale 0.795

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query				
No.	Score	Match	Length	ID	Description
					Pred. No.

No matches found.

Search completed: Thu May 22 08:46:13 1997  
Job time : 10 secs.

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W P S R L

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:32:13 1997; MasPar time 1.92 Seconds  
Tabular output not generated. 33.977 Million cell updates/sec

Title: >US-08-653-294-7  
Description: (1-6) from US08653294.pep  
Perfect score: 49  
Sequence: 1 YRLAIR 6

Scoring table: GAP 150  
PAM 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq26  
1:part1 2:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19

Statistics: Mean 15.681; Variance 40.195; scale 0.390

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	49	100.0	12	18	R95429 HLA-B2702 84-79-84 pa	1.52e+01
2	49	100.0	20	18	R95430 HLA-B2702 84-75T/75-8	1.52e+01
3	49	100.0	20	18	R95428 HLA-B2702 84-75-84 pa	1.52e+01
4	49	100.0	20	16	R92909 HLA-B2702 CTL modul	1.52e+01
5	49	100.0	20	16	R92911 HLA-B2702 CTL modul	1.52e+01
6	49	100.0	20	16	R92907 HLA-B2702 CTL modul	1.52e+01
7	45	91.8	43	11	R87142 Drosophila-12 cadher	4.80e+01
8	45	91.8	43	17	R87142 Protocadherin clone D	4.80e+01
9	44	89.8	724	18	R93081 Bacillus thuringiensis	6.37e+01
10	44	89.8	772	15	R79949 Enzyme M-11.	6.37e+01
11	44	89.8	775	15	R79950 Enzyme Q36.	6.37e+01
12	42	85.7	20	16	R92910 HLA-B2702 CTL modul	1.11e+02
13	42	85.7	20	16	R92908 HLA-B2702 CTL modul	1.11e+02
14	41	83.7	617	8	R42392 McI haemagglutinin.	1.47e+02
15	41	83.7	732	2	R11056 Acylamino acid-isolat	1.47e+02
16	41	83.7	732	3	R20001 Human acyl amino acid	1.47e+02
17	41	83.7	783	13	R70841 E. coli polymerase-II	1.47e+02
18	41	83.7	783	5	R2441 E. coli DNA polymeras	1.47e+02
19	41	83.7	783	1	P94265 Sequence of APH36.1 c	1.47e+02
20	40	81.6	232	1	P80760 Deduced peptide seque	1.93e+02

21	40	81.6	248	3	P60437 Dog 32 kd alveolar su	1.93e+02
22	40	81.6	256	1	R04210 Canine 32K alveolar s	1.93e+02
23	40	81.6	855	6	R29815 S receptor kinase pro	1.93e+02
24	40	81.6	896	1	R05591 The 36 kd antigen of	1.93e+02
25	40	81.6	1157	9	R48678 Insecticidal protoxin	1.93e+02
26	40	81.6	1288	3	R20073 N-methylhydantoinase.	1.93e+02
27	40	81.6	1528	18	R95333 Manduca sexta Bacillu	1.93e+02
28	39	79.6	635	14	R75940 Human myeloproliferat	2.53e+02
29	39	79.6	635	4	R23970 MPLY env protein with	2.53e+02
30	39	79.6	643	18	R97735 Bacillus thuringiensis	2.53e+02
31	39	79.6	643	1	P91462 67-KD protein toxin.	2.53e+02
32	39	79.6	816	12	R63564 Retinoblastoma 94kd t	2.53e+02
33	39	79.6	816	11	R58568 Human retinoblastoma	2.53e+02
34	39	79.6	816	1	P82112 Human retinoblastoma	2.53e+02
35	39	79.6	928	1	R05305 Cancer supressing gen	2.53e+02
36	39	79.6	928	13	R71680 Retinoblastoma p110R	2.53e+02
37	39	79.6	928	14	R74271 Retinoblastoma tumour	2.53e+02
38	39	79.6	928	1	R06289 Predicted retinoblast	2.53e+02
39	39	79.6	928	7	R36534 Retinoblastoma (RB) p	2.53e+02
40	39	79.6	928	13	R71681 Recombinant p110RB p	2.53e+02
41	39	79.6	970	1	P90599 Human retinoblastoma.	2.53e+02
42	39	79.6	1723	19	W00645 Mouse DEC-205.	2.53e+02
43	39	79.6	1743	19	W00644 Human DEC-205.	2.53e+02
44	39	79.6	3398	8	R44430 eRYA region polypepti	2.53e+02
45	38	77.6	341	19	W02699 G-protein coupled hum	3.31e+02

ALIGNMENTS

RESULT 1  
ID R95429 standard; peptide; 12 AA.  
AC R95429;  
DT 12-NOV-1996 (first entry)  
DE HLA-B2702 84-79-84 palindrome.  
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
KW cytolysis; antigen presenting cell.  
OS Synthetic.  
PN W09513288-A1.  
PD 18-MAY-1995.  
PF 10-NOV-1994; U12985.  
PR 10-NOV-1993; US-150493.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PI Clayberger C, Krensky AM,  
DR WFL; 95-194027/25.  
PT Compens. comprising lymphoid surface membrane proteins - which may  
PT inhibit cytolytic activity and differentiation of CTLs.  
PS Example; Page 12; 29pp; English.  
CC R95413, and R95415-R95431 represent palindromes and fragments of  
CC human-leucocyte-associated antigens. This sequence represents the  
CC HLA-B2702 84-79-84 palindrome. These sequences can be used to isolate  
CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
CC protein associated with T-cell activation in mammalian T-cells, and is  
CC also immunologically cross reactive with the heat shock protein Hsc70.  
CC p74 is found in a limited number of cell types, but is particularly  
CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
CC cell with an amphoteric detergent, and then passed through an affinity  
CC column containing a covalently bound HLA-B2702 palindromic peptide.  
CC Compositions comprising the extracellular fragment of p74 combined with  
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate  
CC compounds can be screened for their effect on the cytolytic activity of  
CC T-cells, by combining them with the extracellular portion of p74 and  
CC determining the amount of binding between the candidate compound and p74.  
CC Modulation of CTL activity can be inhibited in a cellular composition  
CC containing T-cells and antigen presenting cells (APCs), by adding to the  
CC mix the extracellular portion of p74, in an amount sufficient to compete  
CC with p74 for the binding of the p74 ligand.  
SQ Sequence 12 AA;  
Query Match 100.0%; Score 49; DB 18; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.52e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6  
 QY 1 YRLAIR 6

RESULT 2

ID R95430 standard; peptide: 20 AA.  
 AC R95430;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B\*2702 84-75T/75-84T palindromic.  
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN W09513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 PI WPI: 95-194027/25.  
 DR Compsns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 12; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B\*2702 84-75T/75-84T palindromic. These sequences can be used to  
 CC isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface  
 CC membrane protein associated with T-cell activation in mammalian T-cells,  
 CC and is also immunologically cross reactive with the heat shock protein  
 CC Hsc70. p74 is found in a limited number of cell types, but is  
 CC particularly expressed on B and T cells. p74 can be isolated by lysis of  
 CC a suitable cell with an amphoteric detergent, and then passed through an  
 CC affinity column containing a covalently bound HLA-B\*2702 palindromic  
 CC peptide. Compositions comprising the extracellular fragment of p74  
 CC combined with HLA-B\*2702.60-84 (see R95416), induces calcium influx, and  
 CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity.  
 CC Candidate compounds can be screened for their effect on the cytolytic  
 CC activity of T-cells, by combining them with the extracellular portion of  
 CC p74 and determining the amount of binding between the candidate compound  
 CC and p74. Modulation of CTL activity can be inhibited in a cellular  
 CC composition containing T-cells and antigen presenting cells (APCs), by  
 CC adding to the mix the extracellular portion of p74, in an amount  
 CC sufficient to compete with p74 for the binding of the p74 ligand.  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 18; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.52e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6  
 QY 1 YRLAIR 6

RESULT 3

ID R95428 standard; peptide: 20 AA.  
 AC R95428;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B\*2702 84-75-84 palindromic.  
 KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN W09513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.

PI Clayberger C, Krensky AM;  
 PI WPI: 95-194027/25.  
 DR Compsns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 12; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B\*2702 84-75-84 palindromic. These sequences can be used to isolate  
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
 CC protein associated with T-cell activation in mammalian T-cells, and is  
 CC also immunologically cross reactive with the heat shock protein Hsc70.  
 CC p74 is found in a limited number of cell types, but is particularly  
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
 CC cell with an amphoteric detergent, and then passed through an affinity  
 CC column containing a covalently bound HLA-B\*2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B\*2702.60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity.  
 CC Candidate compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 18; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.52e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6  
 QY 1 YRLAIR 6

RESULT 4

ID R92909 standard; peptide: 20 AA.  
 AC R92909;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B\*2702 CTL modulating peptide (B2702.84-75/75-84(T)).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B\*2702.  
 OS Synthetic.  
 PN W09528979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Farham P;  
 PI WPI: 95-358582/46.  
 DR Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 CC I MHC HLA-B\*2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 16; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.52e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6  
 QY 1 YRLAIR 6

RESULT 5  
 ID R92911 standard; peptide; 20 AA.

AC R92911;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B\*2702 CTL modulating peptide (B2702.84-75/84-75).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B\*2702.  
 OS Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI: 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC  
 CC HLA-B\*2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 15; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.52e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6  
 QY 1 YRLAIR 6

RESULT 6

ID R92907 standard; peptide; 20 AA.  
 AC R92907;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B\*2702 CTL modulating peptide (B2702.84-75/75-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B\*2702.  
 OS Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI: 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 CC I MHC HLA-B\*2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a

CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 49; DB 16; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.52e+01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlair 6  
 QY 1 YRLAIR 6

RESULT 7

ID R58902 standard; Protein; 43 AA.  
 AC R58902;  
 DT 17-APR-1995 (first entry)  
 DE Drosophila-12 cadherin-related molecule.  
 KW Cadherin; cell adhesion molecule.  
 OS Drosophila.  
 PN W09414960-A.  
 PD 07-JUL-1994.  
 PF 23-DEC-1993; U12588.  
 PR 29-DEC-1992; US-998003.  
 PA (DOHE-) DOHENY EYE INST.  
 PI Suzuki S;  
 DR WPI: 94-293849/36.  
 DR N-PSDB; 068993.  
 PT Polynucleotide sequences encoding new proto-cadherins - useful  
 PT for modulating natural binding and regulating activities.  
 PS Example; Page 63; 14pp; English.  
 CC Two regions of conserved AA sequence, one from the middle of the  
 CC third cadherin extracellular subdomain (EC-3) and the other from the  
 CC C-terminus of the fourth extracellular subdomain (EC-4) were  
 CC identified. The corresp. degenerate oligos (Q68949, Q68950) were  
 CC designed for use as PCR primers. PCR was carried out on a rat brain  
 CC cDNA prep. Two major bands of about 450 bps and 130 bps were found.  
 CC The 450 bp band corresponded to the expected length between the two  
 CC primer sites, but the 130 bp band could not be predicted from any  
 CC of the previously identified cadherin sequences. The 450 bp and 130  
 CC bp bands were extracted and sequenced. Nineteen novel partial cDNA  
 CC clones were isolated. The DNA and deduced AA sequences of the given  
 CC clones (including sequences corresp. to the PCR primers) are given  
 CC in Q68951-Q68969 and R58860-R58878. Various cDNA fragments  
 CC structurally similar to the rat cDNAs were isolated from human,  
 CC mouse and xenopus brain cDNA preps. and from Drosophila and  
 CC C. elegans whole body cDNA preps. by PCR using the above primers.  
 CC The DNA and deduced AA sequences of the resulting PCR fragments  
 CC (including sequences corresp. to the PCR primers) are given in  
 CC Q68971, Q68972-Q68994 and R58882-R58905 and R49143. Comparison  
 CC of the deduced AA sequences indicates a similarity, in particular,  
 CC there are three sets of clones that appear to be cross-species  
 CC homologues: RAT-218, MOUSE-322 and HUMAN-43; RAT-314, MOUSE-321 and  
 CC HUMAN-11; and MOUSE-326 and HUMAN-42.  
 SQ Sequence 43 AA;

Query Match 91.8%; Score 45; DB 11; Length 43;  
 Best Local Similarity 83.3%; Pred. No. 4.80e+01;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 11 yrlvir 16  
 QY 1 YRLAIR 6

RESULT 8

ID R87142 standard; Peptide; 43 AA.  
 AC R87142;  
 DT 29-AUG-1996 (first entry)  
 DE Protocadherin clone DROSOPHILA-12.



Db 8 Yrlqir 13  
||| ||  
QY 1 YRLAIR 6

RESULT 11  
ID R79950 standard; Protein; 775 AA.  
AC R79950;  
DT 24-APR-1996 (first entry)  
DE Enzyme Q36.  
KW Enzyme; M-11; Q36; rhizobium; arthrobacter; trehalose;  
amylaceous saccharide.  
OS Arthrobacter sp. M11.  
FH Key Location/Qualifiers  
FT Misc difference 120..125  
FT /note= "used for production of probe sequence (T04209)"  
FT Misc difference 621..625  
FT /note= "used for production of probe sequence (T04210)"  
PN EP-674005-A2.  
PD 27-SEP-1995.  
PF 23-FEB-1995; 301176.  
PR 23-FEB-1994; JP-047956.  
PR 23-FEB-1994; JP-047940.  
PR 06-APR-1994; JP-090728.  
PR 06-APR-1994; JP-090705.  
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
PI Kubota M, Maruta K, Sugimoto T, Tsusaki K;  
WPI: 95-329870/43.  
DR N-PSDB: T04156.  
PT DNA encoding enzyme reduces amylaceous saccharide to produce  
non-reducing sugar with trehalose end gp. - useful in foods,  
cosmetics, pharmaceuticals, etc.  
PS Claim 3; Page 23-25; 178pp; English.  
CC This sequence represents an enzyme that forms a non-reducing sugar with a  
trehalose end group, from a reducing amylaceous saccharide. The  
amylaceous saccharides have a degree of glucose polymerisation of 3 or  
higher. This sequence was extracted from a liquid culture of  
Arthrobacter species Q36. By using an oligonucleotide probe based on a  
fragment of the enzyme sequence, the DNA encoding sequence was obtained.  
The encoding sequence was then ligated into a vector and used to produce  
M-11 in E.coli transformants. This can also be performed for the DNA  
encoding enzyme M-11 (see T04155), which was obtained from Rhizobium sp.  
M-11. The non-reducing sugars produced by the action of these enzymes  
can be used in foods, cosmetics, pharmaceuticals and feeds. They are  
used as sweeteners, taste and quality improvers, stabilisers, fillers,  
excipients and adjuvants. The sugars can also be used as intermediates  
for trehalose. The advantages with using these sugars, are that, they  
are practically non-reducing (so no browning reaction occurs when they  
are heated with proteins), have a mild but good quality sweetness,  
adequate viscosity and moisture-retaining properties.  
SQ Sequence 775 AA;

Query Match 89.8%; Score 44; DB 15; Length 775;  
Best Local Similarity 83.3%; Pred. No. 6.37e-01;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 8 Yrlqir 13  
||| ||  
QY 1 YRLAIR 6

RESULT 12  
ID R92910 standard; peptide; 20 AA.  
AC R92910;  
DT 16-MAY-1996 (first entry)  
DE HLA-B\*2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).  
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
Immunosuppressant; graft versus host disorder; transplantation; therapy;  
class I MHC; HLA-B\*2702.  
OS Synthetic.  
PN W09526979-A1.  
PD 12-OCT-1995.  
PF 05-APR-1995; U04349.

PR 05-APR-1994; US-222851.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PI Clayberger C, Krensky AM, Parham P;  
DR WPI: 95-358582/46.  
PT Extension of acceptance period of transplants from MHC unmatched  
donor hosts - using Class I B75-84 MHC antigen of the recipient  
host  
PS Example 15; Page 36; 80pp; English.  
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
class I major histocompatibility complex (MHC) antigens. This sequence  
is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
I MHC HLA-B\*2702. These sequences can be used to extend the period of  
acceptance by a recipient of a transplant from an MHC unmatched donor.  
The peptides are administered to a patient in conjunction with a  
subtherapeutic amount of an immunosuppressant. This is administered to  
the patient for a limited period of time (compared to the lifetime  
administration for current treatments). The peptides particularly  
modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
of the patient.  
SQ Sequence 20 AA;

Query Match 85.7%; Score 42; DB 16; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.11e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 Yrlatr 6  
||| |  
QY 1 YRLAIR 6

RESULT 13  
ID R92908 standard; peptide; 20 AA.  
AC R92908;  
DT 16-MAY-1996 (first entry)  
DE HLA-B\*2702 CTL modulating peptide (B2702.84-75(T)/75-84).  
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
Immunosuppressant; graft versus host disorder; transplantation; therapy;  
class I MHC; HLA-B\*2702.  
OS Synthetic.  
PN W09526979-A1.  
PD 12-OCT-1995.  
PF 05-APR-1995; U04349.  
PR 05-APR-1994; US-222851.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PI Clayberger C, Krensky AM, Parham P;  
DR WPI: 95-358582/46.  
PT Extension of acceptance period of transplants from MHC unmatched  
donor hosts - using Class I B75-84 MHC antigen of the recipient  
host  
PS Example 15; Page 36; 80pp; English.  
CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
class I major histocompatibility complex (MHC) antigens. This sequence  
is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
I MHC HLA-B\*2702. These sequences can be used to extend the period of  
acceptance by a recipient of a transplant from an MHC unmatched donor.  
The peptides are administered to a patient in conjunction with a  
subtherapeutic amount of an immunosuppressant. This is administered to  
the patient for a limited period of time (compared to the lifetime  
administration for current treatments). The peptides particularly  
modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
of the patient.  
SQ Sequence 20 AA;

Query Match 85.7%; Score 42; DB 16; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.11e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 Yrlatr 6  
||| |  
QY 1 YRLAIR 6

RESULT 14

ID R42392 standard; Protein; 617 AA.  
AC R42392;  
DT 13-MAY-1994 (first entry)  
DE MCI haemagglutinin.  
KW haemagglutinin; HA; fusion glycoprotein; wild-type;  
KW measles virus; vaccine; infection; consensus polypeptide.  
OS Measles virus strain MCI.  
PN WO9321325-A.  
PD 28-OCT-1993.  
PF 08-APR-1993; U03209.  
PR 08-APR-1992; US-866033.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICE.  
PI Bellini WJ, Rota JS;  
DR WPI: 93-351735/44.  
DR N-PSDB; Q51093.  
PT Haemagglutinin and fusion glycoprotein of several wild-type  
PT measles strains - used to construct vaccines for measles  
PT infection  
PS Claim 11; Page 47-50; 119pp; English.  
CC HA (Q51088-94) and fusion glycoprotein (Q51095-97) sequences of  
CC several wild-type measles strains are given. Shared amino acid  
CC variations in wild-type measles glycoproteins are identified in five  
CC wild-type measles viruses. A consensus polypeptide, the amino acid  
CC sequence of which reflects variation common to more than one wild-  
CC type strain, is the basis for constructing live attenuated vaccines,  
CC or recombinant vaccines to replace older, less efficacious vaccines.  
CC Immunological reagents useful in differentiating wild-type measles  
CC strains from other known strains can also be produced.  
SQ Sequence 617 AA;

Query Match 83.7%; Score 41; DB 8; Length 617;  
Best Local Similarity 66.7%; Pred. No. 1.47e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 555 frlpir 560  
QY 1 YRLAIR 6

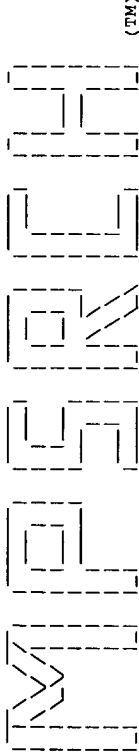
RESULT 15  
ID R11056 standard; Protein; 732 AA.  
AC R11056;  
DT 23-MAY-1991 (first entry)  
DE Acylamino acid-isolating enzyme-like polypeptide.  
KW AARE; pig liver.  
OS Sus scrofa.  
PN J03030673-A.  
PD 08-FEB-1991.  
PF 29-JUN-1989; 165216.  
PR 29-JUN-1989; JP-165216.  
PA (TAKA-) TAKARA SHUZO KK.  
DR WPI: 91-084340/12.  
DR N-PSDB; Q10958.  
PT Acylamino acid-isolating enzyme-like polypeptide - prepd. by  
PT genetic engineering.  
PS Claim 1; Fig 2; 10pp; Japanese.  
CC The sequence was obt'd. from six clones isolated from a pig liver  
CC cDNA library. The clones, lambda AARE 419, 450, 451, 452, 521 and  
CC 522 cover the entire sequence of the gene.  
SQ Sequence 732 AA;

Query Match 83.7%; Score 41; DB 2; Length 732;  
Best Local Similarity 66.7%; Pred. No. 1.47e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 268 frlpir 273  
QY 1 YRLAIR 6

Search completed: Thu May 22 08:32:26 1997  
Job time : 13 secs.

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu May 22 08:29:29 1997; MasPar time 2.04 Seconds  
Tabular output not generated. 62.314 Million cell updates/sec

Title: >US-08-653-294-6  
Description: (1-6) from US08653294.p  
Perfect Score: 53  
Sequence: 1 YRLIR 6

Scoring table: PAM 150  
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot34  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 23.777; Variance 26.124; scale 0.910

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	51	96.2	1489	11	YGPO_YEAST HYPOTHETICAL 171.5 KD	1.06e+00
2	49	92.5	101	11	YEB4_YEAST HYPOTHETICAL 12.2 KD	2.96e+00
3	49	92.5	720	6	NDA4_SCHPO CELL DIVISION CONTROL	2.96e+00
4	48	90.6	221	11	YF88_YEAST HYPOTHETICAL 25.9 KD	4.88e+00
5	48	90.6	239	11	YJ9D_YEAST HYPOTHETICAL 27.6 KD	4.88e+00
6	48	90.6	309	9	TF2B_SULSH TRANSCRIPTION INITIAT	4.88e+00
7	48	90.6	628	4	GIDA_BACSU GLUCOSE INHIBITED DIV	4.88e+00
8	48	90.6	629	4	GIDA_HAEIN GLUCOSE INHIBITED DIV	4.88e+00
9	48	90.6	968	6	MANA_RHOMR MANNAN ENDO-1,4-BETA-	4.88e+00
10	48	90.6	1075	8	RPOB_PINTH DNA-DIRECTED RNA POLY	4.88e+00
11	47	88.7	1089	6	NMD2_YEAST NONSENSE-MEDIATED MRN	7.98e+00
12	46	86.8	234	7	PRC3_DROME PROTEASOME 25 KD SUBU	1.29e+01
13	46	86.8	332	11	YK50_YEAST HYPOTHETICAL 39.4 KD	1.29e+01
14	46	86.8	1070	8	RPOB_TOBAC DNA-DIRECTED RNA POLY	1.29e+01
15	46	86.8	1070	8	RPOB_SPTOL DNA-DIRECTED RNA POLY	1.29e+01
16	45	86.8	1078	8	RPOB_SINAL DNA-DIRECTED RNA POLY	1.29e+01
17	45	84.9	293	8	RL5_CAEEL PROBABLE 60S RIBOSOMA	2.08e+01
18	45	84.9	513	8	RFP_HUMAN TRANSFORMING PROTEIN	2.08e+01
19	45	84.9	1030	3	FBP1_DROME FAT-BODY PROTEIN-1 PR	2.08e+01
20	45	84.9	1638	2	BRM_DROME HOMEOTIC GENE REGULAT	2.08e+01
21	44	83.0	181	10	VC16_VACCC PROTEIN C16/B22.	3.32e+01
22	44	83.0	187	8	RL18_ARATH 60S RIBOSOMAL PROTEIN	3.32e+01

23	44	83.0	233	7	PRC3_XENLA PROTEASOME COMPONENT	3.32e+01
24	44	83.0	258	11	YDF2_SCHPO HYPOTHETICAL 29.3 KD	3.32e+01
25	44	83.0	293	8	RL5_SCHPO 60S RIBOSOMAL PROTEIN	3.32e+01
26	44	83.0	297	8	RLJ_YEAST 60S RIBOSOMAL PROTEIN	3.32e+01
27	44	83.0	515	9	TRPE_BUCAP ANTHRANILATE SYNTHASE	3.32e+01
28	44	83.0	547	9	SNG1_YEAST NITROGUANADINE RESI	3.32e+01
29	44	83.0	590	11	YKTA_CAEEL HYPOTHETICAL 65.5 KD	3.32e+01
30	44	83.0	628	4	GIDA_ECOLI GLUCOSE INHIBITED DIV	3.32e+01
31	44	83.0	975	5	KINH_DROME KINESIN HEAVY CHAIN.	3.32e+01
32	44	83.0	1151	4	GRI1_YEAST GRI1 PROTEIN.	3.32e+01
33	44	83.0	2493	3	CYAA_USTMA ADENYLATE CYCLASE (EC	3.32e+01
34	43	81.1	146	9	SR14_YEAST SIGNAL RECOGNITION PA	5.24e+01
35	43	81.1	185	11	YEM4_YEAST HYPOTHETICAL 21.2 KD	5.24e+01
36	43	81.1	205	11	YIJC_HAEIN HYPOTHETICAL 26.6 KD	5.24e+01
37	43	81.1	234	11	YIJC_ECOLI HYPOTHETICAL 26.6 KD	5.24e+01
38	43	81.1	394	7	PHYV_PSEAE P-HYDROXYBENZOATE HYD	5.24e+01
39	43	81.1	394	7	PHYV_PSEFL P-HYDROXYBENZOATE HYD	5.24e+01
40	43	81.1	601	6	LONH_HAEIN PROTEASE LA HOMOLOG (	5.24e+01
41	43	81.1	779	11	YX31_MYCTU HYPOTHETICAL 84.6 KD	5.24e+01
42	43	81.1	825	8	RCAL_YEAST MITOCHONDRIAL RESPIRA	5.24e+01
43	43	81.1	1592	4	GTF2_STRDO GLUCOSYLTRANSFERASE-I	5.24e+01
44	43	81.1	1597	4	GTF1_STRDO GLUCOSYLTRANSFERASE-I	5.24e+01
45	43	81.1	4092	3	DYHC_YEAST DYNEIN HEAVY CHAIN, C	5.24e+01

ALIGNMENTS

RESULT 1  
ID YGPO\_YEAST STANDARD; PRT; 1489 AA.  
AC PS3115;  
DT 01-OCT-1996 (REL. 34, CREATED)  
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
DE HYPOTHETICAL 171.5 KD HELICASE IN LYSS-ARO2 INTERGENIC REGION.  
GN YGL150C OR G1880.  
OS SACHAROMYCES CEREVISIAE (BAKER'S YEAST).  
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.  
RN [1]  
RX MEDLINE; 96158061.  
RA JAMES C.M., INDGE K.J., OLIVER S.G.;  
RL YEAST 11:1413-1419(1995).  
RN [2]  
RP SEQUENCE OF 138-1489 FROM N.A.  
RA VOLCKAERT G., VOET M., VERHASSELT P., DEFOOR E.;  
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.  
CC -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).  
CC -!- SIMILARITY: TO HELICASES OF THE SNF2/RAD54 FAMILY.  
DR EMBL; 248618; G728695; -.  
DR EMBL; 272672; E243594; -.  
KW HYPOTHETICAL PROTEIN; NUCLEAR PROTEIN; DNA-BINDING; HELICASE;  
KW ATP-BINDING.  
FT DOMAIN 188 193 POLY-ALA.  
FT DOMAIN 259 268 POLY-GLU.  
FT DOMAIN 300 306 POLY-SER.  
FT DOMAIN 568 573 POLY-GLU.  
FT DOMAIN 675 682 POLY-GLU.  
FT NP\_BIND 731 738 ATP (POTENTIAL).  
FT SITE 841 844 DEAQ BOX.  
SQ SEQUENCE 1489 AA; 171454 MW; 8149887E CRC32;  
Query Match 96.2%; Score 51; DB 11; Length 1489;  
Best Local Similarity 83.3%; Pred.No. 1.06e+00;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db 1420 yrlir 1425  
QY 1 YRLIR 6  
RESULT 2  
ID YEB4\_YEAST STANDARD; PRT; 101 AA.  
AC P39999;

DT 01-FEB-1995 (REL. 31, CREATED)  
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL 12.2 KD PROTEIN IN MMS21-UBC8 INTERGENIC REGION.  
 GN YEL014C.  
 OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-S288C / AB972;  
 RA DIETRICH F.S., MULLIGAN J.T., HENNESSEY K.M., ALLEN E., ARAUJO R.,  
 RA AVILES E., BERNO A., BRENNAN T., CARPENTER J., CHEN E., CHERRY J.M.,  
 RA CHUNG E., DUNCAN M., GUZMAN E., HARTZELL G., HUNICK-SMITH S.,  
 RA HYMAN R., KAYSER A., KOMP C., LASHKARI D., LEW H., LIN D.,  
 RA MOSEDALE D., NAKAHARA K., NAMATH A., NORGREN R., OENNER P., OH C.,  
 RA PETEL F.X., ROBERTS D., SEHL P., SCHRAMM S., SHOGREN T., SMITH V.,  
 RA TAYLOR P., WEI Y., YELTON M., BOTSTEIN D., DAVIS R.W.;  
 RL SUBMITTED (DEC-1994) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL; U18530; G602381; -  
 KW HYPOTHETICAL PROTEIN.  
 SQ SEQUENCE 101 AA; 12209 MW; BE5A484B CRC32;

Query Match 92.5%; Score 49; DB 11; Length 101;  
 Best Local Similarity 83.3%; Pred. No. 2.96e+00;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 92 ymlir 97  
 |||||  
 QY 1 YRLIR 6

RESULT 3  
 ID NDA4\_SCHPO STANDARD; PRT; 720 AA.  
 AC P41389;  
 DT 01-NOV-1995 (REL. 32, CREATED)  
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE CELL DIVISION CONTROL PROTEIN NDA4.  
 GN NDA4 OR SPAC3F10.01.  
 OS SCHIOSACCHAROMYCES POMBE (FISSTON YEAST).  
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 94129084.  
 RA MIYAKE S., OKISHIO N., SAMEJIMA I., HIRAKA Y., TODA T., SAITOH I.,  
 RA YANAGIDA M.;  
 RA MOL. BIOL. CELL 4:1003-1015(1993).  
 RL [2]  
 RP SEQUENCE OF 72-720 FROM N.A.  
 RC STRAIN-972;  
 RA MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;  
 RL SUBMITTED (FEB-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
 CC -|- FUNCTION: ROLE IN DNA REPLICATION AND ESSENTIAL FOR VIABILITY.  
 CC -|- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).  
 CC -|- SIMILARITY: BELONGS TO THE MCM2/3/5 FAMILY.  
 DR EMBL; S58467; G545211; -  
 DR EMBL; Z69369; E221200; -  
 DR PIR; A48723; A48723.  
 DR PROSITE; PS00847; MCM235.  
 KW TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;  
 KW DNA REPLICATION; CELL CYCLE; ATP-BINDING.  
 FT DOMAIN 307 312  
 FT DOMAIN 322 529 MCM.  
 FT NP\_BIND 372 379 ATP (POTENTIAL).  
 FT CONFLICT 461 461 A -> R (IN REF. 1).  
 SQ SEQUENCE 720 AA; 80099 MW; 29D61458 CRC32;

Query Match 92.5%; Score 49; DB 6; Length 720;  
 Best Local Similarity 83.3%; Pred. No. 2.96e+00;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 675 ymlir 680  
 |||||

QY 1 YRLIR 6  
 |||||  
 RESULT 4  
 ID YFH8\_YEAST STANDARD; PRT; 221 AA.  
 AC P43592;  
 DT 01-NOV-1995 (REL. 32, CREATED)  
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL 25.9 KD PROTEIN IN MPRI-GCN20 INTERGENIC REGION.  
 GN YFR008W.  
 OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-S288C / AB972;  
 RX MEDLINE; 95400292.  
 RA MURAKAMI Y., NAITOU M., HAGIWARA H., SHIBATA T., OZAWA M.,  
 RA SASANUMA S.-I., SASANUMA M., TSUCHIYA Y., SOEDA E., YOKOYAMA K.,  
 RA YAMAZAKI M., TASHIRO H., EKI T.;  
 RL NAT. GENET. 10:261-268(1995).  
 DR EMBL; D50617; G836763; -  
 KW HYPOTHETICAL PROTEIN.  
 FT DOMAIN 11 22  
 FT POLY-GLN.  
 SQ SEQUENCE 221 AA; 25915 MW; 3D34764A CRC32;

Query Match 90.6%; Score 48; DB 11; Length 221;  
 Best Local Similarity 83.3%; Pred. No. 4.88e+00;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 211 yrlir 216  
 |||||  
 QY 1 YRLIR 6

RESULT 5  
 ID YJ9D\_YEAST STANDARD; PRT; 239 AA.  
 AC P47167;  
 DT 01-FEB-1996 (REL. 33, CREATED)  
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL 27.6 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.  
 GN YJRI35C OR J2122.  
 OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA ROSE M., KOETTER P., ENTIAN K.D.;  
 RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL; Z49635; G1015872; -  
 KW HYPOTHETICAL PROTEIN.  
 SQ SEQUENCE 239 AA; 27567 MW; 0BF23C6E CRC32;

Query Match 90.6%; Score 48; DB 11; Length 239;  
 Best Local Similarity 83.3%; Pred. No. 4.88e+00;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 205 yrlir 210  
 |||||  
 QY 1 YRLIR 6

RESULT 6  
 ID TF2B\_SULSH STANDARD; PRT; 309 AA.  
 AC P50387;  
 DT 01-OCT-1996 (REL. 34, CREATED)  
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE TRANSCRIPTION INITIATION FACTOR IIB HOMOLOG (TFIIB).  
 GN TFB.  
 OS SULFOLOBUS SHIBATAE.  
 OC ARCHAEABACTERIA; CRENARCHAEOTA; SULFOLOBALES.  
 RN [1]



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RX SEQUENCE FROM N.A.
RX MEDLINE; 95320218.
RA KURESHI S.A., KHOO B., BAUMANN P., JACKSON S.P.;
RA PROC. NATL. ACAD. SCI. U.S.A. 92:6077-6081(1995).
RL CC -!- SIMILARITY: BELONGS TO THE IFIIB FAMILY.
CC EMBL; U20899; G836952; -.
KW TRANSCRIPTION REGULATION; DUPLICATION.
FT REPEAT 130 206
FT REPEAT 224 300
SQ SEQUENCE 309 AA; 34756 MW; 0921E52C CRC32;

Query Match 90.6%; Score 48; DB 9; Length 309;
Best Local Similarity 83.3%; Pred. No. 4.88e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 201 yrl1lr 206
QY 1 YRL1LR 6

RESULT 7
ID GIDA_BACSU STANDARD; PRT; 628 AA.
AC P25812;
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE GLUCOSE INHIBITED DIVISION PROTEIN A.
GN GIDA.
OS BACILLUS SUBTILIS.
OC PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / CRK2000;
RX MEDLINE; 92204018.
RA OGASAWARA N., YOSHIKAWA H.;
RL MOL. MICROBIOL. 6:629-634(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE; 96051385.
RA OGASAWARA N., NAKAI S., YOSHIKAWA H.;
RL DNA RES. 1:11-14(1994).
CC -!- FUNCTION: NOT KNOWN.
CC -!- SIMILARITY: TO OTHER BACTERIAL GIDA PROTEIN.
DR EMBL; X62539; G40026; -.
DR EMBL; D26185; G467385; -.
DR PIR; JQ1216; EWSGA.
DR SUBTILIST; BG10059; GIDA.
SQ SEQUENCE 628 AA; 69752 MW; F9B082BB CRC32;

Query Match 90.6%; Score 48; DB 4; Length 628;
Best Local Similarity 83.3%; Pred. No. 4.88e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 435 yrl1lr 440
QY 1 YRL1LR 6

RESULT 8
ID GIDA_HAEIN STANDARD; PRT; 629 AA.
AC P44763;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE GLUCOSE INHIBITED DIVISION PROTEIN A.
GN GIDA OR HI0582.
OS HAEMOPHILUS INFLUENZAE.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC PASTEURELLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20;

RX MEDLINE; 95350630.
RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
RA KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
RA UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
RA FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
RA GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
RA VENTER J.C.; 95350630.
RL SCIENCE 269:496-512(1995).
CC -!- FUNCTION: NOT KNOWN.
CC -!- SIMILARITY: TO OTHER BACTERIAL GIDA PROTEIN.
DR EMBL; L45233; G1004046; -.
DR EMBL; U32739; G925610; -.
SQ SEQUENCE 629 AA; 70103 MW; 6FD83D06 CRC32;

Query Match 90.6%; Score 48; DB 4; Length 629;
Best Local Similarity 83.3%; Pred. No. 4.88e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 435 yrl1lr 440
QY 1 YRL1LR 6

RESULT 9
ID MANA_RHOMR STANDARD; PRT; 968 AA.
AC P49425;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE MANNAN ENDO-1,4-BETA-MANNOSIDASE (EC 3.2.1.78).
GN MANA.
OS RHODOTHERMUS MARINUS.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA;
OC NONPHOTOSYNTHETIC, NONFRUITING GLIDING; CYTOPHAGACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RA POLITZ O., KRAH M., BORRIESS R.;
RL SUBMITTED (AUG-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- CATALYTIC ACTIVITY: RANDOM HYDROLYSIS OF 1,4-BETA-D-
LINKAGES IN MANNANS, GALACTOMANNANS, GLUCOMANNANS, AND
GALACTOGLUCOMANNANS.
CC -!- SIMILARITY: BELONGS TO FAMILY 26 OF GLYCOSYL HYDROLASES.
DR EMBL; X90947; G975706; -.
KW HYDROLASE; GLYCOSIDASE.
SQ SEQUENCE 968 AA; 110219 MW; 0EA79E71 CRC32;

Query Match 90.6%; Score 48; DB 6; Length 968;
Best Local Similarity 83.3%; Pred. No. 4.88e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 692 yrl1lr 697
QY 1 YRL1LR 6

RESULT 10
ID RPOB_PINTH STANDARD; PRT; 1075 AA.
AC P41607;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6).
GN RPOB.
OS PINUS THUNBERGII (GREEN PINE) (JAPANESE BLACK PINE).
OC CHLOROPLAST.
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; CONIFEROPHYCEAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95024047.
RA WAKASUGI T., TSUDZUKI J., ITO S., NAKASHIMA K., TSUDZUKI T.,

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RA SUGIURA M.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 91:9794-9798(1994).  
 CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION  
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS  
 CC SUBSTRATES.  
 CC -1- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +  
 CC RNA(N).  
 CC -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR  
 CC SUBUNITS: ALPHA, BETA, BETA', AND BETA".  
 CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.  
 DR EMBL; D17510; G1262609; -.  
 KW TRANSCRIPTION; DNA-DIRECTED RNA POLYMERASE; CHLOROPLAST.  
 SQ SEQUENCE 1075 AA; 122470 MW; 7643B7A8 CRC32;

Query Match 90.6%; Score 48; DB 8; Length 1075;  
 Best Local Similarity 83.3%; Pred. No. 4.88e+00;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1044 frllir 1049  
 QY 1 YRLIIR 6  
 :|||||

RESULT 11  
 ID NMD2-YEAST STANDARD; PRT; 1089 AA.  
 AC P38798;  
 DT 01-FEB-1995 (REL. 31, CREATED)  
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
 DE NONSENSE-MEDIATED MRNA DEGRADATION PROTEIN 2 (UP-FRAMESHIFT SUPPRESSOR 2).  
 GN NMD2 OR UPF2 OR IF51 OR SUAL OR YHRO77C.  
 OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC MEDLINE; 95189083.  
 RA HE F., JACOBSON A.;  
 RL GENES DEV. 9:437-454(1995).  
 CC [2]  
 CC SEQUENCE FROM N.A.  
 CC STRAIN-FLY136;  
 RC STRAIN-FLY136;  
 RX MEDLINE; 95189082.  
 RA CUI Y., HAGAN K.W., ZHANG S., PELTZ S.W.;  
 RL GENES DEV. 9:423-436(1995).  
 CC [3]  
 CC SEQUENCE FROM N.A.  
 CC MEDLINE; 95327692.  
 RA LEE S.-I., UMEN J.G., VARMUS H.E.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 92:6587-6591(1995).  
 CC [4]  
 CC SEQUENCE FROM N.A.  
 RC STRAIN-S288C / AB972;  
 RX MEDLINE; 94378003.  
 RA JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J.,  
 DU Z., FAVELLO A., FULTON L., GATTUNG S., GEISEL C., KIRSTEN J.,  
 KUCABA T., HILLIER L., JTER M., JOHNSTON L., LANGSTON Y.,  
 LATREILLE P., LOUIS E.J., MACRI C., MARDIS E., MENEZES S., MOUSER L.,  
 NHAN M., RIFKIN L., RILES L., ST PETER H., TREVASKIS E., VAUGHAN K.,  
 VIGNATI D., WILCOX L., WOLLDMAN P., WATERSTON R., WILSON R.,  
 VAUDIN M.;  
 RL SCIENCE 265:2077-2082(1994).  
 CC -1- FUNCTION: INVOLVED IN NONSENSE-MEDIATED DECAY OF MRNAS CONTAINING  
 CC PREMATURE STOP CODONS. IT INTERACTS, VIA ITS C-TERMINUS, WITH  
 CC NAM7/UPF1. COULD BE INVOLVED IN DETERMINING THE EFFICIENCY OF  
 CC TRANSLATIONAL TERMINATION OR REINITIATION OR FACTORS INVOLVED IN  
 CC THE INITIAL ASSEMBLY OF AN INITIATION- AND TERMINATION- COMPETENT  
 CC MRNP.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).  
 DR EMBL; U14974; G555939; -.  
 DR EMBL; U12137; G806704; -.  
 DR EMBL; U28158; G967213; -.  
 DR EMBL; U10556; G500836; -.  
 DR PIR; S46815; S46815.

DR SGD; L0001257; NMD2.  
 FT DOMAIN 843 975 ASP/GLU-RICH (HIGHLY ACIDIC).  
 CC CONFLICT 2 D -> YQQ (IN REF. 3 AND 4).  
 SQ SEQUENCE 1089 AA; 126746 MW; 4B6ADE8F CRC32;

Query Match 88.7%; Score 47; DB 6; Length 1089;  
 Best Local Similarity 83.3%; Pred. No. 7.98e+00;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 580 yrllir 585  
 QY 1 YRLIIR 6  
 :|||||

RESULT 12  
 ID PRC3-DROME STANDARD; PRT; 234 AA.  
 AC P40301;  
 DT 01-FEB-1995 (REL. 31, CREATED)  
 DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE PROTEASOME 25 KD SUBUNIT (EC 3.4.99.46) (MULTICATALYTIC ENDOPEPTIDASE  
 DE COMPLEX 25 KD SUBUNIT).  
 GN PROS-25.  
 OS DROSOPHILA MELANOGASTER (FRUIT FLY).  
 OC EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC STRAIN-CANTON-S;  
 RX MEDLINE; 93363644.  
 RA SEELIG A., TROXELL M., KLOETZEL P.M.;  
 RL BIOCHIM. BIOPHYS. ACTA 1174:215-217(1993).  
 CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX  
 CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH  
 CC ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT  
 CC NEUTRAL OR SLIGHTLY BASIC PH.  
 CC -1- PATHWAY: IS INVOLVED IN AN ATP/UBIQUITIN-DEPENDENT NON-LYSOSOMAL  
 CC PROTEOLYTIC PATHWAY.  
 CC -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL  
 CC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.  
 CC -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND  
 CC ALSO IN THE NUCLEUS.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1A; ALSO KNOWN AS THE  
 CC PROTEASOME A-TYPE FAMILY. BELONGS TO THE C3 SUBFAMILY.  
 DR EMBL; X70304; G397850; -.  
 DR PIR; S36116; S36116  
 DR FLYBASE; FBGN0010405; PROS25.  
 DR PROSITE; PS00388; PROTEASOME\_A.  
 KW PROTEASOME; HYDROLASE; PROTEASE.  
 SQ SEQUENCE 234 AA; 25906 MW; A86BD836 CRC32;

Query Match 86.8%; Score 46; DB 7; Length 234;  
 Best Local Similarity 66.7%; Pred. No. 1.29e+01;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 83 yrllvk 88  
 QY 1 YRLIIR 6  
 :|||||

RESULT 13  
 ID YK50-YEAST STANDARD; PRT; 352 AA.  
 AC P36151;  
 DT 01-JUN-1994 (REL. 29, CREATED)  
 DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL 39.4 KD PROTEIN IN CCP1-SIS2 INTERGENIC REGION.  
 GN YKR070W.  
 OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 RA POHL T.M., POHL F.M.;  
 RL SUBMITTED (MAR-1994) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL; 228295; G486541; -.  
 DR PIR; S38147; S38147.  
 KW HYPOTHETICAL PROTEIN.  
 SQ SEQUENCE 352 AA; 39406 MW; F5B1B2A CRC32;

Query Match 86.8%; Score 46; DB 11; Length 352;  
 Best Local Similarity 66.7%; Pred. No. 1.29e+01;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 223 frllvr 228  
 :|||:|  
 Qy 1 YRLLIR 6

## RESULT 14

ID RPOB\_TOBAC STANDARD; PRT; 1070 AA.  
 AC P08271;  
 DT 01-JAN-1988 (REL. 06, CREATED)  
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6).  
 GN RPOB.  
 OS NICOTIANA TABACUM (COMMON TOBACCO).  
 OC CHLOROPLAST.  
 OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;  
 OC SOLANALES; SOLANACEAE.

(1)  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-CV. BRIGHT YELLOW 4;  
 RA SUGIURA M.;  
 RL SUBMITTED (AUG-1986) TO EMBL/GENBANK/DBJ DATA BANKS.  
 (2)  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-CV. BRIGHT YELLOW 4;  
 RA MEDLINE; 86192857.  
 RA OHME M., TANAKA M., CHUNWONGSE J., SHINOZAKI K., SUGIURA M.;  
 RL FEBS LETT. 200:87-90(1986).  
 (3)  
 RN COMPLETE GENOME.

RA SHINOZAKI K., OHME M., TANAKA M., WAKASUGI T., HAYASHIDA N.,  
 RA MATSUBAYASHI T., ZAITA N., CHUNWONGSE J., OBOKATA J.,  
 RA YAMAGUCHI-SHINOZAKI K., OHTO C., TORAZAWA K., MENG B.Y., SUGITA M.,  
 RA DENO H., KAMOGASHIRA T., YAMADA K., KUSUDA J., TAKAIWA F., KATO A.,  
 RA TOHDOH N., SHIMADA H., SUGIURA M.;  
 RL EMBO J. 5:2043-2049(1986).  
 CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION  
 OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS  
 SUBSTRATES.

CC -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +  
 RNA(N).  
 CC -!- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR  
 SUBUNITS: ALPHA, BETA, BETA', AND BETA".  
 CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.  
 DR EMBL; 200044; G11822; -.  
 DR EMBL; X12745; G11781; -.  
 DR EMBL; M28017; G552958; -.  
 PIR: A24865; RNNTB  
 KW TRANSCRIPTION; DNA-DIRECTED RNA POLYMERASE; CHLOROPLAST.  
 SQ SEQUENCE 1070 AA; 120547 MW; 08C4DF19 CRC32;

Query Match 86.8%; Score 46; DB 8; Length 1070;  
 Best Local Similarity 66.7%; Pred. No. 1.29e+01;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1039 frllvr 1044  
 :|||:|  
 Qy 1 YRLLIR 6

## RESULT 15

ID RPOB\_SPIOI STANDARD; PRT; 1070 AA.  
 AC P11703;  
 DT 01-OCT-1989 (REL. 12, CREATED)

DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
 DE DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6).  
 GN RPOB.  
 OS SPINACIA OLERACEA (SPINACH).  
 OC CHLOROPLAST.  
 OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;  
 OC CARYOPHYLLALES; CHENOPODIACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 88316931.  
 RA HUDSON G.S., HOLTON T.A., WHITFIELD P.R., BOTTOMLEY W.;  
 RL J. MOL. BIOL. 200:639-654(1988).  
 CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION  
 OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS  
 SUBSTRATES.  
 CC -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +  
 RNA(N).  
 CC -!- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR  
 SUBUNITS: ALPHA, BETA, BETA', AND BETA".  
 CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.  
 DR EMBL; M55297; G295121; -.  
 DR PIR; C29959; C29959.  
 KW TRANSCRIPTION; DNA-DIRECTED RNA POLYMERASE; CHLOROPLAST.  
 SQ SEQUENCE 1070 AA; 120899 MW; CDC6F442 CRC32;

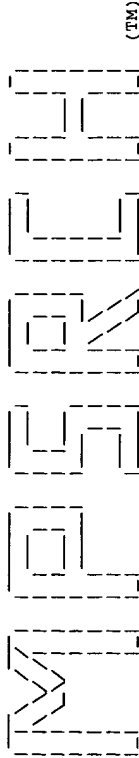
Query Match 86.8%; Score 46; DB 8; Length 1070;  
 Best Local Similarity 66.7%; Pred. No. 1.29e+01;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1039 frllvr 1044  
 :|||:|  
 Qy 1 YRLLIR 6

Search completed: Thu May 22 08:29:41 1997  
 Job time : 12 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:42:58 1997; MasPar time 2.50 Seconds  
68.327 Million cell updates/sec

Tabular output not generated.

Title: >US-08-653-294-5  
Description: (1-6) from US08653294.pep  
Perfect Score: 53  
Sequence: 1 RILLY 6

Scoring table: PAM 150  
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Maximum DB seq length 60

Database: pir50  
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3  
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8  
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 22.859; Variance 32.635; scale 0.700

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB ID	Description	Pred. No.
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No matches found.

Search completed: Thu May 22 08:43:09 1997  
Job time : 11 secs.

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WATERMAN (TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:43:26 1997; MasPar time 1.79 Seconds  
71.236 Million cell updates/sec

Tabular output not generated.

Title: >US-08-653-294-5  
Description: (1-6) from US08653294.pep  
Perfect Score: 53  
Sequence: 1 RILLY 6

Scoring table: PAM 150  
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Maximum DB seq length 60

Database: swiss-prot34  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 23.812; Variance 26.364; scale 0.903

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query				
No.	Score	Match	Length	ID	Description
-----					
					Pred. No.

No matches found.

Search completed: Thu May 22 08:43:33 1997  
Job time : 7 secs.

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MSRHH (TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu May 22 08:29:58 1997; MasPar time 2.69 Seconds  
Tabular output not generated. 63.585 Million cell updates/sec

Title: >US-08-653-294-6  
Description: (1-6) from US08653294.pep  
Perfect Score: 53  
Sequence: 1 YRLLR 6

Scoring table: PAM 150  
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: p1r50  
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3  
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8  
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 22.841; Variance 31.665; scale 0.721

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	%	ID	Description	Pred. No.
1	51	96.2	1489	11	S60416	DNA helicase YGL150c
2	49	92.5	101	11	S50445	hypothetical protein
3	49	92.5	720	11	A48723	cell division contro
4	48	90.6	173	9	S27599	hypothetical protein
5	48	90.6	221	11	S56263	hypothetical protein
6	48	90.6	239	11	S57158	hypothetical protein
7	48	90.6	389	10	JC4001	macrolide 3-O-acyl
8	48	90.6	628	4	BWBSGA	gida protein - Bacil
9	48	90.6	629	8	I64078	glucose inhibited di
10	47	88.7	1089	11	S48244	NMD2 protein - yeast
11	46	86.8	234	5	S36116	multicatalytic endop
12	46	86.8	352	11	S38147	hypothetical protein
13	46	86.8	1070	5	C29359	DNA-directed RNA pol
14	46	86.8	1070	1	RNNTB	DNA-directed RNA pol
15	46	86.8	1078	5	S48842	finger protein rfp -
16	45	84.9	506	6	S37583	transforming protein
17	45	84.9	513	2	TVHURE	transforming protein
18	45	84.9	801	15	TVHURE	transforming protein
19	45	84.9	1030	12	SV1034	gene P1 protein - fr
20	45	84.9	1638	12	A42091	transcriptional acti
21	44	83.0	96	8	S40544	hypothetical protein

22	44	83.0	96	4	IEECE9	hypothetical 11k pro	9.80e+01
23	44	83.0	153	8	A36837	Dil protein - vaciol	9.80e+01
24	44	83.0	181	8	C42528	B2R protein - varci	9.80e+01
25	44	83.0	234	5	JH0421	proteasome chain XC3	9.80e+01
26	44	83.0	297	7	S42144	ribosomal protein L5	9.80e+01
27	44	83.0	322	12	S66766	probable membrane pr	9.80e+01
28	44	83.0	355	10	I40819	butyrate kinase - Cl	9.80e+01
29	44	83.0	515	2	I40052	anthranilate synthas	9.80e+01
30	44	83.0	547	12	S53920	SNG1 protein - yeast	9.80e+01
31	44	83.0	590	12	S40707	hypothetical protein	9.80e+01
32	44	83.0	628	4	BVECQA	gida protein - Esche	9.80e+01
33	44	83.0	975	3	A31497	kinesin heavy chain	9.80e+01
34	44	83.0	1151	11	A41529	GRII protein - yeast	9.80e+01
35	44	83.0	2493	12	A55481	adenylate cyclase (E	9.80e+01
36	43	81.1	146	12	S51616	signal recognition p	1.44e+02
37	43	81.1	158	4	W6WL18	E6 protein - human p	1.44e+02
38	43	81.1	294	11	S19226	cold-regulated prote	1.44e+02
39	43	81.1	363	12	S59337	RNS5 protein - yeast	1.44e+02
40	43	81.1	394	1	WHP5BA	4-hydroxybenzoate 3-	1.44e+02
41	43	81.1	416	16	S26836	type II site-specifi	1.44e+02
42	43	81.1	505	10	C64502	hypothetical protein	1.44e+02
43	43	81.1	556	14	A49579	amphotropic murine r	1.44e+02
44	43	81.1	870	11	S65158	PAL1 protein - yeast	1.44e+02
45	43	81.1	2148	14	A56011	transcription factor	1.44e+02

## ALIGNMENTS

1	RESULT	S60416	#type complete
	ENTRY	DNA helicase YGL150c - yeast (Saccharomyces cerevisiae)	
	TITLE	protein G1880	
	ALTERNATE_NAMES	#formal_name Saccharomyces cerevisiae	
	ORGANISM	15-Feb-1995 #sequence_revision 12-Apr-1996 #text_change	
	DATE	19-Jul-1996	
	ACCESSIONS	S60416; S53049; S60421; S64166; S64164	
	REFERENCE	S60416	
	#authors	James, C.M.; Indge, K.J.; Oliver, S.G.	
	#submission	submitted to the EMBL Data Library, March 1995	
	#description	DNA sequence analysis of a 35kb segment from Saccharomyces cerevisiae chromosome VII reveals 19 open reading frames including RAD54, ACE1/CUP2, PMR1, RCK1, AMS1 and CAL1/CDC43.	
	#accession	S60416	
	#molecule_type	DNA	
	#residues	1-1489 #label JAM	
	#cross-references	EMBL:Z48618	
	REFERENCE	S53045	
	#authors	James, C.M.; Indge, K.J.; Oliver, S.G.	
	#submission	submitted to the EMBL Data Library, March 1995	
	#description	DNA sequence analysis of a 35Kb segment from S.cerevisiae chromosome VII reveals 39 ORFs including RAD54, ACE1(CUP2), PMR1, RCK1, AMS1 and CAL1/CDC43.	
	#accession	S53049	
	#molecule_type	DNA	
	#residues	816-1489 #label JAW	
	#cross-references	EMBL:Z48618	
	REFERENCE	S60417	
	#authors	James, C.M.; Indge, K.J.; Oliver, S.G.	
	#journal	Yeast (1995) 11:1413-1419	
	#title	DNA sequence analysis of a 35 kb segment from Saccharomyces cerevisiae chromosome VII reveals 19 open reading frames including RAD54, ACE1/CUP2, PMR1, RCK1, AMS1 and CAL1/CDC43.	
	#accession	S60421	
	#status	nucleic acid sequence not shown	
	#molecule_type	DNA	
	#residues	728-767:808-862:865-969;1001-1021;1296-1347;1360-1468	
	#cross-references	EMBL:Z48618	
	REFERENCE	S64165	
	#authors	James, C.M.; Indge, K.J.; Oliver, S.G.	
	#submission	submitted to the Protein Sequence Database, May 1996	

```

#accession S64166
#molecule_type DNA
#residues 1-1489 #label JAA
#cross-references EMBL:272672
#experimental_source strain S288C
REFERENCE S64153
#authors Volckaert, G.; Voet, M.; Verhasselt, P.; Defoor, E.
#submission submitted to the Protein Sequence Database, May 1996
#accession S64164
#molecule_type DNA
#residues 1-137 #label VOL
#cross-references EMBL:272672
#experimental_source strain S288C
GENETICS
#map_position 7L
SUMMARY #length 1489 #molecular-weight 171454 #checksum 2554
Query Match 96.2%; Score 51; DB 11; Length 1489;
Best Local Similarity 83.3%; Pred. No. 5.56e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 1420 yrllvr 1425
|:|:|:|
QY 1 YRLLIR 6

RESULT 2
ENTRY S50445 #type complete
TITLE hypothetical protein YEL014c - yeast (Saccharomyces cerevisiae)
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 24-Feb-1995
ACCESSIONS S50445
REFERENCE S50428
#authors Dietrich, F.S.
#submission submitted to the EMBL Data Library, December 1994
#description Saccharomyces cerevisiae chromosome V cosmids 9871, 8199, 9867, 9495 and lambda clones 6693 and 5898.
#accession S50445
#molecule_type DNA
#residues 1-101 #label DIE
#cross-references EMBL:U18530
GENETICS
#map_position 5L
SUMMARY #length 101 #molecular-weight 12209 #checksum 4508
Query Match 92.5%; Score 49; DB 11; Length 101;
Best Local Similarity 83.3%; Pred. No. 1.30e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 92 yrmlir 97
|:|:|:|
QY 1 YRLLIR 6

RESULT 3
ENTRY A48723 #type complete
TITLE cell division control protein nda4 - fission yeast (Schizosaccharomyces pombe)
ORGANISM #formal_name Schizosaccharomyces pombe
DATE 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 04-Dec-1994
ACCESSIONS A48723
REFERENCE A48723
#authors Miyake, S.; Okishio, N.; Samejima, I.; Hiraoka, Y.; Toda, T.; Saitoh, I.; Yanagida, M.
#journal Mol. Biol. Cell (1993) 4:1003-1015
#title Fission yeast genes nda4(+) and nda4(+), mutations of which lead to S-phase block, chromatin alteration and Ca(2+) suppression, are members of the CDC46/MCM2 family.
#accession A48723
#status preliminary; not compared with conceptual translation

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#molecule_type DNA
#residues 1-720 #label MIY
GENETICS
#gene nda4+
KEYWORDS cell division control
FEATURE 319-532 #domain MCM2 core domain similarity #label MCM
SUMMARY #length 720 #molecular-weight 80184 #checksum 1029
Query Match 92.5%; Score 49; DB 11; Length 720;
Best Local Similarity 83.3%; Pred. No. 1.30e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 675 yrmlir 680
|:|:|:|
QY 1 YRLLIR 6

RESULT 4
ENTRY S27599 #type complete
TITLE hypothetical protein 3 - Nostoc sp.
ORGANISM #formal_name Nostoc sp.
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995
ACCESSIONS S27599
REFERENCE S27596
#authors Walton, D.K.; Gendel, S.M.; Atherly, A.G.
#submission submitted to the EMBL Data Library, February 1992
#accession S27599
#status preliminary
#molecule_type DNA
#residues 1-173 #label WAL
#cross-references EMBL:M81381
SUMMARY #length 173 #molecular-weight 19346 #checksum 1671
Query Match 90.6%; Score 48; DB 9; Length 173;
Best Local Similarity 83.3%; Pred. No. 1.97e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 164 yrllir 169
|:|:|:|
QY 1 YRLLIR 6

RESULT 5
ENTRY S56263 #type complete
TITLE hypothetical protein YFR008w - yeast (Saccharomyces cerevisiae)
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
ACCESSIONS S56263
REFERENCE S56186
#authors Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanuma, M.; Tsuchiya, Y.; Soeda, E.; Yokoyama, K.; Yamazaki, M.; Tashiro, H.; Eki, T.
#submission submitted to the EMBL Data Library, May 1995
#description Analysis of the nucleotide sequence of chromosome VI from Saccharomyces cerevisiae.
#accession S56263
#status preliminary
#molecule_type DNA
#residues 1-221 #label MUR
#cross-references EMBL:D50617
GENETICS
#map_position 6R
SUMMARY #length 221 #molecular-weight 25915 #checksum 5555
Query Match 90.6%; Score 48; DB 11; Length 221;
Best Local Similarity 83.3%; Pred. No. 1.97e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 211 yrllir 216

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QY 1 YRLLR 6
||||:|
#authors Ogasawara, N.; Yoshikawa, H.
#journal Mol. Microbiol. (1992) 6:629-634
#title Genes and their organization in the replication origin region
of the bacterial chromosome.
#cross-references MUID:92204018
#accession I40440
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-628 #label RES
#cross-references EXBL:X62539; NID:G40020; CDS_PID:G40026
#experimental_source strain CRK2000
CLASSIFICATION #superfamily gida protein
SUMMARY #length 628 #molecular-weight 69752 #checksum 5500

Query Match 90.6%; Score 48; DB 4; Length 628;
Best Local Similarity 83.3%; Pred. No. 1.97e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 435 YRLLR 440
||||:|
QY 1 YRLLR 6

RESULT 9
ENTRY
TITLE I64078 #type complete
glucose inhibited division protein (gida) homolog -
Haemophilus influenzae (strain Rd KW20)
ORGANISM #formal_name Haemophilus influenzae
DATE 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
I64078
ACCESSIONS A64000
REFERENCE
#authors Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
Kirkness, E.F.; Kervage, A.R.; Bult, C.J.; Tomb, J.F.;
Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
Fitzhugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton,
M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann,
J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.;
Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
#journal Science (1995) 269:496-512
#title Whole-genome random sequencing and assembly of Haemophilus
influenzae Rd.
#accession I64078
#status preliminary
#molecule_type DNA
#residues 1-629 #label TIGR
#cross-references GB:L42023; TIGR:HI0582
#note named as homolog to a protein from Escherichia coli
CLASSIFICATION #superfamily gida protein
SUMMARY #length 629 #molecular-weight 70103 #checksum 317

Query Match 90.6%; Score 48; DB 8; Length 629;
Best Local Similarity 83.3%; Pred. No. 1.97e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 435 YRLLR 440
||||:|
QY 1 YRLLR 6

RESULT 10
ENTRY
TITLE S48244 #type complete
NMD2 protein - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES IF51 protein; protein YHR077c
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 28-Oct-1994 #sequence_revision 10-Feb-1995 #text_change
06-Sep-1996
ACCESSIONS S48244; S46815; S64648; S64738
REFERENCE S48244
#authors He, F.; Jacobson, A.

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QY 1 YRLLR 6
||||:|
#authors Ogasawara, N.; Yoshikawa, H.
#journal Mol. Microbiol. (1992) 6:629-634
#title Genes and their organization in the replication origin region
of the bacterial chromosome.
#cross-references MUID:92204018
#accession I40440
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-628 #label RES
#cross-references EXBL:X62539; NID:G40020; CDS_PID:G40026
#experimental_source strain CRK2000
CLASSIFICATION #superfamily gida protein
SUMMARY #length 628 #molecular-weight 69752 #checksum 5500

Query Match 90.6%; Score 48; DB 11; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.97e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 205 YRLLR 210
||||:|
QY 1 YRLLR 6

RESULT 7
ENTRY
TITLE JC4001 #type complete
macrolide 3-O-acyltransferase (EC 2.3.1.-) - Streptomyces sp.
ORGANISM #formal_name Streptomyces sp.
DATE 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change
14-Jul-1995
ACCESSIONS JC4001
REFERENCE
#authors Arisawa, A.; Tsunekawa, H.; Okamura, K.; Okamoto, R.
#journal Biosci. Biotechnol. Biochem. (1995) 59:582-588
#title Nucleotide sequence analysis of the carbomycin biosynthetic
genes including the 3-O-acyltransferase gene from
Streptomyces thermotolerans.
#accession JC4001
#molecule_type DNA
#residues 1-389 #label ABI
#cross-references DBJ:D30759
#note the source was designated as Streptomyces thermotolerans
GENETICS
#gene acyA
KEYWORDS acyltransferase
SUMMARY #length 389 #molecular-weight 42879 #checksum 3458

Query Match 90.6%; Score 48; DB 10; Length 389;
Best Local Similarity 83.3%; Pred. No. 1.97e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 158 YRLLR 163
||||:|
QY 1 YRLLR 6

RESULT 8
ENTRY
TITLE BWBSGA #type complete
gida protein - Bacillus subtilis
ORGANISM #formal_name Bacillus subtilis
DATE 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change
23-Aug-1996
ACCESSIONS I40440; JQ1216; S18076
REFERENCE I40435

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#submission submitted to the EMBL Data Library, September 1994
#description Identification of a novel component of the nonsense-mediated
#RNA decay pathway using an interacting protein screen.
#accession S48244
##molecule_type DNA
##residues 1-1089 ##label HEF
##cross-references EMBL:U14974
REFERENCE
#authors Favellio, T.
#submission submitted to the EMBL Data Library, June 1994
#description The sequence of S. cerevisiae cosmid 9205.
#accession S46815
##molecule_type DNA
##residues 'MYO', 3-1089 ##label FAV
##cross-references EMBL:U10556
REFERENCE
#authors Lee, S.I.; Umen, J.G.; Varnus, H.E.
#journal Proc. Natl. Acad. Sci. U.S.A. (1995) 92:6587-6591
#title A genetic screen identifies cellular factors involved in
retroviral -1 frameshifting.
#accession S64648
##status nucleic acid sequence not shown
##molecule_type DNA
##residues 1-1089 ##label LEE
##cross-references EMBL:U28158
REFERENCE
#authors Varnus, H.E.
#submission submitted to the EMBL Data Library, May 1995
#accession S64738
##molecule_type DNA
##residues 'MYO', 3-1089 ##label VAR
##cross-references EMBL:U28158
GENETICS
#gene NMD2; IFS1
#map_position 8R
#introns 2/3
SUMMARY
#length 1089 #molecular-weight 126746 #checksum 7254
Query Match 88.7%; Score 47; DB 11; Length 1089;
Best Local Similarity 83.3%; Pred. No. 2.97e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 580 Yrllir 585
QY 1 Yrllir 6
RESULT 11
ENTRY
TITLE
ALTERNATE_NAMES S36116 #type complete
PROS-Dm25 - fruit fly (Drosophila melanogaster)
ORGANISM proteasome chain PROS-Dm25
#formal_name Drosophila melanogaster
#formal_name Drosophila melanogaster
DATE 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
19-May-1995
ACCESSIONS S36116; S36117; A49550
REFERENCE
#authors Seelig, A.; Troxell, M.; Klotzel, P.M.
#journal Blochm. Biophys. Acta (1993) 1174:215-217
#title Sequence and genomic organization of the Drosophila
proteasome PROS-Dm25 gene.
#accession S36116
##molecule_type DNA
##residues 1-234 ##label SE1
##cross-references EMBL:X70304
#accession S36117
##molecule_type protein
##residues 7-36;178-192;228-234 ##label SE2
##note the authors translated the codon ACG for residue 116 as
Pro
REFERENCE A49550
#authors Seelig, A.; Multhaup, G.; Pesold-Hurt, B.; Beyreuther, K.;
Klotzel, P.M.

```

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#journal J. Biol. Chem. (1993) 268:25561-25567
#title Drosophila proteasome Dm25 subunit substitutes the mouse MC3
subunit in hybrid proteasomes. The N-terminal domain is
essential for subunit incorporation.
#accession A49550
##status not compared with conceptual translation
##molecule_type mRNA
##residues 1-234 ##label SE3
##cross-references GB:X70696
GENETICS
#introns 13/3; 39/3; 125/3; 177/3
#superfamily multicatalytic endopeptidase complex chain C9
#classification hydrolase; proteinase
#keywords
#summary #length 234 #molecular-weight 25906 #checksum 7606
Query Match 86.8%; Score 46; DB 5; Length 234;
Best Local Similarity 66.7%; Pred. No. 4.45e+01;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 83 Yrllvk 88
QY 1 Yrllir 6
RESULT 12
ENTRY
TITLE S38147 #type complete
hypothetical protein YKR070w - yeast (Saccharomyces
cerevisiae)
ORGANISM #formal_name Saccharomyces cerevisiae
#formal_name Saccharomyces cerevisiae
DATE 03-May-1994 #sequence_revision 03-May-1994 #text_change
12-Apr-1996
ACCESSIONS S38147
REFERENCE
#authors Pohl, T.M.; Pohl, F.M.
#submission submitted to the Protein Sequence Database, March 1994
#accession S38147
##molecule_type DNA
##residues_type 1-352 ##label POH
##cross-references EMBL:Z28295
#experimental_source strain S288C
GENETICS
#map_position 11R
SUMMARY #length 352 #molecular-weight 39406 #checksum 754
Query Match 86.8%; Score 46; DB 11; Length 352;
Best Local Similarity 66.7%; Pred. No. 4.45e+01;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 223 Yrllvr 228
QY 1 Yrllir 6
RESULT 13
ENTRY
TITLE C29959 #type complete
DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - spinach
chloroplast
ORGANISM #formal_name chloroplast Spinacia oleracea #common_name
spinach
DATE 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change
12-Apr-1995
ACCESSIONS C29959
REFERENCE
#authors Hudson, G.S.; Holton, T.A.; Whitfield, P.R.; Bottomley, W.
#journal J. Mol. Biol. (1988) 200:639-654
#title Spinach chloroplast rpoBC genes encode three subunits of the
chloroplast RNA polymerase.
#cross-references MUID:88316931
#accession C29959
##molecule_type DNA
##residues 1-1070 ##label HUD
##cross-references GB:M55297
GENETICS

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```

#gene
#genome
CLASSIFICATION #superfamily DNA-directed RNA polymerase beta chain
KEYWORDS chloroplast; nucleotidyltransferase
SUMMARY #length 1070 #molecular-weight 120899 #checksum 2671

Query Match 86.8%; Score 46; DB 5; Length 1070;
Best Local Similarity 66.7%; Pred. NO. 4.45e+01;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1039 frllvr 1044
:||||
Qy 1 YRLLIR 6

RESULT 14
ENTRY #type complete
TITLE DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - common
ORGANISM tobacco chloroplast
#formal_name chloroplast Nicotiana tabacum #common_name
common tobacco
DATE 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change
03-Feb-1994
ACCESSIONS A24865; A00690
REFERENCE A24865
#authors Ohme, M.; Tanaka, M.; Chunwongse, J.; Shinozaki, K.; Sugliura,
M.
#journal FEBS Lett. (1986) 200:87-90
#title A tobacco chloroplast DNA sequence possibly coding for a
polypeptide similar to E. coli RNA polymerase beta-subunit.
#cross-references MUID:86192857
#accession A24865
#molecule_type DNA
#residues 1-1070 #label OHM
#cross-references GB:M28017
REFERENCE A38013
#authors Shinozaki, K.; Ohme, M.; Tanaka, M.; Wakasugi, T.; Hayashida,
N.; Matsubayashi, T.; Zaita, N.; Chunwongse, J.; Obokata,
J.; Yamaguchi-Shinozaki, K.; Ohto, C.; Torazawa, K.; Meng,
B.Y.; Sugita, M.; Deno, H.; Kamogashira, T.; Yamada, K.;
Kusuda, J.; Takaiwa, F.; Kato, A.; Tondoh, N.; Shimada, H.;
Sugliura, M.
#journal EMBO J. (1986) 5:2043-2049
#title The complete nucleotide sequence of the tobacco chloroplast
genome: its gene organization and expression.
#contents annotation; gene organization, sites, features
GENETICS
#gene rpoB
#genome chloroplast
CLASSIFICATION #superfamily DNA-directed RNA polymerase beta chain
KEYWORDS chloroplast; nucleotidyltransferase; transcription
SUMMARY #length 1070 #molecular-weight 120546 #checksum 1605

Query Match 86.8%; Score 46; DB 1; Length 1070;
Best Local Similarity 66.7%; Pred. NO. 4.45e+01;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1039 frllvr 1044
:||||
Qy 1 YRLLIR 6

RESULT 15
ENTRY #type complete
TITLE DNA-directed RNA polymerase (EC 2.7.7.6) beta chain : white
mustard chloroplast
ORGANISM #formal_name chloroplast Sinapis alba #common_name white
mustard
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
03-May-1996
ACCESSIONS S48842
REFERENCE S48842
#authors Julicher, K.; Pfannschmidt, T.; Liere, K.; Link, G.

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#submission submitted to the EMBL Data Library, October 1994
#accession S48842
#molecule_type DNA
#residues 1-1078 #label JUL
#cross-references EMBL:X82417
GENETICS
#gene rpoB
#genome chloroplast
CLASSIFICATION #superfamily DNA-directed RNA polymerase beta chain
KEYWORDS chloroplast; nucleotidyltransferase; transcription
SUMMARY #length 1078 #molecular-weight 121669 #checksum 2477

Query Match 86.8%; Score 46; DB 5; Length 1078;
Best Local Similarity 66.7%; Pred. NO. 4.45e+01;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1047 frllvr 1052
:||||
Qy 1 YRLLIR 6

Search completed: Thu May 22 08:30:18 1997
Job time : 20 secs.

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RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA SIMS M.;  
RL SUBMITTED (JUN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.  
CC -!- FUNCTION: THIS PROTEIN BINDS 5S RNA (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.  
DR EMBL; Z49967; G886450; -;  
DR WORMPEP; F54C9.5; CE02255.  
KW RIBOSOMAL PROTEIN; RNA-BINDING.  
SQ SEQUENCE 293 AA; 33386 MW; 8FFEC7EE CRC32;

Query Match 85.7%; Score 42; DB 8; Length 293;  
Best Local Similarity 66.7%; Pred. No. 2.15e+01;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 49 yrlivlr 54  
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QY 1 YRLAIR 6

RESULT 15  
ID YHR4\_PBSY STANDARD; PRT; 375 AA.  
AC P20400;  
DT 01-FEB-1991 (REL. 17, CREATED)  
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE HYPOTHETICAL 40 KD PROTEIN IN HRP LOCUS (ORF1).  
OS PSEUDOMONAS SYRINGAE (PV. SYRINGAE).  
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;  
OC PSEUDOMONADACEAE.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NR32;  
RX MEDLINE: 89053865.  
RA MUKHOPADHYAY P., WILLIAMS J., MILLS D.;  
RL J. BACTERIOL. 170:5479-5488(1988).  
CC -!- FUNCTION: MAY BE INVOLVED IN REGULATION OF HRP OR OTHER HRP LOCI.  
CC -!- SIMILARITY: TO THE C-TERMINAL HALF OF E.COLI MDOG.  
DR EMBL; M23555; -; NOT\_ANNOTATED\_CDS.  
DR PIR; A31383; A31383.  
KW HYPOTHETICAL PROTEIN.  
SQ SEQUENCE 375 AA; 41515 MW; 5FB9D42C CRC32;

Query Match 85.7%; Score 42; DB 11; Length 375;  
Best Local Similarity 66.7%; Pred. No. 2.15e+01;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 219 yrltlr 224  
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QY 1 YRLAIR 6

Search completed: Thu May 22 08:31:19 1997  
Job time : 11 secs.

Query Match 85.7%; Score 42; DB 1; Length 148;  
 Best Local Similarity 66.7%; Pred. No. 2.15e+01;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 132 yklavr 137  
 |::|  
 Qy 1 YRLAIR 6

RESULT 11  
 ID COAT\_CTV36 STANDARD; PRT; 223 AA.  
 AC Q00686;  
 DT 01-APR-1993 (REL. 25, CREATED)  
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
 DE COAT PROTEIN.  
 OS CITRUS TRISTEZA VIRUS (ISOLATE T36) (CTV).  
 OC VIRIDAE; SS-RNA NONENVELOPED VIRUSES; CAPILLOVIRIDAE.  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-38.  
 RX MEDLINE: 91237334.  
 RA SEKIYA M.E., LAWRENCE S.D., MCCAFFERY M., CLINE K.;  
 RL J. GEN. VIROL. 72:1013-1020(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 94160579.  
 RA PAPPU H.R., KARASEV A.V., ANDERSON E.J., PAPPU S.S., HILF M.E.,  
 RA FEBRES V., ECKLOFF R.M.G., MCCAFFERY M., BOYKO V., GOWDA S.,  
 RA DOLJA V.V., KOONIN E.V.;  
 RL VIROLOGY 199:35-46(1994).  
 CC -!- PTM: CONSISTS OF AT LEAST TWO SIZE VARIANTS, CP1 AND CP2, WHICH  
 CC RESULT OF POST-TRANSLATIONAL PROTEOLYSIS AT SITES APPROXIMATIVELY  
 CC 12 TO 15 AND 26 AA FROM THE N-TERMINUS RESPECTIVELY.  
 CC EMBL: M76485; G323416; -.  
 DR EMBL: U16304; G806746; -.  
 KW COAT PROTEIN.  
 SQ SEQUENCE 223 AA; 24909 MW; F3AA6BB6 CRC32;

Query Match 85.7%; Score 42; DB 2; Length 223;  
 Best Local Similarity 66.7%; Pred. No. 2.15e+01;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 85 yrlavk 90  
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 Qy 1 YRLAIR 6

RESULT 12  
 ID FRDC\_WOLSU STANDARD; PRT; 256 AA.  
 AC P17413;  
 DT 01-AUG-1990 (REL. 15, CREATED)  
 DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)  
 DE FUMARATE REDUCTASE CYTOCHROME B SUBUNIT.  
 GN FRDC.  
 OS WOLINELLA SUCCINOGENES.  
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; ANAEROBIC RODS;  
 CC BACTEROIDACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE: 90355847.  
 RA KOERTNER C., LAUTERBACH F., TRIPIER D., UNDEN G., KROEGER A.;  
 RL MOL. MICROBIOL. 4:855-860(1990).  
 CC -!- FUNCTION: DI-HEME CYTOCHROME OF THE FUMARATE REDUCTASE COMPLEX.  
 CC -!- SUBUNIT: PART OF AN ENZYME COMPLEX CONTAINING THREE SUBUNITS;  
 CC A FLAVOPROTEIN, AN IRON-SULFUR PROTEIN AND A CYTOCHROME B.  
 CC -!- SIMILARITY: TO CYTOCHROME B-558 FROM B.SUBTILIS SUCCINATE  
 CC DEHYDROGENASE.  
 DR EMBL: X51509; G48512; -.  
 DR FIR: S10184; S10164.  
 KW TRICARBOXYLIC ACID CYCLE; TRANSMEMBRANE; ELECTRON TRANSPORT; HEME.  
 FT TRANSMEM 32 54  
 RN TRANSMEM 77 98  
 POTENTIAL.

FT TRANSMEM 123 149 POTENTIAL.  
 FT TRANSMEM 171 192 POTENTIAL.  
 FT TRANSMEM 214 232 POTENTIAL.  
 FT BINDING 44 44 HEME (POTENTIAL).  
 FT BINDING 93 93 HEME (POTENTIAL).  
 FT BINDING 143 143 HEME (POTENTIAL).  
 FT BINDING 182 182 HEME (POTENTIAL).  
 SQ SEQUENCE 256 AA; 29723 MW; C3AB8928 CRC32;

Query Match 85.7%; Score 42; DB 4; Length 256;  
 Best Local Similarity 66.7%; Pred. No. 2.15e+01;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 188 yrlavk 193  
 |::|  
 Qy 1 YRLAIR 6

RESULT 13  
 ID YIAT\_HAEIN STANDARD; PRT; 268 AA.  
 AC P44996;  
 DT 01-NOV-1995 (REL. 32, CREATED)  
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE HYPOTHETICAL TRANSCRIPTIONAL REGULATOR HI1032.  
 GN HI1032.  
 OS HAEMOPHILUS INFLUENZAE.  
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;  
 CC PASTEURELLACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-RD / KW20;  
 RX MEDLINE: 95350630.  
 RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,  
 RA KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,  
 RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,  
 RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,  
 RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,  
 RA UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,  
 RA FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,  
 RA GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,  
 RA VENTER J.C.;  
 RL SCIENCE 269:496-512(1995).  
 CC -!- SIMILARITY: STRONG, TO E.COLI YIAT.  
 CC -!- SIMILARITY: BELONGS TO THE ICLR FAMILY OF TRANSCRIPTIONAL  
 CC REGULATORS.

Query Match 85.7%; Score 42; DB 11; Length 268;  
 Best Local Similarity 66.7%; Pred. No. 2.15e+01;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 73 yrltik 78  
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 Qy 1 YRLAIR 6

RESULT 14  
 ID RL5\_CAEEL STANDARD; PRT; 293 AA.  
 AC P49405;  
 DT 01-FEB-1996 (REL. 33, CREATED)  
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
 DE PROBABLE 60S RIBOSOMAL PROTEIN L5.  
 GN F34C9.5.  
 OS CAENORHABDITIS ELEGANS.  
 OC EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.  
 RN [1]



EMBL:	A03204;	72333;	
DR	PIR;	A24962;	EVASAL1.
DR	PIR;	A24042;	A24042.
DR	PROSITE;	PS00104;	EPSP_SYNTHASE_1.
DR	PROSITE;	PS00885;	EPSP_SYNTHASE_2.
DR	PROSITE;	PS01028;	DEHYDROQUINASE_1.
DR	PROSITE;	PS01128;	SHIKIMATE_KINASE.
DR	KW	AROMATIC AMINO ACID BIOSYNTHESIS;	MULTIFUNCTIONAL ENZYME;
DR	KW	OXIDOREDUCTASE; LYASE;	TRANSFERASE; KINASE; NADP: ATP-BINDING.
DR	FT	DOMAIN	1 384
DR	FT	DOMAIN	397 843
DR	FT	DOMAIN	863 1056
DR	FT	DOMAIN	1057 1277
DR	FT	DOMAIN	1290 1603
DR	FT	DOMAIN	3-DEHYDROQUINASE.
DR	FT	DOMAIN	SHIKIMATE DEHYDROGENASE.
DR	FT	DOMAIN	EPSP SYNTHASE.
DR	FT	DOMAIN	SHIKIMATE KINASE.
DR	FT	DOMAIN	3-DEHYDROQUINASE.
DR	FT	DOMAIN	SHIKIMATE DEHYDROGENASE.

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RESULT 4  
 ID TCPAARATH STANDARD; PRT; 545 AA.  
 AC P28769;  
 DT 01-DEC-1992 (REL. 24, CREATED)  
 DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA).  
 GN CCT1.  
 OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).  
 OC EUKARYOTA: PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;  
 OC CAPPARALE; CRUCIFERAE.  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE; 93138412.  
 RX MORI M., MURATA K., KUBOTA H., YAMAMOTO A., MATSUSHIRO A.,  
 RA MORITA T.;  
 RL GENE 122:381-382(1992).  
 CC -1- FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON  
 CC ATP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN THE FOLDING OF  
 CC ACTIN AND TUBULIN.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -1- SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 KD THAT  
 CC FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER.  
 CC -1- SIMILARITY: TO OTHER MEMBERS OF TCP-1 CHAPERONIN FAMILY.  
 DR EMBL; D11351; G217871; -.  
 DR PIR; JN0448; JN0448.  
 DR PROSITE; PS00750; TCPI\_1.  
 DR PROSITE; PS00751; TCPI\_2.  
 DR PROSITE; PS00995; TCPI\_3.  
 KW CHAPERONE; ATP-BINDING; MULTIGENE FAMILY.  
 SQ SEQUENCE 545 AA; 59229 MW; 8E52A94B CRC32;  
  
 Query Match 89.8%; Score 44; DB 9; Length 545;  
 Best Local Similarity 83.3%; Pred. No. 7.58e+00;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
 Db 124 yrlamr 129  
 QY 1 YRLAIR 6  
  
 RESULT 5  
 ID RL5\_SCHPO STANDARD; PRT; 293 AA.  
 AC P52822;  
 DT 01-OCT-1996 (REL. 34, CREATED)  
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE 60S RIBOSOMAL PROTEIN L5.  
 GN RPL5.  
 OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE; 96212235.  
 RX MICHAEL W.M., DREYFUSS G.;  
 RL J. BIOL. CHEM. 271:11571-11574(1996).  
 CC -1- FUNCTION: THIS PROTEIN BINDS 5S RNA.  
 CC -1- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.  
 DR EMBL; U48270; G1206017; -.  
 KW RIBOSOMAL PROTEIN.  
 SQ SEQUENCE 293 AA; 33255 MW; 4D72400A CRC32;  
  
 Query Match 87.8%; Score 43; DB 8; Length 293;  
 Best Local Similarity 66.7%; Pred. No. 1.28e+01;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
 Db 48 yrlvvr 53  
 QY 1 YRLAIR 6  
  
 RESULT 6

ID RLL\_YEAST STANDARD; PRT; 297 AA.  
 AC P26321;  
 DT 01-MAY-1992 (REL. 22, CREATED)  
 DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE 60S RIBOSOMAL PROTEIN L1 (L5) (YL3) (RIBOSOMAL 5 S RNA-BINDING  
 DE PROTEIN).  
 GN RPL1 OR YPL131W OR LPL14W.  
 OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-S288C;  
 RX MEDLINE; 91177855.  
 RA TANG B., NAZAR R.N.;  
 RL J. BIOL. CHEM. 266:6120-6123(1991).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE; 92388126.  
 RA TANG B., NAZAR R.N.;  
 RL J. BIOL. CHEM. 267:17738-17742(1992).  
 [3]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE; 90360986.  
 RA TZAGOLOFF A., CAPITANTO N., NOBREGA M.P., GATTI D.;  
 RL EMBO J. 9:2759-2764(1990).  
 [4]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE; 93233645.  
 RA DESHMUKH M.P., TSAY Y.F., PAULOVICH A.G., WOOLFORD J.L.;  
 RL MOL. CELL. BIOL. 13:2835-2845(1993).  
 [5]  
 RN SEQUENCE FROM N.A.  
 RA HALL J., DEPAULO T., AHMED A., BUSSEY H., FORTIN N., FRIESEN J.D.,  
 RA STORMS R.K., VO D.H., WANG Y., WINNETT E.;  
 RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.  
 CC -1- FUNCTION: THIS PROTEIN BINDS 5S RNA.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -1- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.  
 DR EMBL; M65036; G173232; -.  
 DR EMBL; M94864; G173235; -.  
 DR EMBL; L01796; G172424; -.  
 DR EMBL; U43703; G1244783; -.  
 DR PIR; S14172; S14172.  
 DR PIR; S48089; S48089.  
 DR LISTA; SC01009; RPL1.  
 DR SGD; L0001699; RPL1.  
 KW RIBOSOMAL PROTEIN; RNA-BINDING.  
 FT CONFLICT 112 112 R -> K (IN REF. 4 AND 5).  
 SQ SEQUENCE 297 AA; 33743 MW; 2D9F1304 CRC32;  
  
 Query Match 87.8%; Score 43; DB 8; Length 297;  
 Best Local Similarity 66.7%; Pred. No. 1.28e+01;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
 Db 49 yrlvvr 54  
 QY 1 YRLAIR 6  
  
 RESULT 7  
 ID PABP\_LACLA STANDARD; PRT; 470 AA.  
 AC P27629;  
 DT 01-AUG-1992 (REL. 23, CREATED)  
 DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4.1.3.-) (ADC SYNTHASE).  
 GN PABP.  
 OS LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).  
 OC PROKARYOTA; FIRMICUTES; COCCI; STREPTOCOCCAEAE.  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-NCDO 496;



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WIREH

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:31:08 1997; MasPar time 1.96 Seconds  
Tabular output not generated. 64.775 Million cell updates/sec

Title: >US-08-653-294-7  
Description: (1-6) from US08653294.pep  
Perfect Score: 49  
Sequence: 1 YRLAIR 6

Scoring table: PAM 150  
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot34  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 22.440; Variance 22.471; scale 0.999

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	46	93.9	1333	8	RPOA_SCHPO RETROTRANSPPOSABLE ELE	2.57e+00
2	45	91.8	1132	10	VHSJ_LAMBD HOST SPECIFICITY PROT	4.44e+00
3	45	91.8	2616	6	NDL_DROME SERINE PROTEASE NUDEL	4.44e+00
4	44	89.8	545	9	TCPLA_ARATH T-COMPLEX PROTEIN 1.	7.58e+00
5	43	87.8	293	8	RL5_SCHPO 60S RIBOSOMAL PROTEIN	1.28e+01
6	43	87.8	297	8	RL1_YEAST 60S RIBOSOMAL PROTEIN	1.28e+01
7	43	87.8	470	7	PABB_LACLA PARA-AMINOBENZONATE SY	1.28e+01
8	43	87.8	1603	1	ARO1_EMENT PENTAFUNCTIONAL AROM	1.28e+01
9	42	85.7	83	10	V187_BPT3 GENE 18.7 PROTEIN.	2.15e+01
10	42	85.7	148	1	3DHQ_BACSU PUTATIVE CATABOLIC 3-	2.15e+01
11	42	85.7	223	2	COAT_CTV36 COAT PROTEIN.	2.15e+01
12	42	85.7	256	4	FRC_CWLSU FUMARATE REDUCTASE CY	2.15e+01
13	42	85.7	268	11	YIAJ_HAEIN HYPOTHETICAL TRANSCRI	2.15e+01
14	42	85.7	293	8	RL5_CAPEL PROBABLE 60S RIBOSOMA	2.15e+01
15	42	85.7	373	11	YHR4_PSESY HYPOTHETICAL 40 KD PR	2.15e+01
16	42	85.7	397	3	DP3B_MYCSM DNA POLYMERASE III, B	2.15e+01
17	42	85.7	399	3	DP3B_MYCLE DNA POLYMERASE III, B	2.15e+01
18	42	85.7	621	3	DCBE_RHIME C4-DICARBOXYLATE TRAN	2.15e+01
19	42	85.7	937	1	ADAC_RAT ALPHA-ADAPTIN (C) (CL	2.15e+01
20	42	85.7	938	1	ADAC_MOUSE ALPHA-ADAPTIN (C) (CL	2.15e+01
21	42	85.7	958	5	HIG_DROME LOCOMOTION-RELATED PR	2.15e+01
22	42	85.7	977	1	ADRA_MOUSE ALPHA-ADAPTIN (A) (CL	2.15e+01

23	42	85.7	1538	9	SIN3_YEAST PAIRED AMPHIPATHIC HE	2.15e+01
24	42	85.7	1692	3	CYAA_SCHPO ADENYLATE CYCLASE (EC	2.15e+01
25	42	85.7	2035	5	HMP2_YEREN HIGH-MOLECULAR-WEIGHT	2.15e+01
26	41	83.7	349	6	NTRB_SALTY NITROGEN REGULATION P	3.56e+01
27	41	83.7	349	6	NTRB_SCOLI NITROGEN REGULATION P	3.56e+01
28	41	83.7	353	8	PSBA_MARPO PHOTOSYSTEM Q(B) PROT	3.56e+01
29	41	83.7	360	8	PSBA_SYNY4 PHOTOSYSTEM Q(B) PROT	3.56e+01
30	41	83.7	360	8	PSBA_ANTSP PHOTOSYSTEM Q(B) PROT	3.56e+01
31	41	83.7	360	8	PSBA_PEDI PHOTOSYSTEM Q(B) PROT	3.56e+01
32	41	83.7	360	8	PSBA_PROMA PHOTOSYSTEM Q(B) PROT	3.56e+01
33	41	83.7	360	8	PSB2_SYNEN PHOTOSYSTEM Q(B) PROT	3.56e+01
34	41	83.7	360	8	PSB1_SYNV3 PHOTOSYSTEM Q(B) PROT	3.56e+01
35	41	83.7	360	8	PSB1_SYNVU PHOTOSYSTEM Q(B) PROT	3.56e+01
36	41	83.7	360	8	PSB1_SYN7 PHOTOSYSTEM Q(B) PROT	3.56e+01
37	41	83.7	360	8	PSB1_ANASP PHOTOSYSTEM Q(B) PROT	3.56e+01
38	41	83.7	410	6	MDP1_RABIT MICROSOMAL DIBEPIDAS	3.56e+01
39	41	83.7	446	1	AP50_SCHPO PUTATIVE CLATHRIN COA	3.56e+01
40	41	83.7	620	4	HEMA_MEASY HEMAGGLUTININ-NEURAMI	3.56e+01
41	41	83.7	626	3	DPO2_SULSO DNA POLYMERASE II (EC	3.56e+01
42	41	83.7	732	1	ACPH_HUMAN ACYLAMINO-ACID-RELEASE	3.56e+01
43	41	83.7	732	1	ACPH_RAT ACYLAMINO-ACID-RELEASE	3.56e+01
44	41	83.7	782	3	DPO2_SCOLI DNA POLYMERASE II (EC	3.56e+01
45	41	83.7	1997	8	PTPB_HUMAN PROTEIN-TYROSINE PHOS	3.56e+01

ALIGNMENTS

RESULT 1  
ID RPOA\_SCHPO STANDARD; PRT; 1333 AA.  
AC Q05654;  
DT 01-OCT-1996 (REL. 34, CREATED)  
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
DE RETROTRANSPPOSABLE ELEMENT TF2 155 KD PROTEIN.  
GN SPAC26A3.13C.  
OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).  
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972;  
RX MEDLINE; 93380663.  
RA WEAVER D.C., SHPAKOVSKI G.V., CAPUTO E., LEVIN H.L., BOEKE J.D.;  
RL GENE 131:135-139(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972;  
RA MCLEAN J., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;  
RL SUBMITTED (FEB-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
CC -!- SIMILARITY: REGIONALLY, TO PROTEASE, REVERSE TRANSCRIPTASE,  
CC RNASE H AND INTEGRASE FROM OTHER RETROTRANSPPOSONS AND  
CC RETROVIRUSES.  
DR EMBL; L10324; G173439; -.  
DR EMBL; Z69240; E220685; -.  
KW TRANSPOSABLE ELEMENT.  
FT SIMILAR 1 400 TO CAPSID PROTEIN FROM RETROVIRUSES.  
FT CONFLICT 206 206 L-> P (IN REF. 1).  
SQ SEQUENCE 1333 AA; 154932 MW; 78D5D7DA CRC32;

Query Match 93.9%; Score 46; DB 8; Length 1333;  
Best Local Similarity 83.3%; Pred. No. 2.57e+00;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 411 yrlpir 416  
|||:  
|||:  
Qy 1 YRLAIR 6

RESULT 2  
ID VHSJ\_LAMBD STANDARD; PRT; 1132 AA.  
AC P03749;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:30:35 1997; MasPar time 1.92 Seconds  
Tabular output not generated. 34.026 Million cell updates/sec

Title: >US-08-653-294-6  
Description: (1-6) from US08653294.pep  
Perfect Score: 53  
Sequence: 1 YRLIIR 6

Scoring table: PAM 150  
Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq26  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19

Statistics: Mean 16.490; Variance 45.535; scale 0.362

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	48	90.6	389	3	R15428		3-acetylation enzyme.	4.52e+01
2	47	88.7	724	18	R93081		Bacillus thuringiensis	5.89e+01
3	47	88.7	764	19	W01897		Nonsense-mediated MRN	5.89e+01
4	47	88.7	1089	19	W01896		Nonsense-mediated MRN	5.89e+01
5	46	86.8	43	11	R5902		Drosophila-12 cadher	7.66e+01
6	46	86.8	43	17	R87142		Protocadherin clone D	7.66e+01
7	45	84.9	434	18	R95698		Erythrobacter longus	9.94e+01
8	44	83.0	4472	19	R97246		Virulence gene cluste	1.29e+02
9	43	81.1	10	11	R61548		Peptide fragment (1.0	1.66e+02
10	43	81.1	158	12	R63866		HPV18 E6/E7 proteins.	1.66e+02
11	43	81.1	158	14	R79656		HPV-18 E6 protein.	1.66e+02
12	43	81.1	271	5	R27728		HPV 18 E6 protein fra	1.66e+02
13	43	81.1	451	5	R27642		Human calcium channel	1.66e+02
14	43	81.1	652	12	R63808		Human amphotropic ret	1.66e+02
15	43	81.1	1592	6	R32925		Glucosyltransferase	1.66e+02
16	43	81.1	4987	3	R10834		Rianodin receptor.	1.66e+02
17	43	81.1	5035	5	R25450		MH mutant porcine rya	1.66e+02
18	43	81.1	5072	2	R1510		Ryanodine receptor de	1.66e+02
19	42	79.2	12	18	R95429		HLA-B2702 84-79-84 pa	2.15e+02
20	42	79.2	20	18	R95428		HLA-B2702 84-75-84 pa	2.15e+02

21	42	79.2	20	18	R95430	HLA-B2702 84-75T/75-8	2.15e+02
22	42	79.2	20	16	R92907	HLA-B2702 CTL modul	2.15e+02
23	42	79.2	20	16	R92909	HLA-B2702 CTL modul	2.15e+02
24	42	78.2	20	16	R92911	HLA-B2702 CTL modul	2.15e+02
25	42	79.2	78	7	R39225	Hydrophobic protein d	2.15e+02
26	42	79.2	205	7	R39353	EpiQ protein.	2.15e+02
27	42	79.2	402	10	R54204	snac gene product inv	2.15e+02
28	42	79.2	643	18	R97735	Bacillus thuringiens	2.15e+02
29	42	79.2	643	1	P91462	67-kD protein toxin.	2.15e+02
30	42	78.2	772	15	R79949	Enzyme W-11.	2.15e+02
31	42	79.2	775	15	R79950	Enzyme Q36.	2.15e+02
32	42	79.2	3079	11	R59926	GAP protein Ira2.	2.15e+02
33	41	77.4	64	15	R78151	zebrafish sonic hedge	2.76e+02
34	41	77.4	108	18	R93159	Murine monoclonal ant	2.76e+02
35	41	77.4	391	12	R63233	ATP-sensitive K chann	2.76e+02
36	41	77.4	457	14	R78184	E.coli cell division	2.76e+02
37	41	77.4	501	13	R62115	Nocardia coralina al	2.76e+02
38	41	77.4	501	17	R81471	Nocardia coralina al	2.76e+02
39	41	77.4	1025	8	R38863	GC-B.	2.76e+02
40	41	77.4	1047	3	R10867	NPRB(Pro655, Glu656,	2.76e+02
41	41	77.4	1047	3	R10399	Human Natriuretic Pep	2.76e+02
42	41	77.4	3077	1	P93283	Sequence of clone HIV	2.76e+02
43	41	77.4	3211	1	P81769	Sequence encoded by t	2.76e+02
44	40	75.5	169	19	W05507	HCW Toledo strain UL	3.54e+02
45	40	75.5	1138	8	R39820	tie receptor kinase.	3.54e+02

ALIGNMENTS

RESULT 1  
ID R15428 standard; Protein; 389 AA.  
AC R15428;  
DE 25-FEB-1992 (first entry)  
DE 3-acetylation enzyme.  
KW Macrolide antibiotics; acylation; Streptomyces; tylosin;  
KW spiramycin; leucomycin; nidamycin; acya.  
OS Streptomyces thermotolerans ATCC 11416.  
PN EP-459525-A.  
PD 04-DEC-1991.  
PF 03-JUN-1991; 109033.  
PR 01-JUN-1990; JP-141625.  
PR 22-FEB-1991; JP-048753.  
PA (SAOC) MERCIAN CORP.  
PI Arisawa A, Kawamura N, Kojima I, Tone H, Okamoto R;  
PI Okamura K.  
DR WPI; 91-355809/49.  
DR N-PSDB; Q14978.  
PT Gene encoding 3-acetylation enzyme for macrolide antibiotics - used  
PT to transform Streptomyces sp. to have acylation activity, for use  
PT in medicine.  
PS Disclosure; Fig 7; 45pp; English.  
CC The sequence was deduced from DNA sequence obtd. from plasmid p53A,  
CC a subclone of a DNA library prepd. from genomic DNA of S.thermotol-  
CC erans. The 3-acetylation enzyme is involved in the synthesis of  
CC macrolide antibiotics. Microorganisms, ep. Streptomyces, trans-  
CC formed with the gene can be used for the commercial prodn. of  
CC macrolide antibiotics, e.g. 3-acetylated tylosin.  
SQ Sequence 389 AA;  
  
Query Match 90.6%; Score 48; DB 3; Length 389;  
Best Local Similarity 83.3%; Pred. No. 4.52e+01;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Db 158 yrllir 163  
| | | | |  
Oy 1 YRLIIR 6  
  
RESULT 2  
ID R93081 standard; Protein; 724 AA.  
AC R93081;  
DR 04-OCT-1996 (first entry)  
DE Bacillus thuringiensis insecticidal protein JEG80.

KW Insecticidal crystal toxin; jeg80; anti-diptera; mosquito; larvae;  
 KW Aedes aegypti; Anopheles stephensi; Culex pipiens; Btjeg 367.  
 OS Bacillus thuringiensis ser. jegathesan 367.  
 PN WO9606171-A2.  
 PD 29-FEB-1996.  
 PF 24-AUG-1995; F01116.  
 PR 25-AUG-1994; FR-010299.  
 PA (INSP ) INST PASTEUR.  
 PI Delecluse A, Thierry I;  
 DR WPI: 96-151374/15.  
 DR N-PSDB; T17044.  
 PR New B.thuringiensis ser. jegathesan insecticidal proteins - and  
 PT related DNA, with high activity against dipteran larvae, e.g.  
 PT A.aegypti, A.stephensi or C.pipiens  
 PS Claim 17; Fig 5; 55pp; French.  
 CC The present sequence is that of the JEG80 protein which was isolated  
 CC from Bacillus thuringiensis ser. Jegathesan 367 (Btjeg367); it is  
 CC a crystal toxin of mol. wt. 80 kD which is active against dipteran  
 CC insects, esp. mosquitoes. The full-length, recombinant JEG80 toxin,  
 CC had mean LC50 values (in ng/ml) after 48 hours of 18.8, 42.7 and  
 CC 10.1 against larvae of Aedes aegypti, Anopheles stephensi and Culex  
 CC pipiens, respectively. Wild-type Btjeg367 crystals gave values of  
 CC 47.4, 54.5 and 9.6. The JEG80 protein is far more toxic (6-40 times  
 CC more toxic against the mosquito species tested) than the Bt CryIVD  
 CC toxin, despite their close sequence similarity.  
 SQ Sequence 724 AA;

Query Match 88.7%; Score 47; DB 18; Length 724;  
 Best Local Similarity 83.3%; Pred. No. 5.89e+01;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 548 yrlilr 553  
 |||:|  
 QY 1 YRLILR 6

RESULT 3  
 ID W01897 standard; Protein; 764 AA.  
 AC W01897.  
 DT 24-NOV-1996 (first entry)  
 DE Nonsense-mediated mRNA decay 2 C-terminal.  
 KW Nonsense-mediated mRNA decay; NMD2; Upflp; inhibition.  
 OS Saccharomyces cerevisiae.  
 PN WO9622301-A1.  
 PD 25-JUL-1996.  
 PF 27-DEC-1995; U16930.  
 PR 20-JAN-1995; US-375300.  
 PA (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.  
 PI He F, Jacobson AS;  
 DR WPI: 96-354469/35.  
 DR N-PSDB; T31994.  
 PT Isolated nonsense-mediated mRNA decay gene and protein - used to  
 PT develop methods for inhibiting the decay pathway for producing  
 PT heterologous or endogenous proteins  
 PS Claim 10; Page 54-56; 73pp; English.  
 CC The NMD2 gene (T31993) is named after its role in the Nonsense-  
 CC Mediated mRNA Decay pathway. The protein, Nmd2p, binds to Upflp.  
 CC A C-terminal fragment of the protein (T31994) also binds Upflp and,  
 CC when overexpressed in the host cell, the fragment inhibits the  
 CC function of Upflp, thereby inhibiting the nonsense-mediated  
 CC mRNA decay pathway.  
 SQ Sequence 764 AA;

Query Match 88.7%; Score 47; DB 19; Length 764;  
 Best Local Similarity 83.3%; Pred. No. 5.89e+01;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 255 yrlilr 260  
 ||:|  
 QY 1 YRLILR 6

RESULT 4

ID W01896 standard; Protein; 1089 AA.  
 AC W01896.  
 DT 24-NOV-1996 (first entry)  
 DE Nonsense-mediated mRNA decay 2 protein.  
 KW Nonsense-mediated mRNA decay; NMD2; Upflp; inhibition.  
 OS Saccharomyces cerevisiae.  
 PN WO9622301-A1.  
 PD 25-JUL-1996.  
 PF 27-DEC-1995; U16930.  
 PR 20-JAN-1995; US-375300.  
 PA (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.  
 PI He F, Jacobson AS;  
 DR WPI: 96-354469/35.  
 DR N-PSDB; T31993.  
 PT Isolated nonsense-mediated mRNA decay gene and protein - used to  
 PT develop methods for inhibiting the decay pathway for producing  
 PT heterologous or endogenous proteins  
 PS Claim 8; Page 49-52; 73pp; English.  
 CC The NMD2 gene (T31993) is named after its role in the Nonsense-  
 CC Mediated mRNA Decay pathway. The protein, Nmd2p, binds to Upflp.  
 CC A C-terminal fragment of the protein (T31994) also binds Upflp and,  
 CC when overexpressed in the host cell, the fragment inhibits the  
 CC function of Upflp, thereby inhibiting the nonsense-mediated  
 CC mRNA decay pathway.  
 SQ Sequence 1089 AA;

Query Match 88.7%; Score 47; DB 19; Length 1089;  
 Best Local Similarity 83.3%; Pred. No. 5.89e+01;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 580 yrlilr 585  
 ||:|  
 QY 1 YRLILR 6

RESULT 5  
 ID R58902 standard; Protein; 43 AA.  
 AC R58902.  
 DT 17-APR-1995 (first entry)  
 DE Drosophila-12 cadherin-related molecule.  
 KW Cadherin; cell adhesion molecule.  
 OS Drosophila.  
 PN WO9414960-A.  
 PD 07-JUL-1994.  
 PF 23-DEC-1993; U12588.  
 PR 29-DEC-1992; US-998003.  
 PA (DOHE-) DOHENY EYE INST.  
 PI Suzuki S;  
 DR WPI: 94-293849/36.  
 DR N-PSDB; O68993.  
 PT Polynucleotide sequences encoding new proto:cadherins - useful  
 PT for modulating natural binding and regulating activities.  
 PS Example; Page 63; 114pp; English.  
 CC Two regions of conserved AA sequence, one from the middle of the  
 CC third cadherin extracellular subdomain (EC-3) and the other from the  
 CC C-terminus of the fourth extracellular subdomain (EC-4) were  
 CC identified. The corresp. degenerate oligos (Q68949, Q68950) were  
 CC designed for use as PCR primers. PCR was carried out on a rat brain  
 CC cDNA prep. Two major bands of about 450 bps and 130 bps were found.  
 CC The 450 bp band corresponded to the expected length between the two  
 CC primer sites, but the 130 bp band could not be predicted from any  
 CC of the previously identified cadherin sequences. The 450 bp and 130  
 CC bp bands were extracted and sequenced. Nineteen novel partial cDNA  
 CC clones were isolated. The DNA and deduced AA sequences of the  
 CC clones (including sequences corresp. to the PCR primers) are given  
 CC in Q68951-Q68969 and R58860-R58878. Various cDNA fragments  
 CC structurally similar to the rat cDNAs were isolated from human,  
 CC mouse and Xenopus brain cDNA preps. and from Drosophila and  
 CC C. elegans whole body cDNA preps. by PCR using the above primers.  
 CC The DNA and deduced AA sequences of the resulting PCR fragments  
 CC (including sequences corresp. to the PCR primers) are given in  
 CC Q68971, Q68972-Q68994 and R58882-R58905 and R49143. Comparison  
 CC of the deduced AA sequences indicates a similarity, in particular,

CC there are three sets of clones that appear to be cross-species  
 CC homologues: RAT-218, MOUSE-322 and HUMAN-43; RAT-314, MOUSE-321 and  
 CC HUMAN-11; and MOUSE-326 and HUMAN-42.  
 SQ Sequence 43 AA;

Query Match 86.8%; Score 46; DB 11; Length 43;  
 Best Local Similarity 83.3%; Pred. No. 7.66e+01;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 11 yrlvir 16  
 |||||  
 QY 1 YRLLR 6

## RESULT 6

ID R87142 standard; Peptide; 43 AA.  
 AC R87142.  
 DT 29-AUG-1996 (first entry)  
 DE Protocadherin clone DROSOPHILA-12.  
 KW Protocadherin; pc3; pc4; pc5; human; rat; cadherin; cell adhesion; mouse;  
 QS catenin; therapy; clone; frog; fruit fly.  
 OS Drosophila melanogaster.  
 FH Key Location/Qualifiers  
 FT Misc\_difference 38  
 FT /note= "encoded by CGA"  
 FT Misc\_difference 39  
 FT /note= "encoded by ATG"  
 FT Misc\_difference 40  
 FT /note= "encoded by ACA"  
 FT Misc\_difference 41  
 FT /note= "encoded by ATG"  
 FT Misc\_difference 42  
 FT /note= "encoded by CGC"  
 FT Misc\_difference 43  
 FT /note= "encoded by CGC"  
 PN WO9600289-A1.  
 PD 04-JAN-1996.  
 PF 26-JUN-1995; U08071.  
 PR 27-JUN-1994; US-268161.  
 PA (DOHE-) DOHENY EYE INST.  
 PI Suzuki S;  
 DR WPI; 96-068873/07.  
 DR N-PSDB; T03617.  
 DT Polynucleotide(s) encoding human protocadherins pc3 and pc4 and rat  
 PT pc5 - involved in cell-cell adhesion and regulation activities  
 PS Example 2; Page 67-68; 146pp; English.  
 CC R87142-R87144 represent partial fragments of the drosophila protocadherin  
 CC sequence. The cDNAs encoding these sequences were isolated after  
 CC screening a drosophila whole body cDNA preparation with the primers shown  
 CC in T03575 and T03576. The primers were constructed from portions of the  
 CC amino acid sequences of the third and fourth extracellular domains of  
 CC published cadherin sequences. The cytoplasmic domain of cadherin  
 CC interacts with the cytoskeleton through catenins and other cytoskeleton  
 CC associated proteins. The cytoplasmic domain is not present in all  
 CC cadherins, but in those which possess it, it is essential for the  
 CC cadherins adhesive function. The cadherins which do not possess a  
 CC cytoplasmic domain appear to function via a different method from those  
 CC with a cytoplasmic domain. These protein sequences are involved in  
 CC cell-cell adhesion. These sequences may have regulatory functions in the  
 CC cell, as well as the cell-cell adhesive properties. Antibodies produced  
 CC against these sequences are useful for modulating the binding activity of  
 CC these protocadherins, and can be used therapeutically.  
 SQ Sequence 43 AA;

Query Match 86.8%; Score 46; DB 17; Length 43;  
 Best Local Similarity 83.3%; Pred. No. 7.66e+01;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 11 yrlvir 16  
 |||||  
 QY 1 YRLLR 6

## RESULT 7

ID R95698 standard; Protein; 434 AA.  
 AC R95698.  
 DT 20-SEP-1996 (first entry)  
 DE Erythrocyte longus lycopene cyclase protein.  
 KW Phytoene dehydrogenase; Erythrocyte longus; Erwinia hebicola; probe;  
 KW open reading frame; lycopene cyclase; Rhodobacter sphaeroides;  
 KW beta-carotene; food colourant; additive; anti-cancer.  
 OS Erythrocyte longus.  
 PN J0809241-A.  
 PD 09-APR-1996.  
 PF 30-SEP-1994; 236621.  
 PR 30-SEP-1994; JP-236621.  
 PA (ASAH ) ASAH KASEI KOGYO KK.  
 DR WPI; 96-233337/24.  
 DR N-PSDB; T31799.  
 DT Erythrocyte sp. phytoene dehydrogenase and lycopene cyclase genes  
 FT - for the prodn. of beta-carotene useful as a food colourant  
 PS Example 1; Page 6-7; 7pp; Japanese.  
 CC Erythrocyte longus ATCC 14126. The corresp. gene was isolated from an  
 CC E. longus genomic DNA library using a 1 kb fragment of the phytoene  
 CC dehydrogenase gene from Erwinia hebicola as a probe. The probe isolated  
 CC a nucleotide fragment which contained two open reading frames (ORF).  
 CC ORF2 (1578 bp) encodes the phytoene dehydrogenase (T31798) whereas ORF1  
 CC (1302 bp) encodes lycopene cyclase. The two ORFs were inserted into the  
 CC plasmid pRK415 to generate pRKCD. This plasmid was transformed into  
 CC Rhodobacter sphaeroides for prodn. of the proteins. The phytoene  
 CC dehydrogenase and lycopene cyclase can be used to produce beta-carotene  
 CC for use as a food colourant or as a food additive with anti-cancer  
 CC effects.  
 SQ Sequence 434 AA;

Query Match 84.9%; Score 45; DB 18; Length 434;  
 Best Local Similarity 83.3%; Pred. No. 9.94e+01;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 340 yrlvir 345  
 |||||  
 QY 1 YRLLR 6

## RESULT 8

ID R97246 standard; Protein; 4472 AA.  
 AC R97246.  
 DT 07-JAN-1997 (first entry)  
 DE Virulence gene cluster polypeptide product.  
 KW Mutant; adaptation; virulence factor; identification; screening;  
 KW vaccine; drugs; infection; treatment.  
 OS Salmonella typhimurium.  
 FH Key Location/Qualifiers  
 ET Region  
 FT /note= "All x's in this sequence correspond to  
 FT termination codons in the virulence gene  
 FT cluster sequence given in T09224."  
 PN W09617951-A2.  
 PD 13-JUN-1996.  
 PF 11-DEC-1995; G02875.  
 PR 09-DEC-1994; GB-024921.  
 PR 31-JAN-1995; GB-001881.  
 PR 05-MAY-1995; GB-009239.  
 PA (RPMs-) RPMs TECHNOLOGY LTD.  
 PI Holden DW;  
 DR WPI; 96-287194/29.  
 DT Identifying virulence genes in microorganisms - by introducing  
 PT mutants with insertion inactivated genes into environment and  
 PT retrieval and analysis of mutants  
 PS Claim 51; Figure 11; 131pp; English.  
 CC A method for identifying a microorganism having a reduced adaptation  
 CC to a particular environment comprising the steps of: (1) providing a  
 CC plurality of microorganisms each of which is independently mutated by  
 CC the insertional inactivation of a gene with a nucleic acid comprising  
 CC a unique marker sequence so that each mutant contains a different

CC marker sequence, or clones of the said microorganism; (2) providing  
 CC individually a stored sample of each mutant produced by step (1) and  
 CC providing individually stored nucleic acid comprising the unique  
 CC marker sequence from each individual mutant; (3) introducing a  
 CC plurality of mutants produced by step (1) into the said particular  
 CC environment and allowing those microorganisms which are able to do so  
 CC to grow in the said environment; (4) retrieving microorganisms from  
 CC the said environment or a selected part thereof and isolating the  
 CC nucleic acid from the retrieved microorganisms; (5) comparing any  
 CC marker sequences in the nucleic acid isolated in step (4) to the  
 CC unique marker sequence of each individual mutant stored as in step  
 CC (2); and (6) selecting an individual mutant which does not contain any  
 CC of the marker sequences as isolated in step (4). The products and  
 CC methods can be used for identifying virulence genes in microorganisms.  
 CC The mutant microorganisms can be used in vaccines or to screen for  
 CC drugs which reduce virulence or compounds useful for preventing,  
 CC ameliorating or treating infections in animals or plants.  
 SQ Sequence 4472 AA;

Query Match 83.0%; Score 44; DB 19; Length 4472;  
 Best Local Similarity 66.7%; Pred. No. 1.29e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 200 yllmr 205  
 QY 1 YRLLR 6

RESULT 9  
 ID R61548 standard; peptide; 10 AA.  
 AC R61548;  
 DT 11-MAY-1995 (first entry)  
 DE Peptide fragment (1.0914) of HPV binds HLA-A2.1.  
 KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;  
 KW HIV; plasma specific antigen; hepatitis B virus; Epstein Barr;  
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;  
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;  
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;  
 KW diagnostic; MHC class I molecule; major histocompatibility complex;  
 KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen.  
 OS Human papilloma virus strain 18.  
 PN WO9420127-A.  
 PD 15-SEP-1994.  
 PF 04-MAR-1994; U02353.  
 PR 05-MAR-1993; US-027146.  
 PR 04-JUN-1993; US-073205.  
 PR 29-NOV-1993; US-159184.  
 PA (CYTE-) CYTEL CORP.  
 PI Grey HM, Kast WM, Sette A, Sidney J;  
 DR WPI: 94-302678/37.  
 PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used  
 PT for treatment or prophylaxis of cancer, virus infection or  
 PT autoimmune diseases.  
 PS Example 5; Page 109; 138pp; English.  
 CC R59496-R61666 are immunogenic 10mer peptides that contain a HLA-A2.1  
 CC binding motif. These peptides bind HLA-A2.1 and have a binding  
 CC affinity of at least 1% as compared to a reference peptide (R71293).  
 CC R61548 has an IC50 of 0.0036 and the sequence occurs at position 24  
 CC in the HPV E6 protein. The peptides of the invention can induce  
 CC cytotoxic T lymphocytes which can react with target cells. They can  
 CC be used for the treatment or prophylaxis of cancer, eg. prostate  
 CC cancer or lymphoma, etc.  
 SQ Sequence 10 AA;

Query Match 81.1%; Score 43; DB 11; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 1.66e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 3 ylllr 8  
 QY 1 YRLLR 6

RESULT 10  
 ID R63866 standard; Protein; 158 AA.  
 AC R63866; 1995 (first entry)  
 DT 28-JUN-1995  
 DE HPV18 E6/E7 proteins.  
 KW HPV; HPV18; E6 protein; E7 protein; diagnosis; cervical dysplasia;  
 KW cervix cancer.  
 OS Human papillomavirus strain 18.  
 PN WO9426934-A.  
 PD 24-NOV-1994.  
 PF 06-MAY-1994; U05085.  
 PR 06-MAY-1993; US-058920.  
 PA (BAXT ) BAXTER DIAGNOSTICS INC.  
 PI Brown JT;  
 DR WPI: 95-006821/01.  
 DR P-PSDB; Q75471.  
 PT Human papilloma virus detection assay - by amplification using  
 PT self sustained sequence replication and hybridisation with a  
 PT detector probe  
 PS Disclosure; Page 27-28; 79pp; English.  
 CC The sequences of the E6 and E7 polypeptide-encoding regions of human  
 CC papillomavirus (HPV) 16 and 18 are given in Q75470-71 and the  
 CC encoded proteins in R63865-66, respectively. Probes and primers  
 CC based on these sequences were used for HPV infection diagnosis;  
 CC expression of E6 and E7 is diagnostic for cervical cancer or pre-  
 CC malignant states.  
 CC Sequence 158 AA;

Query Match 81.1%; Score 43; DB 12; Length 158;  
 Best Local Similarity 83.3%; Pred. No. 1.66e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 99 ylllr 104  
 QY 1 YRLLR 6

RESULT 11  
 ID R79656 standard; Protein; 158 AA.  
 AC R79656;  
 DT 06-DEC-1995 (first entry)  
 DE HPV-18 E6 protein.  
 KW Ubiquitin-conjugating enzyme; HPV-18 E6 protein; cell cycle;  
 KW cell proliferation; cancer; psoriasis; fibrosis.  
 OS Homo sapiens.  
 PN WO9518974-A.  
 PD 13-JUL-1995.  
 PF 04-JAN-1995; U00164.  
 PR 04-JAN-1994; US-176937.  
 PR 23-MAY-1994; US-247904.  
 PR 27-MAY-1994; US-250795.  
 PR 13-SEP-1994; US-305520.  
 PA (MITO-) MITOTIX INC.  
 PI Cottarel G, Draetta G, Eckstein JW, Gyuris J, Rolfe M;  
 DR WPI: 95-255137/33.  
 DR N-PSDB; Q97848.  
 PT Identifying inhibitors of ubiquitin mediated proteolysis of cell cycle  
 PT regulatory proteins - also new ubiquitin conjugating enzymes, their  
 PT related nucleic acid, vectors, antibodies etc., useful for regulating  
 PT e.g. cell proliferation  
 PS Disclosure; Page 100-101; 157pp; English.  
 CC HPV-18 E6 cDNA (given in Q97848) was amplified from a HeLa cell  
 CC cDNA library using the primers given in Q97846-47. The gene  
 CC was subcloned into a baculovirus vector for expression of  
 CC recombinant E6 in Sf9 insect cells for use as a component of an  
 CC in vitro ubiquitin conjugating system.  
 SQ Sequence 158 AA;

Query Match 81.1%; Score 43; DB 14; Length 158;  
 Best Local Similarity 83.3%; Pred. No. 1.66e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 99 ylllr 104



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QY      1 YRLIIR 6
      1 | | | |
RESULT  12
ID R27728 standard; Protein; 271 AA.
AC R27728;
DT 09-MAR-1993 (first entry)
DE HPV 18 E6 protein fragment.
KW Virus vector; vaccinia virus; papillomavirus; HPV; human;
KW amplification; immunotherapeutic.
OS Human papillomavirus 18.
FH Key Location/Qualifiers
FT Peptide 2..259
FT /note="HPV-18 E6 protein"
PN W09216636-A.
PD 01-OCT-1992.
PF 10-MAR-1992; G00424.
PR 14-MAR-1991; GB-005383.
PA (IMMU ) IMMUNOLOGY LTD.
PI Boursnell MEG, Inglis SC, Munro AJ;
DR WPI; 92-349219/42.
DR N-PSDB; Q29390.
PT Recombinant virus vectors encoding human papillomavirus proteins
PT - for treating and vaccinating against HPV infections and
PT conditions caused by them, such as cervical cancer
PS Disclosure; Fig 1b; 83pp; English.
CC The fragment of DNA contg. the HPV-18 E6/E7 coding region was
CC prep'd. by PCR from plasmid pBR322/HPV16 (Boshart et al., EMBO J. 3:
CC 1151) using oligonucleotides S01 and S02. The prod. of the
CC second reading frame is the HPV-18 E7 protein whereas the third
CC reading frame encodes HPV-18 E6. The E6 and E7 ORFs are fused
CC together to form a single continuous ORF via site directed mutagenesis
CC and the immortalising potential of E7 is removed by altering two key
CC codons of the HPV E7 sequence. The single ORF of HPV-18 E6/E7 may be
CC inserted into vaccinia virus DNA at neutral sites (pref. by inserting
CC two sets of the DNA in opposite orientations to overcome the problem
CC of intertypic recombination) to make a recombinant virus vector for
CC use immunotherapeutically to activate cells of the immune system
CC against HPV. See also R27723-43.
CC Sequence 271 AA;
      Query Match      81.1%; Score 43; DB 5; Length 271;
      Best Local Similarity 83.3%; Pred. No. 1.66e+02;
      Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 100 ymlir 105
      1 | | | |
QY      1 YRLIIR 6

RESULT  13
ID R27642 standard; Protein; 451 AA.
AC R27642;
DT 03-MAR-1993 (first entry)
DE Human calcium channel 27980/4.
KW Plasmid p1247-10.1.1.1; Ca-flux assay; SS.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc.difference 417
FT /note="encoded by GNN codon, N is unknown"
PN EP-507170-A.
PD 07-OCT-1992.
PF 23-MAR-1992; 104970.
PR 04-APR-1991; DE-110785.
PA (FARB ) BAYER AG.
PI Franz J, Rae P, Unterbeck A, Weingaertner B;
DR WPI; 92-333446/41.
DR P-PSDB; R27642.
PT Cloned human neuronal calcium channel sub-types - useful in
PT calcium flux assays to screen for neurone-specific calcium
PT channel ligands
PS Claim 2; Page 24-27; 101pp; German.

CC Human neuroblastoma cell line, hippocampus, frontal and temporal
CC cortex and visual cortex cDNA banks were screened with a probe
CC containing carp skeletal muscle ca-channel cDNA. The cDNA clone
CC p1247-10.1.1.1 was sequenced and found to encode amino acids 1050 to
CC 1512 including the end of the third domain (IIS6) and the entire
CC domain IV and about 130 C-terminal flanking amino acids which
CC correspond to the last cytoplasmic part of the protein. The human
CC neuronal calcium channel proteins can be used for screening for Ca
CC channel ligands (agonists or antagonists). See also Q29259-Q29275.
CC Sequence 451 AA;
      Query Match      81.1%; Score 43; DB 5; Length 451;
      Best Local Similarity 86.7%; Pred. No. 1.66e+02;
      Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 380 ykllir 385
      1 | | | |
QY      1 YRLIIR 6

RESULT  14
ID R63808 standard; Protein; 652 AA.
AC R63808;
DT 28-JUN-1995 (first entry)
DE Human amphotropic retrovirus receptor GLVR2.
KW Amphotropic retrovirus receptor; gibbon leukemia virus receptor 2;
KW GLVR2; gene therapy.
OS Homo sapiens.
PN EP-622377-A.
PD 02-NOV-1994.
PF 28-MAR-1994; 104889.
PR 16-APR-1993; US-050584.
PA (AMCY ) AMERICAN CYANAMID CO.
PI Johann SV, Ohara BM, Van Zeijl M, O'hara BM;
DR WPI; 94-334580/42.
DR N-PSDB; Q74311.
PT Nucleic acid sequence encoding an amphotropic retrovirus receptor
PT - used to create viral vectors useful in gene therapy.
PS Claim 4; Fig 2; 24pp; English.
CC Q74311 encodes R63808 the amphotropic retrovirus receptor, gibbon
CC leukaemia virus receptor 2 (GLVR2). Nucleotide fragments of Q74311
CC can be used to create vectors, for use in human gene therapy and
CC for the transformation of host cells enabling them to express the
CC GLVR2 gene and receptor. The nucleotide fragments can also be used
CC as probes to study GLVR2 distribution in cells from various species
CC and tissues.
CC Sequence 652 AA;
      Query Match      81.1%; Score 43; DB 12; Length 652;
      Best Local Similarity 83.3%; Pred. No. 1.66e+02;
      Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 377 yrlir 382
      1 | | | |
QY      1 YRLIIR 6

RESULT  15
ID R32925 standard; Protein; 1592 AA.
AC R32925;
DT 28-JUN-1993 (first entry)
DE Glucosyltransferase I.
KW GT-I; Streptococcus; dental; caries.
OS Streptococcus sobrinus.
PN J05023188-A.
PD 02-FEB-1993.
PF 25-JUL-1991; 186592.
PR 25-JUL-1991; JP-186592.
PA (FUKU/) FUKUI I.
PA (KATO/) KATO K.
DR WPI; 93-079449/10.
DR N-PSDB; Q37760.
PT DNA sequence glucosyl:transferase-I - comprises Streptococcus

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PT sobrinus DNA sequence with at least one nucleotide added or  
 deleted  
 PS Claim 13; Page 15; 29pp; Japanese.  
 CC The DNA sequence from Streptococcus sobrinus strain 6715 encodes  
 CC glucosyltransferase-I (and mutants). The DNA was obtd. by treating  
 CC S. sobrinus 6715 with mutanolysin, extracting the chromosomal DNA,  
 CC partially digesting with Sau3AI and fractionating on agarose gel.  
 CC The 3-5 kbp fragment was ligated into pUC18 and E. coli JM109  
 CC transformed with it. A GT-1 expressing clone was isolated and  
 CC sequenced. The clone may be used in the development of a drug for  
 CC dental caries.  
 SQ Sequence 1592 AA;

Query Match 81.1%; Score 43; DB 6; Length 1592;  
 Best Local Similarity 83.3%; Pred.No. 1.66e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 371 yrllnr 376  
 |||||  
 QY 1 YRLILR 6

Search completed: Thu May 22 08:30:51 1997  
 Job time : 16 secs.

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O I O  IntelliGenetics
> O <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "seq2" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.
Selected sequence key from "seq2.key": SEQ 10 NO.2
seq2 (AA) ID seq2 AA preliminary pattern
1 followed by
2 any character
2 g or r
2 r or l
2 any character
2 i or n
2 r or g
2 l
2 d or s or n
2 e or v
2 r

Selected data banks and files:

Data bank : A-GeneSeq 26, all entries
Data bank : PIR 50, all entries
Data bank : Swiss-Prot 34, all entries

-- Output Parameters --

Format Options:
Nucleic acid code matching Exact File Options:
Find non-matching hits only No Indirect file
Report key used Yes Sequence or key file
List of hits Yes
Note position of hit Yes Hit display
Display full annotations Yes Name and annotations
Sequence context 10

-- Run Parameters --

Run mode Batch
Time to start comparison now
Notify at end of run No

-----
1 match found in sequence:
R92909 : HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
(from "A-GeneSeq 26")
ID R92909 standard; peptide; 20 AA.
AC R92909;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
class I major histocompatibility complex (MHC) antigens. This sequence
is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC
HLA-B2702. These sequences can be used to extend the period of
acceptance by a recipient of a transplant from an MHC unmatched donor.
The peptides are administered to a patient in conjunction with a
subtherapeutic amount of an immunosuppressant. This is administered to
the patient for a limited period of time (compared to the lifetime
administration for current treatments). The peptides particularly
modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
of the patient.
SQ Sequence 20 AA;
SQ 2 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 0 G; 0 H;
SQ 1 I; 4 L; 0 K; 0 M; 0 F; 0 P; 0 S; 1 T; 0 W; 2 Y; 0 V;
Found using 'seq2' (seq2.key)

-----
1 match found in sequence:
R92913 : HLA-B7 CTL modulating peptide (B7.84-75/75-84).
(from "A-GeneSeq 26")
ID R92913 standard; peptide; 20 AA.
AC R92913;
DT 16-MAY-1996 (first entry)
DE HLA-B7 CTL modulating peptide (B7.84-75/75-84).

```

```

CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
CC I MHC HLA-B2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;
SQ 2 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 0 G; 0 H;
SQ 1 I; 4 L; 0 K; 0 M; 0 F; 0 P; 0 S; 1 T; 0 W; 2 Y; 0 V;
Found using 'seq2' (seq2.key)

-----
1 yrlairlnerrlnrtalry
1 10
...

-----
2 matches found in sequence:
R92911 : HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
(from "A-GeneSeq 26")
ID R92911 standard; peptide; 20 AA.
AC R92911;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
class I major histocompatibility complex (MHC) antigens. This sequence
is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC
HLA-B2702. These sequences can be used to extend the period of
acceptance by a recipient of a transplant from an MHC unmatched donor.
The peptides are administered to a patient in conjunction with a
subtherapeutic amount of an immunosuppressant. This is administered to
the patient for a limited period of time (compared to the lifetime
administration for current treatments). The peptides particularly
modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
of the patient.
SQ Sequence 20 AA;
SQ 2 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 0 G; 0 H;
SQ 2 I; 4 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 2 Y; 0 V;
Found using 'seq2' (seq2.key)

-----
1 yrlairlnerrlnrtalry
1 10 20
...

-----
1 match found in sequence:
R92913 : HLA-B7 CTL modulating peptide (B7.84-75/75-84).
(from "A-GeneSeq 26")
ID R92913 standard; peptide; 20 AA.
AC R92913;
DT 16-MAY-1996 (first entry)
DE HLA-B7 CTL modulating peptide (B7.84-75/75-84).

```

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KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW Immunosuppressant; graft versus host disorder; transplantation; therapy;
KW Class I MHC; HLA-B7.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PR 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B7-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
CC I MHC HLA-B7. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;
SQ 0 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Q; 2 E; 0 Z; 2 G; 0 H;
SQ 0 I; 4 L; 0 K; 0 M; 0 F; 0 P; 2 S; 0 T; 0 W; 2 Y; 0 V;
Found using 'seq2' (seq2.key)

1 ygrlnrlsrreslnlrgy
1 10
...
-----
1 match found in sequence:
R92907 ; HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
(from "A-GeneSeq 26")
ID R92907 standard; peptide; 20 AA.
AC R92907;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW Immunosuppressant; graft versus host disorder; transplantation; therapy;
KW Class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PR 05-APR-1995; U04349.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B7-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
CC I MHC HLA-B2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;
SQ 2 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Q; 2 E; 0 Z; 0 G; 0 H;
SQ 2 I; 4 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 2 Y; 0 V;
Found using 'seq2' (seq2.key)

```

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SQ 2 I; 4 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 2 Y; 0 V;
Found using 'seq2' (seq2.key)

1 yrlairlnrerlnrlaly
1 10
...
-----
1 match found in sequence:
R95428 ; HLA-B2702 84-75-84 palindrome.
(from "A-GeneSeq 26")
ID R95428 standard; peptide; 20 AA.
AC R95428;
DT 12-NOV-1996 (first entry)
DE HLA-B2702 84-75-84 palindrome.
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW Cytolysis; antigen presenting cell.
OS Synthetic.
PN W09513288-A1.
PD 18-MAY-1995.
PR 10-NOV-1994; U12985.
PR 10-NOV-1994; US-150493.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI: 95-194027/25.
PT Compsns. comprsing lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 12; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLA-B2702 84-75-84 palindrome. These sequences can be used to isolate
CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane
CC protein associated with T-cell activation in mammalian T-cells, and is
CC also immunologically cross reactive with the heat shock protein Hsc70.
CC p74 is found in a limited number of cell types, but is particularly
CC expressed on B and T cells. p74 can be isolated by lysis of a suitable
CC cell with an amphoteric detergent, and then passed through an affinity
CC column containing a covalently bound HLA-B2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
CC compounds can be screened for their effect on the cytolytic activity of
CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition
CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.
SQ Sequence 20 AA;
SQ 2 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 0 G; 0 H;
SQ 2 I; 4 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 2 Y; 0 V;
Found using 'seq2' (seq2.key)

```

```

1 yrlairlnrerlnrlaly
1 10
...
-----
1 match found in sequence:
R95415 ; HLA-B7.84-75-84 Palindrome.
(from "A-GeneSeq 26")
ID R95415 standard; peptide; 20 AA.
AC R95415;
DT 12-NOV-1996 (first entry)
DE HLA-B7.84-75-84 Palindrome.
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;

```

KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
KW cytolysis; antigen presenting cell.  
OS Synthetic.  
PN WO9513288-A1.  
PD 18-MAY-1995.  
PF 10-NOV-1994; U12985.  
PR 10-NOV-1993; US-150493.  
PA (STUD ) UNIV LELAND STANFORD JUNIOR.  
PI Clayberger C, Krensky AM;  
DR WPI: 95-194027/25.  
PT Compsns. comprising lymphoid surface membrane proteins - which may  
PT inhibit cytolytic activity and differentiation of CTLs.  
PS Example; Page 18; 29pp; English.  
CC R95413, and R95415-R95431 represent palindromes and fragments of  
CC human-leucocyte-associated antigens. These sequences can be used to isolate  
CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
CC protein associated with T-cell activation in mammalian T-cells, and is  
CC also immunologically cross reactive with the heat shock protein Hsc70.  
CC p74 is found in a limited number of cell types, but is particularly  
CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
CC cell with an amphoteric detergent, and then passed through an affinity  
CC column containing a covalently bound HLA-B2702 palindromic peptide.  
CC Compositions comprising the extracellular fragment of p74 combined with  
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate  
CC compounds can be screened for their effect on the cytolytic activity of  
CC T-cells, by combining them with the extracellular portion of p74 and  
CC determining the amount of binding between the candidate compound and p74.  
CC Modulation of CTL activity can be inhibited in a cellular composition  
CC containing T-cells and antigen presenting cells (APCs), by adding to the  
CC mix the extracellular portion of p74, in an amount sufficient to compete  
CC with p74 for the binding of the p74 ligand.  
SQ Sequence 20 AA;  
SQ 0 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 2 G; 0 H;  
SQ 0 I; 4 L; 0 K; 0 M; 0 F; 0 P; 2 S; 0 T; 0 W; 2 Y; 0 V;  
Found using 'seq2' (seq2.key)

1 ygrlnrlserreslnlrgy  
10

-- Search Statistics --

Times:	CPU	Total Elapsed
	00:07:08.00	00:07:13.00
Number of sequences searched:		241556
Number of sequence hits:		6
Number of separate matches:		7
Number of sequence hits saved:		0

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MPERCH (TM)

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu May 22 08:48:41 1997; MasPar time 2.83 Seconds  
201.600 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-653-294-31  
Description: (1-20) from US08653294.pep  
Perfect Score: 154  
Sequence: 1 YRLAIRLNERYLRLAIRLNER 20

Scoring table: PAM 150  
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Maximum DB seq length 60

Database: pir50  
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3  
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8  
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 28.882; Variance 64.246; scale 0.450

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
---------------	-------	-------	--------	----	----	-------------	-----------

No matches found.

Search completed: Thu May 22 08:49:00 1997  
Job time : 19 secs.

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WPIRLH (TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:48:13 1997; MasPar time 2.10 Seconds  
Tabular output not generated. 202.262 Million cell updates/sec

Title: >US-08-653-294-31  
Description: (1-20) from US08653294.pap  
Perfect Score: 154  
Sequence: 1 YRLAIRLNERYLRLAIRLNER 20

Scoring table: PAM 150  
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Maximum DB seq length 60

Database: swiss-prot34  
1:part1 2:part3 3:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 30.299; Variance 54.375; scale 0.557

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query				
No.	Score	Match	Length	ID	Description
Pred. No.					

No matches found.

Search completed: Thu May 22 08:48:23 1997  
Job time : 10 secs.

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MAILED (TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:49:18 1997; MasPar time 1.99 Seconds  
Tabular output not generated. 109.404 Million cell updates/sec

Title: >US-08-653-294-31  
Description: (1-20) from US08653294.pep  
Perfect Score: 154  
Sequence: 1 YRLAIRLNERVLAIRLNER 20

Scoring table: PAM 150  
Gap 15

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Maximum DB seq length 60

Database: a-geneseq26

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19

Statistics: Mean 19.740; Variance 84.009; scale 0.235

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	154	100.0	20	16	HLA-B2702 CTL modul	6.55e-07
2	83	53.9	20	18	HLA-B2702 84-75-84 pa	1.33e+00
3	83	53.9	20	16	HLA-B2702 CTL modul	1.33e+00
4	78	50.6	20	16	HLA-B2702 CTL modul	3.49e+00
5	76	49.4	20	16	HLA-B2702 CTL modul	5.10e+00
6	72	46.8	20	18	HLA-B2702 84-75/75-8	1.09e+01
7	71	46.1	20	16	HLA-B2702 CTL modul	1.31e+01

Note: Post-processor removed 38 summaries from list due to search parameters chosen.

#### ALIGNMENTS

RESULT 1  
ID R92911 standard; peptide; 20 AA.

AC R92911;

DT 16-MAY-1996 (first entry)

DE HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).

KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
KW class I MHC; HLA-B2702.  
OS Synthetic.  
PN W09526979-A1.  
PD 12-OCT-1995.  
PF 05-APR-1995; U04349.  
PR 05-APR-1994; US-222851.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PI Clayberger C, Krensky AM, Parham P;  
DR WPI; 95-358582/46.  
PT Extension of acceptance period of transplants from MHC unmatched  
PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
PT host  
PS Example 15; Page 36; 80pp; English.  
CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
CC class I major histocompatibility complex (MHC) antigens. This sequence  
CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC  
CC HLA-B2702. These sequences can be used to extend the period of  
CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
CC The peptides are administered to a patient in conjunction with a  
CC subtherapeutic amount of an immunosuppressant. This is administered to  
CC the patient for a limited period of time (compared to the lifetime  
CC administration for current treatments). The peptides particularly  
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
CC of the patient.  
SQ Sequence 20 AA;

Query Match 100.0%; Score 154; DB 16; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.55e-07;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 yrlairlneryvlairlner 20

QY 1 YRLAIRLNERVLAIRLNER 20

#### RESULT 2

ID R95428 standard; peptide; 20 AA.  
AC R95428;  
DT 12-NOV-1996 (first entry)  
DE HLA-B2702 84-75-84 palindrome.  
KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
KW Cytolysis; antigen presenting cell.  
OS Synthetic.  
PN W09513288-A1.  
PD 18-MAY-1995.  
PF 10-NOV-1994; U12985.  
PR 10-NOV-1993; US-150493.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PI Clayberger C, Krensky AM;  
DR WPI; 95-194027/25.  
PT Compsns. comprising lymphoid surface membrane proteins - which may  
PT inhibit cytolytic activity and differentiation of CTLs.  
PS Example; Page 12; 29pp; English.  
CC R95413, and R95415-R95431 represent palindromes and fragments of  
CC human-leucocyte-associated antigens. This sequence represents the  
CC HLA-B2702 84-75-84 palindrome. These sequences can be used to isolate  
CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
CC protein associated with T-cell activation in mammalian T-cells, and is  
CC also immunologically cross reactive with the heat shock protein Hsc70.  
CC p74 is found in a limited number of cell types, but is particularly  
CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
CC cell with an amphoteric detergent, and then passed through an affinity  
CC column containing a covalently bound HLA-B2702 palindromic peptide.  
CC Compositions comprising the extracellular fragment of p74 combined with  
CC HLA-B2702 60-84 (see R95416), induces calcium influx, and inhibits  
CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate  
CC compounds can be screened for their effect on the cytolytic activity of  
CC T-cells, by combining them with the extracellular portion of p74 and  
CC determining the amount of binding between the candidate compound and p74.  
CC Modulation of CTL activity can be inhibited in a cellular composition

CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 20 AA;

Query Match 53.9%; Score 83; DB 18; Length 20;  
 Best Local Similarity 65.0%; Pred. No. 1.33e+00;  
 Matches 13; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Db 1 yrlairlner-renltrialr 19  
 ||||| ||||| : : :  
 QY 1 YRLAIRLNERYLRLAIRLNER 20

## RESULT 3

ID R92907 standard; peptide; 20 AA.

AC R92907;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN WO9526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host

PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 CC I MHC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 53.9%; Score 83; DB 16; Length 20;  
 Best Local Similarity 65.0%; Pred. No. 1.33e+00;  
 Matches 13; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Db 1 yrlairlner-renltrialr 19  
 ||||| ||||| : : :  
 QY 1 YRLAIRLNERYLRLAIRLNER 20

## RESULT 4

ID R92909 standard; peptide; 20 AA.

AC R92909;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN WO9526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched

PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 CC I MHC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 50.6%; Score 78; DB 16; Length 20;  
 Best Local Similarity 65.0%; Pred. No. 3.49e+00;  
 Matches 13; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Db 1 yrlairlner-renltrialr 19  
 ||||| ||||| : : :  
 QY 1 YRLAIRLNERYLRLAIRLNER 20

## RESULT 5

ID R92908 standard; peptide; 20 AA.

AC R92908;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN WO9526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host

PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 CC I MHC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 49.4%; Score 76; DB 16; Length 20;  
 Best Local Similarity 60.0%; Pred. No. 5.10e+00;  
 Matches 12; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Db 1 yrlairlner-renltrialr 19  
 ||||| ||||| : : :  
 QY 1 YRLAIRLNERYLRLAIRLNER 20

## RESULT 6

ID R95430 standard; peptide; 20 AA.

AC R95430;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B2702 84-75T/75-84T palindrome.  
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;

KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW Cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN W09513288-A1.  
 PD 18-MAY-1995.  
 PR 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI; 95-194027/25.  
 PT Compsns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 12: 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B2702 84-75T/75-84T palindrome. These sequences can be used to  
 CC isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface  
 CC membrane protein associated with T-cell activation in mammalian T-cells,  
 CC and is also immunologically cross reactive with the heat shock protein  
 CC Hsc70. p74 is found in a limited number of cell types, but is  
 CC particularly expressed on B and T cells. p74 can be isolated by lysis of  
 CC a suitable cell with an amphoteric detergent, and then passed through an  
 CC affinity column containing a covalently bound HLA-B2702 palindromic  
 CC peptide. Compositions comprising the extracellular fragment of p74  
 CC combined with HLA-B2702 60-84 (see R95416), induces calcium influx, and  
 CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity.  
 CC Candidate compounds can be screened for their effect on the cytolytic  
 CC activity of T-cells, by combining them with the extracellular portion of  
 CC p74 and determining the amount of binding between the candidate compound  
 CC and p74. Modulation of CTL activity can be inhibited in a cellular  
 CC composition containing T-cells and antigen presenting cells (APCs), by  
 CC adding to the mix the extracellular portion of p74, in an amount  
 CC sufficient to compete with p74 for the binding of the p74 ligand.  
 SQ Sequence 20 AA;

Query Match 46.8%; Score 72; DB 18; Length 20;  
 Best Local Similarity 72.2%; Pred. No. 1.09e+01;  
 Matches 13; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 Db 1 yrlairlnetrenlrtrial 18  
 QY 1 YRLAIRLINE-RYRLAIRL 17

RESULT 7  
 ID R92910 standard; peptide; 20 AA.  
 AC R92910;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995.  
 PR 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B\*75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is an inverted dimer of residues 75-84 of the alpha1 domain of the class  
 CC I MHC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime

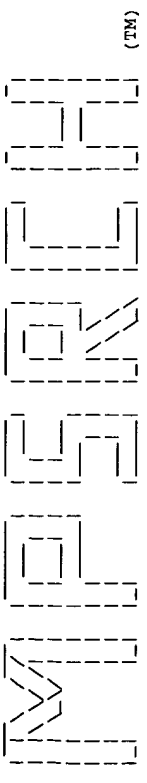
CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 46.1%; Score 71; DB 16; Length 20;  
 Best Local Similarity 60.0%; Pred. No. 1.31e+01;  
 Matches 12; Conservative 1; Mismatches 6; Indels 1; Gaps 1;  
 Db 1 yrlairlnetrenlrtrial 19  
 QY 1 YRLAIRLINE-RYRLAIRL 20

Search completed: Thu May 22 08:49:27 1997  
 Job time : 9 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:47:21 1997; MasPar time 2.92 Seconds  
195.000 Million cell updates/sec

Tabular output not generated.

Title: >US-08-653-294-26  
Description: (1-20) from US08653294.pep  
Perfect Score: 154  
Sequence: 1 YRLAIRLNERRENLRALRY 20

Scoring table: PAM 150  
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Maximum DB seq length 60

Database: pir50  
1:unnn1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3  
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8  
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 30.116; Variance 61.232; scale 0.492

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	ID	Description	Pred. No.
-----						

No matches found.

Search completed: Thu May 22 08:47:32 1997  
Job time : 11 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

(TM)

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Run on: Thu May 22 08:46:58 1997; MasPar time 2.04 Seconds

Tabular output not generated. 207.603 Million cell updates/sec

Title: >US-08-653-294-26  
Description: (1-20) from US08653294.pep  
Perfect Score: 154  
Sequence: 1 YRLAIRLNERRENRLRY 20

Scoring table: PAM 150  
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Maximum DB seq length 60

Database: swiss-prot34  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 31.472; Variance 50.872; scale 0.619

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query	No.	Score	Match	Length	DB	ID	Description	Pred. No.
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No matches found.

Search completed: Thu May 22 08:47:04 1997  
Job time : 6 secs.

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immunosuppressant; graft versus host disorder; transplantation; therapy;  
 class I MHC; HLA-B2702.  
 Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI: 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 donor hosts - using Class I B75-84 MHC antigen of the recipient  
 host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
 class I major histocompatibility complex (MHC) antigens. This sequence  
 is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 I MHC HLA-B2702. These sequences can be used to extend the period of  
 acceptance by a recipient of a transplant from an MHC unmatched donor.  
 The peptides are administered to a patient in conjunction with a  
 subtherapeutic amount of an immunosuppressant. This is administered to  
 the patient for a limited period of time (compared to the lifetime  
 administration for current treatments). The peptides particularly  
 modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 of the patient.  
 CC Sequence 20 AA;

Query Match 100.0%; Score 154; DB 16; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.21e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 yrlairlnerrenlrtrialy 20  
 QY 1 YRLAIRLNERRENLRTRIALY 20

RESULT 3  
 ID R92909 standard; peptide; 20 AA.  
 AC R92909;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI: 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 donor hosts - using Class I B75-84 MHC antigen of the recipient  
 host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
 class I major histocompatibility complex (MHC) antigens. This sequence  
 is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 I MHC HLA-B2702. These sequences can be used to extend the period of  
 acceptance by a recipient of a transplant from an MHC unmatched donor.  
 The peptides are administered to a patient in conjunction with a  
 subtherapeutic amount of an immunosuppressant. This is administered to  
 the patient for a limited period of time (compared to the lifetime  
 administration for current treatments). The peptides particularly  
 modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 of the patient.  
 CC Sequence 20 AA;

Query Match 95.5%; Score 147; DB 16; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 6.09e-07;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 yrlairlnerrenlrtrialy 20  
 QY 1 YRLAIRLNERRENLRTRIALY 20

RESULT 4  
 ID R92908 standard; peptide; 20 AA.  
 AC R92908;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI: 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 donor hosts - using Class I B75-84 MHC antigen of the recipient  
 host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
 class I major histocompatibility complex (MHC) antigens. This sequence  
 is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 I MHC HLA-B2702. These sequences can be used to extend the period of  
 acceptance by a recipient of a transplant from an MHC unmatched donor.  
 The peptides are administered to a patient in conjunction with a  
 subtherapeutic amount of an immunosuppressant. This is administered to  
 the patient for a limited period of time (compared to the lifetime  
 administration for current treatments). The peptides particularly  
 modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 of the patient.  
 CC Sequence 20 AA;

Query Match 95.5%; Score 147; DB 16; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 6.09e-07;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 yrlairlnerrenlrtrialy 20  
 QY 1 YRLAIRLNERRENLRTRIALY 20

RESULT 5  
 ID R92910 standard; peptide; 20 AA.  
 AC R92910;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84(T)).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI: 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 donor hosts - using Class I B75-84 MHC antigen of the recipient  
 host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
 class I major histocompatibility complex (MHC) antigens. This sequence  
 is an inverted dimer of residues 75-84 of the alpha-1 domain of the class  
 I MHC HLA-B2702. These sequences can be used to extend the period of  
 acceptance by a recipient of a transplant from an MHC unmatched donor.  
 The peptides are administered to a patient in conjunction with a

CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 90.9%; Score 140; DB 16; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 3.05e-06;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 YRLAIRLNRERLRLALRY 20  
 QY 1 YRLAIRLNRERLRLALRY 20

## RESULT 6

ID R95430 standard; peptide; 20 AA.  
 AC R95430;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B2702 84-75T/75-84T palindromic.  
 KW HLA: p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN WO9513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI: 95-194027/25

PT Compsns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 12; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B2702 84-75T/75-84T palindromic. These sequences can be used to  
 CC isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface  
 CC membrane protein associated with T-cell activation in mammalian T-cells,  
 CC and is also immunologically cross reactive with the heat shock protein  
 CC Hsc70. p74 is found in a limited number of cell types, but is  
 CC particularly expressed on B and T cells. p74 can be isolated by lysis of  
 CC a suitable cell with an amphoteric detergent, and then passed through an  
 CC affinity column containing a covalently bound HLA-B2702 palindromic  
 CC peptide. Compositions comprising the extracellular fragment of p74  
 CC combined with HLA-B2702.60-84 (see R95415), induces calcium influx, and  
 CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis.  
 CC Candidate compounds can be screened for their effect on the cytolytic  
 CC activity of T-cells, by combining them with the extracellular portion of  
 CC p74 and determining the amount of binding between the candidate compound  
 CC and p74. Modulation of CTL activity can be inhibited in a cellular  
 CC composition containing T-cells and antigen presenting cells (APCs), by  
 CC adding to the mix the extracellular portion of p74, in an amount  
 CC sufficient to compete with p74 for the binding of the p74 ligand.  
 SQ Sequence 20 AA;

Query Match 85.1%; Score 131; DB 18; Length 20;  
 Best Local Similarity 94.7%; Pred. No. 2.39e-05;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 YRLAIRLNRERLRLALRY 19  
 QY 1 YRLAIRLNRERLRLALRY 19

## RESULT 7

ID R92911 standard; peptide; 20 AA.  
 AC R92911;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;

KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN WO9526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI: 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC  
 CC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;

Query Match 53.9%; Score 83; DB 16; Length 20;  
 Best Local Similarity 65.0%; Pred. No. 9.02e-01;  
 Matches 13; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Db 1 YRLAIRLNRERLRLALRY 20  
 QY 1 YRLAIRLNRERLRLALRY 19

## RESULT 8

ID R83062 standard; peptide; 10 AA.  
 AC R83062;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.75-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN WO9526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI: 95-358582/46.

PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Claim 15; Page 9; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC  
 CC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 10 AA;

Query Match 50.0%; Score 77; DB 16; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 YRLAIRLNRERLRLALRY 19  
 QY 1 YRLAIRLNRERLRLALRY 19

Db 1 renltrialy 10  
 QY 11 RENLRIALRY 20

RESULT 9  
 ID R95413 standard; peptide; 10 AA.  
 AC R95413;  
 DT 12-NOV-1996 (first entry)  
 DE Alpha1-helix of HLA-B2702.  
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN W09513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI; 95-194027/25.  
 PT Compens. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 11: 29pp; English.  
 CC This sequence represents the alpha1-helix of the  
 CC human-leucocyte-associated antigen B2702 (HLA-B2702). This sequence,  
 CC epitopes, and palindromes of it (such as R95428) can be used to isolate  
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
 CC protein associated with T-cell activation in mammalian T-cells, and is  
 CC also immunologically cross reactive with the heat shock protein Hsc70.  
 CC p74 is found in a limited number of cell types, but is particularly  
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
 CC cell with an amphoteric detergent, and then passed through an affinity  
 CC column containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 10 AA;

Query Match 50.0%; Score 77; DB 18; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 renltrialy 10  
 QY 11 RENLRIALRY 20

RESULT 10  
 ID R41208 standard; peptide; 10 AA.  
 AC R41208;  
 DT 15-MAR-1994 (first entry)  
 DE Peptide fragment of Class I HLA peptide.  
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;  
 KW parasitic disease; cytotoxic T lymphocyte; modulation.  
 OS Synthetic.  
 PN W09317699-A.  
 PD 16-SEP-1993.  
 PR 25-FEB-1993; U01758.  
 PF 02-MAR-1992; US-844716.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger CA, Krensky AM;  
 DR WPI; 93-303134/38.  
 PT New peptide(s) based on Class I HLA antigen domains - used for  
 PT modulating cytotoxic T-lymphocyte activity towards targets

PS Claim 11; Page 54; 61pp; English.  
 CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)  
 CC activity, either by inhibition or stimulation. It can be used  
 CC for inhibiting CTL toxicity in transplantations, for inducing CTL  
 CC activity in parasitic diseases and neoplasia and in studies on viral  
 CC infection. The peptide can also be used for identifying CTLs which  
 CC bind to it and removing subsets of CTLs from a T-cell composition.  
 CC This peptide sequence is more commonly found within larger peptide  
 CC compounds of not more than 30 amino acids in length.  
 SQ Sequence 10 AA;

Query Match 50.0%; Score 77; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 renltrialy 10  
 QY 11 RENLRIALRY 20

RESULT 11  
 ID R92912 standard; peptide; 15 AA.  
 AC R92912;  
 DT 16-MAY-1996 (first entry)  
 DE HLA-B2702 CTL modulating peptide (B2702.70-84).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW class I MHC; HLA-B2702.  
 OS Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI; 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient  
 PT host  
 PS Example 15; Page 36; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R83097-R83093 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC corresponds to residues 70-84 of the alpha-1 domain of the class I MHC  
 CC HLA-B2702. These sequences can be used to extend the period of  
 CC acceptance by a recipient of a transplant from an MHC unmatched donor.  
 CC The peptides are administered to a patient in conjunction with a  
 CC subtherapeutic amount of an immunosuppressant. This is administered to  
 CC the patient for a limited period of time (compared to the lifetime  
 CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 15 AA;

Query Match 50.0%; Score 77; DB 16; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 renltrialy 15  
 QY 11 RENLRIALRY 20

RESULT 12  
 ID R95422 standard; peptide; 25 AA.  
 AC R95422;  
 DT 12-NOV-1996 (first entry)  
 DE HLAB38.6084.  
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN W09513288-A1.

18-MAY-1995.  
 10-NOV-1994; U12985.  
 10-NOV-1993; US-150493.  
 (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI: 95-194027/25.  
 PT Compens. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 9; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B\*38.6084. These sequences can be used to isolate the protein p74 from  
 CC a T-cell lysate. p74 is a T-cell surface membrane protein associated  
 CC with T-cell activation in mammalian T-cells, and is also immunologically  
 CC cross reactive with the heat shock protein Hsc70. p74 is found in a  
 CC limited number of cell types, but is particularly expressed on B and T  
 CC cells. p74 can be isolated by lysis of a suitable cell with an  
 CC amphoteric detergent, and then passed through an affinity column  
 CC containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 25 AA;

Query Match 50.0%; Score 77; DB 18; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 renalrlyal 25  
 QY 11 RENLRLALRY 20

RESULT 13

ID R95416 standard; peptide; 25 AA.  
 AC R95416;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B2702.60-84.  
 KW HLA: p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytotoxic; antigen presenting cell.  
 OS Synthetic.  
 PN W09513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI: 95-194027/25.  
 PT Compens. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 9; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents  
 CC HLA-B\*38.6084. These sequences can be used to isolate the protein p74  
 CC from a T-cell lysate. p74 is a T-cell surface membrane protein  
 CC associated with T-cell activation in mammalian T-cells, and is also  
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is  
 CC found in a limited number of cell types, but is particularly expressed on  
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an  
 CC amphoteric detergent, and then passed through an affinity column  
 CC containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC this sequence, induces calcium influx, and inhibits cytotoxic T  
 CC lymphocyte (CTL) differentiation or cytotoxicity. Candidate compounds can

CC be screened for their effect on the cytolytic activity of T-cells, by  
 CC combining them with the extracellular portion of p74 and determining the  
 CC amount of binding between the candidate compound and p74. Modulation of  
 CC CTL activity can be inhibited in a cellular composition containing  
 CC T-cells and antigen presenting cells (APCs), by adding to the mix the  
 CC extracellular portion of p74, in an amount sufficient to compete with p74  
 CC for the binding of the p74 ligand.  
 SQ Sequence 25 AA;

Query Match 50.0%; Score 77; DB 18; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 renalrlyal 25  
 QY 11 RENLRLALRY 20

RESULT 14

ID R41205 standard; peptide; 25 AA.  
 AC R41205;  
 DT 15-MAR-1994 (first entry)  
 DE Peptide fragment of Class I HLA peptide.  
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;  
 KW parasitic disease; cytotoxic T lymphocyte; modulation.  
 OS Synthetic.  
 PN W09317599-A.  
 PD 16-SEP-1993.  
 PF 25-FEB-1993; U01758.  
 PR 02-MAR-1992; US-844716.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger CA, Krensky AM;  
 DR WPI: 93-303134/38.  
 PT New peptide(s) based on Class I HLA antigen domains - used for  
 PT modulating cytotoxic T-lymphocyte activity towards targets  
 PS Claim 8; Page 53; 61pp; English.  
 CC The peptide (or a fragment of at least 10 amino acids, joined at at  
 CC least one terminus to a sequence other than that of wild type HLA  
 CC antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity,  
 CC either by inhibition or stimulation. It can be used for  
 CC inhibiting CTL toxicity in transplantations, for inducing CTL  
 CC activity in parasitic diseases and neoplasia, and in studies on viral  
 CC infection. The peptide can also be used for identifying CTLs which  
 CC bind to it and removing subsets of CTLs from a T-cell composition.  
 SQ Sequence 25 AA;

Query Match 50.0%; Score 77; DB 8; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 renalrlyal 25  
 QY 11 RENLRLALRY 20

RESULT 15

ID R83093 standard; peptide; 25 AA.  
 AC R83093;  
 DT 16-MAY-1996 (first entry)  
 DE HLAB38 CTL modulating peptide (B38.6084).  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW immunosuppressant; graft versus host disorder; transplantation; therapy;  
 KW Class I MHC; HLAB38.  
 OS Synthetic.  
 PN W09526979-A1.  
 PD 12-OCT-1995.  
 PF 05-APR-1995; U04349.  
 PR 05-APR-1994; US-222851.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM, Parham P;  
 DR WPI: 95-358582/46.  
 PT Extension of acceptance period of transplants from MHC unmatched  
 PT donor hosts - using Class I B75-84 MHC antigen of the recipient

PT host  
 PS Example 13; Page 32; 80pp; English.  
 CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of  
 CC class I major histocompatibility complex (MHC) antigens. This sequence  
 CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC  
 CC HLAB38. These sequences can be used to extend the period of acceptance  
 CC by a recipient of a transplant from an MHC unmatched donor. The peptides  
 CC are administered to a patient in conjunction with a subtherapeutic amount  
 CC of an immunosuppressant. This is administered to the patient for a  
 CC limited period of time (compared to the lifetime administration for  
 CC current treatments). The peptides particularly modulate (or inhibit) the  
 CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.  
 SQ Sequence 25 AA;

Query Match 50.0%; Score 77; DB 16; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.13e+00;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 16 renlrialry 25  
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Search completed: Thu May 22 08:47:56 1997  
 Job time : 6 secs.



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Quest - Quick User-directed Expression Search Tool  
Release 5.4

-- Outline of search "seq1" --

Selected search type is key against sequence data banks or files.  
Selected scope is Sequence. "seq1.key": *SEQ 10 No; 1*  
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SQ Sequence 366 AA;
SQ 38 A; 30 R; 5 N; 19 D; 0 B; 8 C; 21 Q; 28 E; 0 Z; 29 G; 9 H;
SQ 9 I; 30 L; 10 K; 6 M; 7 F; 18 P; 27 S; 24 T; 12 W; 13 Y; 23 V;
Found using 'seq1' (seq1.key)
...
89 qkykrqaqdrvslnrlrgyynqseagsh
108
|-----|
1 match found in sequence:
R12466 ; HLA-C exon Cb-2.
(from "A-GeneSeq 26")
AC R12466;
DE HLA-C exon Cb-2.
DE Human leukocyte antigen; probe; major histocompatibility complex;
KW MHC; class I.
OS Homo sapiens.
PN J03112485-A.
PD 14-MAY-1991.
PF 22-SEP-1989; 247695.
PR 22-SEP-1989; JP-247695.
PA (OLYU ) OLYMPUS OPTICAL KK.
DR WPI; 91-182989/25.
DR N-PSDB; Q12117.
PT HLA-C gene, DNA probe and transformant cells - for immunisation
PT of animals and monoclonal antibody development.
PS Claim 4; Page 2; 13pp; Japanese.
CC Probes comprising part of the DNA sequence encoding the protein can
CC be used to identify Class I genes. The DNA can be expressed for
CC immunisation of animals and prodn. of monoclonal antibodies specific
CC for the HLA-C antigen. See also R12465 (same patent) and J03112485
CC and J03112487.
SQ Sequence 366 AA;
SQ 40 A; 32 R; 5 N; 20 D; 0 B; 9 C; 19 Q; 29 E; 0 Z; 29 G; 9 H;
SQ 9 I; 30 L; 10 K; 6 M; 6 F; 18 P; 22 S; 24 T; 11 W; 15 Y; 23 V;
Found using 'seq1' (seq1.key)
...
89 qkykrqaqdrvslnrlrgyynhreaagst
108
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1 match found in sequence:
R12463 ; HLA-Bw53 exon.
(from "A-GeneSeq 26")
ID R12463 standard; Protein; 362 AA.
AC R12463;
DE HLA-Bw53 exon.
DE Human leukocyte antigen; probe; major histocompatibility complex;
KW MHC; class I.
OS Homo sapiens.
PN J03112487-A.
PD 14-MAY-1991.
PF 22-SEP-1989; 247697.
PR 22-SEP-1989; JP-247697.
PA (OLYU ) OLYMPUS OPTICAL KK.
DR WPI; 91-182991/25.
DR N-PSDB; Q12114.
PT HLA-Bw53 gene, DNA probe and transformant cells - used for
PT immunisation, identifying specificity of antiserum etc.
PS Claim 2; Page 1; 11pp; Japanese.

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CC Probes comprising part of the sequence encoding the protein can be
CC used to identify Class I genes. The DNA can be expressed for
CC immunisation of animals and prodn. of monoclonal antibodies
CC specific for the HLA-Bw53 antigen. See also J03112485 and
CC J03112486.
SQ Sequence 362 AA;
SQ 38 A; 29 R; 6 N; 20 D; 0 B; 5 C; 21 Q; 24 E; 0 Z; 27 G; 8 H;
SQ 13 I; 29 L; 9 K; 6 M; 7 F; 18 P; 24 S; 29 T; 11 W; 15 Y; 23 V;
SQ 0 Others;
Found using 'seq1' (seq1.key)
...
89 qifkntqtyrenlrlrgyynqseagshi
99
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1 match found in sequence:
R12464 ; HLA-B35 antigen.
(from "A-GeneSeq 26")
ID R12464 standard; Protein; 362 AA.
AC R12464;
DE 29-AUG-1991 (first entry)
DE HLA-B35 antigen.
DE Human leukocyte antigen; probe; major histocompatibility complex;
KW MHC; class I.
OS Homo sapiens.
PN J03112486-A.
PD 14-MAY-1991.
PF 22-SEP-1989; 247697.
PR 22-SEP-1989; JP-247697.
PA (OLYU ) OLYMPUS OPTICAL KK.
DR WPI; 91-182991/25.
DR N-PSDB; Q12115.
PT HLA-B35 gene - used in DNA probe and transformant cells for
PT immunising animals, for developing monoclonal antibody.
PS Claim 1; Page 1; 11pp; Japanese.
CC Probes comprising part of the sequence encoding this sequence can
CC be used to identify Class I genes. The DNA can be expressed for
CC immunisation of animals and prodn. of monoclonal antibodies
CC specific for the HLA-B35 antigen. See also J03112485 and J03112487.
SQ Sequence 362 AA;
SQ 37 A; 29 R; 6 N; 20 D; 0 B; 5 C; 21 Q; 24 E; 0 Z; 28 G; 8 H;
SQ 12 I; 29 L; 9 K; 5 M; 7 F; 18 P; 25 S; 29 T; 11 W; 15 Y; 24 V;
Found using 'seq1' (seq1.key)
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89 qifkntqtyreslnrlrgyynqseagshi
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1 match found in sequence:
R41205 ; Peptide fragment of Class I HLA peptide.
(from "A-GeneSeq 26")
ID R41205 standard; peptide; 25 AA.
AC R41205;
DE 15-MAR-1994 (first entry)
DE Peptide fragment of Class I HLA peptide.
DE Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW parasitic disease; cytotoxic T lymphocyte; modulation.
OS Synthetic.
PN W09317699-A.
PD 16-SEP-1993.
PF 25-FEB-1993; J01758.
PR 02-MAR-1992; US-844716.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.

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PI Clayberger CA, Krensky AM;  
 DR WPI; 93-303134/38.  
 PT New peptide(s) based on Class I HLA antigen domains - used for  
 PT modulating cytotoxic T-lymphocyte activity towards targets  
 PS Claim 8; Page 53; 6lpp; English.  
 CC The peptide (or a fragment of at least 10 amino acids, joined at at  
 CC least one terminus to a sequence other than that of wild type HLA  
 CC antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity,  
 CC either by inhibition or stimulation. It can be used for  
 CC inhibiting CTL toxicity in transplantations, for inducing CTL  
 CC activity in parasitic diseases and neoplasia and in studies on viral  
 CC infection. The peptide can also be used for identifying CTLs which  
 CC bind to it and removing subsets of CTLs from a T-cell composition.  
 SQ Sequence 25 AA;  
 SQ 3 A; 4 R; 1 N; 2 D; 0 B; 1 C; 2 Q; 2 E; 0 Z; 0 G; 0 H;  
 SQ 2 I; 2 L; 2 K; 0 M; 0 F; 0 P; 0 S; 2 T; 1 W; 1 Y; 0 V;  
 Found using 'seq1' (seq1.key)

...  
 6 qickakagtrenlralry 25  
 16  
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 qickakagtrenlralry

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 1 match found in sequence:  
 R41206 ; Peptide fragment of Class I HLA peptide.  
 (from "A-Geneseq 26")  
 ID R41206 standard; peptide; 25 AA.  
 AC R41206;  
 DE 15-MAR-1994 (first entry)  
 DE Peptide fragment of Class I HLA peptide.  
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;  
 KW parasitic disease; cytotoxic T lymphocyte; modulation.  
 OS Synthetic.  
 PN WO9317699-A.  
 PD 16-SEP-1993.  
 PF 25-FEB-1993; U01758.  
 PR 02-MAR-1992; US-844716.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger CA, Krensky AM;  
 DR WPI; 93-303134/38.  
 PT New peptide(s) based on Class I HLA antigen domains - used for  
 PT modulating cytotoxic T-lymphocyte activity towards targets  
 PS Claim 9; Page 53; 6lpp; English.  
 CC The peptide (or a fragment of at least 10 amino acids, joined at at  
 CC least one terminus to a sequence other than that of wild type HLA  
 CC antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity,  
 CC either by inhibition or stimulation. It can be used for  
 CC inhibiting CTL toxicity in transplantations, for inducing CTL  
 CC activity in parasitic diseases and neoplasia and in studies on viral  
 CC infection. The peptide can also be used for identifying CTLs which  
 CC bind to it and removing subsets of CTLs from a T-cell composition.  
 SQ Sequence 25 AA;  
 SQ 1 A; 1 N; 2 D; 0 B; 0 C; 3 Q; 1 E; 0 Z; 1 G; 0 H;  
 SQ 0 I; 2 L; 2 K; 0 M; 0 F; 0 P; 1 S; 2 T; 1 W; 2 Y; 1 V;  
 Found using 'seq1' (seq1.key)

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 6 qkykrqagtdrvsnlrgy 25  
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 qkykrqagtdrvsnlrgy

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 1 match found in sequence:  
 R41207 ; Peptide fragment of Class I HLA peptide.  
 (from "A-Geneseq 26")  
 ID R41207 standard; peptide; 25 AA.  
 AC R41207;  
 DE 15-MAR-1994 (first entry)  
 DE Peptide fragment of Class I HLA peptide.  
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;

KW parasitic disease; cytotoxic T lymphocyte; modulation.  
 OS Synthetic.  
 PN WO9317699-A.  
 PD 16-SEP-1993.  
 PF 25-FEB-1993; U01758.  
 PR 02-MAR-1992; US-844716.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger CA, Krensky AM;  
 DR WPI; 93-303134/38.  
 PT New peptide(s) based on Class I HLA antigen domains - used for  
 PT modulating cytotoxic T-lymphocyte activity towards targets  
 PS Claim 10; Page 54; 6lpp; English.  
 CC The peptide (or a fragment of at least 10 amino acids, joined at at  
 CC least one terminus to a sequence other than that of wild type HLA  
 CC antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity,  
 CC either by inhibition or stimulation. It can be used for  
 CC inhibiting CTL toxicity in transplantations, for inducing CTL  
 CC activity in parasitic diseases and neoplasia and in studies on viral  
 CC infection. The peptide can also be used for identifying CTLs which  
 CC bind to it and removing subsets of CTLs from a T-cell composition.  
 SQ Sequence 25 AA;  
 SQ 0 A; 4 R; 2 N; 1 D; 0 B; 0 C; 2 Q; 2 E; 0 Z; 1 G; 0 H;  
 SQ 1 I; 2 L; 1 K; 0 M; 0 F; 0 P; 2 S; 4 T; 1 W; 2 Y; 0 V;  
 Found using 'seq1' (seq1.key)

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 6 qiskntqtyreslnlrgy 25  
 16  
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 qiskntqtyreslnlrgy

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 1 match found in sequence:  
 R41208 ; Peptide fragment of Class I HLA peptide.  
 (from "A-Geneseq 26")  
 ID R41208 standard; peptide; 10 AA.  
 AC R41208;  
 DE 15-MAR-1994 (first entry)  
 DE Peptide fragment of Class I HLA peptide.  
 KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;  
 KW parasitic disease; cytotoxic T lymphocyte; modulation.  
 OS Synthetic.  
 PN WO9317699-A.  
 PD 16-SEP-1993.  
 PF 25-FEB-1993; U01758.  
 PR 02-MAR-1992; US-844716.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger CA, Krensky AM;  
 DR WPI; 93-303134/38.  
 PT New peptide(s) based on Class I HLA antigen domains - used for  
 PT modulating cytotoxic T-lymphocyte activity towards targets  
 PS Claim 11; Page 54; 6lpp; English.  
 CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)  
 CC activity, either by inhibition or stimulation. It can be used  
 CC for inhibiting CTL toxicity in transplantations, for inducing CTL  
 CC activity in parasitic diseases and neoplasia and in studies on viral  
 CC infection. The peptide can also be used for identifying CTLs which  
 CC bind to it and removing subsets of CTLs from a T-cell composition.  
 CC This peptide sequence is more commonly found within larger peptide  
 CC compounds of not more than 30 amino acids in length.  
 SQ Sequence 10 AA;  
 SQ 1 A; 3 R; 1 N; 0 D; 0 B; 0 C; 0 Q; 1 E; 0 Z; 0 G; 0 H;  
 SQ 1 I; 2 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 1 Y; 0 V;  
 Found using 'seq1' (seq1.key)

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 1 renlralry 10  
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 renlralry

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 1 match found in sequence:  
 R41209 ; Peptide fragment of Class I HLA peptide.  
 (from "A-Geneseq 26")

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ID R41209 standard; peptide; 10 AA.
AC R41209;
DT 15-MAR-1994 (first entry)
DE Peptide fragment of Class I HLA peptide.
KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW Parasitic disease; cytotoxic T lymphocyte; modulation.
OS Synthetic.
PN WO9317699-A.
PD 16-SEP-1993.
PF 25-FEB-1993; U01758.
PR 02-MAR-1992; US-844716.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger CA, Krensky AM;
DR WPI; 93-303134/38.
PT New peptide(s) based on Class I HLA antigen domains - used for
PT modulating cytotoxic T-lymphocyte activity towards targets
PS Claim 11; Page 54; 61pp; English.
CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
CC activity, either by inhibition or stimulation. It can be used
CC for inhibiting CTL toxicity in transplantations, for inducing CTL
CC activity in parasitic diseases and neoplasia and in studies on viral
CC infection. The peptide can also be used for identifying CTLs which
CC bind to it and removing subsets of CTLs from a T-cell composition.
CC This peptide sequence is more commonly found within larger peptide
CC compounds of not more than 30 amino acids in length.
SQ Sequence 10 AA;
SQ 0 A; 3 R; 1 N; 0 D; 0 B; 0 C; 0 Q; 1 E; 0 Z; 1 G; 0 H;
SQ 0 I; 2 L; 0 K; 0 M; 0 F; 0 P; 1 S; 0 T; 0 W; 1 Y; 0 V;
Found using 'seq1' (seq1.key)

1 |-----|
1 reslnlrgy
10

1 match found in sequence:
R48286 : Peptide fragment of HLA-B38 antigen.
(from "A-GeneSeq 26")
ID R48286 standard; peptide; 25 AA.
AC R48286;
DT 15-MAR-1994 (first entry)
DE Peptide fragment of HLA-B38 antigen.
KW Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
KW Parasitic disease; cytotoxic T lymphocyte; modulation.
OS Synthetic.
PN WO9317699-A.
PD 16-SEP-1993.
PF 25-FEB-1993; U01758.
PR 02-MAR-1992; US-844716.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger CA, Krensky AM;
DR WPI; 93-303134/38.
PT New peptide(s) based on Class I HLA antigen domains - used for
PT modulating cytotoxic T-lymphocyte activity towards targets
PS Example 13; Page 39; 61pp; English.
CC The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
CC activity, either by inhibition or stimulation. It can be used for
CC inhibiting CTL toxicity in transplantations, for inducing CTL
CC activity in parasitic diseases and neoplasia and in studies on viral
CC infection. The peptide can also be used for identifying CTLs which
CC bind to it and removing subsets of CTLs from a T-cell composition.
CC This peptide is derived from the HLA-B38 antigen and corresponds
CC to the amino acid positions 60-84 of that antigen.
SQ Sequence 25 AA;
SQ 1 A; 4 R; 3 N; 1 D; 0 B; 1 C; 2 Q; 1 E; 0 Z; 0 G; 0 H;
SQ 2 I; 2 L; 1 K; 0 M; 0 F; 0 P; 0 S; 4 T; 1 W; 2 Y; 0 V;
Found using 'seq1' (seq1.key)

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1 |-----|
1 reslnlrgy
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1 match found in sequence:
R83061 : HLA-B7 CTL modulating peptide (B7.75-84).
(from "A-GeneSeq 26")
ID R83061 standard; peptide; 10 AA.
AC R83061;
DT 15-MAY-1996 (first entry)
DE HLA-B7 CTL modulating peptide (B7.75-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW Immunosuppressant; graft versus host disorder; transplantation; therapy;
KW Class I MHC; HLA-B7.
OS Synthetic.
PN WO9526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PS Claim 13; Page 66; 80pp; English.
CC This sequence represents a fragment of a class I major histocompatibility
CC complex (MHC) antigen. This sequence corresponds to residues 75-84 of
CC the alpha-1 domain of the class I MHC HLA-B7. This sequence, and the
CC peptide fragments represented by R83062-R83085, R83090-R83096 and
CC R92907-R92913 can be used to extend the period of acceptance by a
CC recipient of a transplant from an MHC unmatched donor. The peptides are
CC administered to a patient in conjunction with a subtherapeutic amount of
CC an immunosuppressant. This is administered to the patient for a limited
CC period of time (compared to the lifetime administration for current
CC treatments). The peptides particularly modulate (or inhibit) the
CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.
SQ Sequence 10 AA;
SQ 0 A; 3 R; 1 N; 0 D; 0 B; 0 C; 0 Q; 1 E; 0 Z; 1 G; 0 H;
SQ 0 I; 2 L; 0 K; 0 M; 0 F; 0 P; 1 S; 0 T; 0 W; 1 Y; 0 V;
Found using 'seq1' (seq1.key)

1 |-----|
1 reslnlrgy
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1 match found in sequence:
R83062 : HLA-B2702 CTL modulating peptide (B2702.75-84).
(from "A-GeneSeq 26")
ID R83062 standard; peptide; 10 AA.
AC R83062;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.75-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW Immunosuppressant; graft versus host disorder; transplantation; therapy;
KW Class I MHC; HLA-B2702.
OS Synthetic.
PN WO9526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PS Claim 15; Page 9; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC
CC HLA-B2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a

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CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 10 AA;
SQ 1 A; 3 R; 1 N; 0 D; 0 B; 0 C; 0 Q; 1 E; 0 Z; 0 G; 0 H;
SQ 1 I; 2 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 1 Y; 0 V;
Found using 'seq1' (seq1.key)

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1 match found in sequence:
R92912 ; HLA-B*2702 CTL modulating peptide (B2702.70-84).
(from "A-GeneSeq 26")
ID R92912 standard; peptide; 15 AA.
AC R92912;
DT 16-MAY-1996 (first entry)
DE HLA-B*2702 CTL modulating peptide (B2702.70-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B*2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B*75-84 MHC antigen of the recipient
PT host
Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 70-84 of the alpha-1 domain of the class I
CC HLA-B*2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 15 AA;
SQ 2 A; 3 R; 1 N; 1 D; 0 B; 0 C; 1 Q; 1 E; 0 Z; 0 G; 0 H;
SQ 1 I; 2 L; 1 K; 0 M; 0 F; 0 P; 0 S; 1 T; 0 W; 1 Y; 0 V;
Found using 'seq1' (seq1.key)

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1 15

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1 match found in sequence:
R92913 ; HLA-B*7 CTL modulating peptide (B7.84-75/75-84).
(from "A-GeneSeq 26")
ID R92913 standard; peptide; 20 AA.
AC R92913;
DT 16-MAY-1996 (first entry)
DE HLA-B*7 CTL modulating peptide (B7.84-75/75-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B*7.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.

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PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B*75-84 MHC antigen of the recipient
PT host
Example 15; Page 36; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
CC I MHC HLA-B*7. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;
SQ 0 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 2 G; 0 H;
SQ 0 I; 4 L; 0 K; 0 M; 0 F; 0 P; 2 S; 0 T; 0 W; 2 Y; 0 V;
Found using 'seq1' (seq1.key)

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1 ygrlnrlserreslrlrgy
1 11
20

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1 match found in sequence:
R83072 ; HLA-B*46 CTL modulating peptide (Bw46.60-84).
(from "A-GeneSeq 26")
ID R83072 standard; peptide; 25 AA.
AC R83072;
DT 16-MAY-1996 (first entry)
DE HLA-B*46 CTL modulating peptide (Bw46.60-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B*46.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI: 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B*75-84 MHC antigen of the recipient
PT host
Example 13; Page 32; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 60-84 of the alpha-1 domain of the class
CC I MHC HLA-B*46. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 25 AA;
SQ 1 A; 5 R; 1 N; 2 D; 0 B; 0 C; 3 Q; 1 E; 0 Z; 1 G; 0 H;
SQ 0 I; 2 L; 2 K; 0 M; 0 F; 0 P; 1 S; 2 T; 1 W; 2 Y; 1 V;
Found using 'seq1' (seq1.key)

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6 qkykrqaqtdrvslrlrgy
16 25

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1 match found in sequence:
R83073 : HLA-Bw62 CTL modulating peptide (Bw62.60-84).
(from "A-Geneseq 26")
ID R83073 standard; peptide; 25 AA.
AC R83073;
DT 16-MAY-1996 (first entry)
DE HLA-Bw62 CTL modulating peptide (Bw62.60-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-Bw62.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 13; Page 32; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
CC HLA-Bw62. These sequences can be used to extend the period of acceptance
CC by a recipient of a transplant from an MHC unmatched donor. The peptides
CC are administered to a patient in conjunction with a subtherapeutic amount
CC of an immunosuppressant. This is administered to the patient for a
CC limited period of time (compared to the lifetime administration for
CC current treatments). The peptides particularly modulate (or inhibit) the
CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.
SQ Sequence 25 AA;
SQ 0 A; 4 R; 2 N; 1 D; 0 B; 0 C; 2 Q; 2 E; 0 Z; 1 G; 0 H;
SQ 1 I; 2 L; 1 K; 0 M; 0 F; 0 P; 2 S; 4 T; 1 W; 2 Y; 0 V;
Found using 'seq1' (seq1.key)

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qickakagtddrenlrlaly
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1 match found in sequence:
R83090 : HLA-B2702 CTL modulating peptide (B2702.60-84).
(from "A-Geneseq 26")
ID R83090 standard; peptide; 25 AA.
AC R83090;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.60-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 13; Page 32; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
CC HLA-B2702. These sequences can be used to extend the period of acceptance
CC by a recipient of a transplant from an MHC unmatched donor. The peptides
CC are administered to a patient in conjunction with a subtherapeutic amount
CC of an immunosuppressant. This is administered to the patient for a
CC limited period of time (compared to the lifetime administration for
CC current treatments). The peptides particularly modulate (or inhibit) the
CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.
SQ Sequence 25 AA;
SQ 0 A; 4 R; 2 N; 1 D; 0 B; 0 C; 2 Q; 2 E; 0 Z; 1 G; 0 H;
SQ 1 I; 2 L; 1 K; 0 M; 0 F; 0 P; 2 S; 4 T; 1 W; 2 Y; 0 V;
Found using 'seq1' (seq1.key)

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6 qickntqttyrenlrlaly
16
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qickakagtddrenlrlaly
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1 match found in sequence:
R83094 : HLA-B2702 CTL modulating peptide (B2702.75-84(D)).
(from "A-Geneseq 26")
ID R83094 standard; peptide; 10 AA.
AC R83094;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.75-84(D)).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.

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CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 25 AA;
SQ 3 A; 4 R; 1 N; 2 D; 0 B; 1 C; 2 Q; 2 E; 0 Z; 0 G; 0 H;
SQ 2 I; 2 L; 2 K; 0 M; 0 F; 0 P; 0 S; 2 T; 1 W; 1 Y; 0 V;
Found using 'seq1' (seq1.key)

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6 qickakagtddrenlrlaly
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qickakagtddrenlrlaly
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1 match found in sequence:
R83093 : HLAB38 CTL modulating peptide (B38.6084).
(from "A-Geneseq 26")
ID R83093 standard; peptide; 25 AA.
AC R83093;
DT 16-MAY-1996 (first entry)
DE HLAB38 CTL modulating peptide (B38.6084).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLAB38.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 13; Page 32; 80pp; English.
CC R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
CC HLAB38. These sequences can be used to extend the period of acceptance
CC by a recipient of a transplant from an MHC unmatched donor. The peptides
CC are administered to a patient in conjunction with a subtherapeutic amount
CC of an immunosuppressant. This is administered to the patient for a
CC limited period of time (compared to the lifetime administration for
CC current treatments). The peptides particularly modulate (or inhibit) the
CC activity of the cytotoxic T lymphocytes (CTLs) of the patient.
SQ Sequence 25 AA;
SQ 1 A; 4 R; 3 N; 1 D; 0 B; 1 C; 2 Q; 1 E; 0 Z; 0 G; 0 H;
SQ 2 I; 2 L; 1 K; 0 M; 0 F; 0 P; 0 S; 4 T; 1 W; 2 Y; 0 V;
Found using 'seq1' (seq1.key)

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qickakagtddrenlrlaly
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1 match found in sequence:
R83094 : HLA-B2702 CTL modulating peptide (B2702.75-84(D)).
(from "A-Geneseq 26")
ID R83094 standard; peptide; 10 AA.
AC R83094;
DT 16-MAY-1996 (first entry)
DE HLA-B2702 CTL modulating peptide (B2702.75-84(D)).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.

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PF 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 14; Page 34; 80pp; English.
CC R3061-R3085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC
CC HLA-B*2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with
CC a subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 10 AA:
SQ 1 A; 3 R; 0 N; 1 D; 0 B; 0 C; 0 Q; 1 E; 0 Z; 0 G; 0 H;
SQ 1 I; 2 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 1 Y; 0 V;
Found using 'seq1' (seq1.key)

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1 match found in sequence:

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R83096 : HLA-B*2702 CTL modulating peptide (B2702.75-84(L)).
(from "A-Geneseq 26")

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ID R3096 standard; peptide; 10 AA.
AC R3096;
DE 16-MAY-1996 (first entry)
DE HLA-B*2702 CTL modulating peptide (B2702.75-84(L)).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B*2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PR 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 14; Page 34; 80pp; English.
CC R3061-R3085, R83090-R83096 and R92907-R92913 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC corresponds to residues 75-84 of the alpha-1 domain of the class I MHC
CC HLA-B*2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with
CC a subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 10 AA;
SQ 0 A; 3 R; 1 N; 0 D; 0 B; 0 C; 0 Q; 1 E; 0 Z; 0 G; 0 H;
SQ 1 I; 3 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 1 Y; 0 V;
Found using 'seq1' (seq1.key)

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renrtrialy
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1 match found in sequence:
R92907 : HLA-B*2702 CTL modulating peptide (B2702.84-75/75-84).
(from "A-Geneseq 26")
ID R92907 standard; peptide; 20 AA.
AC R92907;
DE 16-MAY-1996 (first entry)
DE HLA-B*2702 CTL modulating peptide (B2702.84-75/75-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B*2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PR 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R3061-R3085, R83090-R83096 and R92907-R92914 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
CC I MHC HLA-B*2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime
CC administration for current treatments). The peptides particularly
CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
CC of the patient.
SQ Sequence 20 AA;
SQ 2 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 0 G; 0 H;
SQ 2 I; 4 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 2 Y; 0 V;
Found using 'seq1' (seq1.key)

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yrlairlnerenrtrialy
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1 match found in sequence:

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R92908 : HLA-B*2702 CTL modulating peptide (B2702.84-75(T)/75-84).
(from "A-Geneseq 26")

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ID R92908 standard; peptide; 20 AA.
AC R92908;
DE 16-MAY-1996 (first entry)
DE HLA-B*2702 CTL modulating peptide (B2702.84-75(T)/75-84).
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW immunosuppressant; graft versus host disorder; transplantation; therapy;
KW class I MHC; HLA-B*2702.
OS Synthetic.
PN W09526979-A1.
PD 12-OCT-1995.
PR 05-APR-1995; U04349.
PR 05-APR-1994; US-222851.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM, Parham P;
DR WPI; 95-358582/46.
PT Extension of acceptance period of transplants from MHC unmatched
PT donor hosts - using Class I B75-84 MHC antigen of the recipient
PT host
PS Example 15; Page 36; 80pp; English.
CC R3061-R3085, R83090-R83096 and R92907-R92914 represent fragments of
CC class I major histocompatibility complex (MHC) antigens. This sequence
CC is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
CC I MHC HLA-B*2702. These sequences can be used to extend the period of
CC acceptance by a recipient of a transplant from an MHC unmatched donor.
CC The peptides are administered to a patient in conjunction with a
CC subtherapeutic amount of an immunosuppressant. This is administered to
CC the patient for a limited period of time (compared to the lifetime

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CC administration for current treatments). The peptides particularly  
 CC modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)  
 CC of the patient.  
 SQ Sequence 20 AA;  
 SQ 2 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 0 G; 0 H;  
 SQ 1 I; 4 L; 0 K; 0 M; 0 F; 0 P; 0 S; 1 T; 0 W; 2 Y; 0 V;  
 Found using 'seq1' (seq1.key)

1 yrlairlnerrenlrialy 20  
 11

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 1 match found in sequence:  
 R95413 : Alpha1-helix of HLA-B2702.  
 (from "A-GeneSeq 26")  
 ID R95413 standard; peptide: 10 AA.  
 AC R95413;  
 DE 12-NOV-1996 (first entry)  
 DE Alpha1-helix of HLA-B2702.  
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN WO9513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI: 95-194027/25.  
 PT Compsns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 11; 29pp; English.  
 CC This sequence represents the alpha1-helix of the  
 CC human-leucocyte-associated antigen B2702 (HLA-B2702). This sequence,  
 CC epitopes, and palindromes of it (such as R95428) can be used to isolate  
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
 CC protein associated with T-cell activation in mammalian T-cells, and is  
 CC also immunologically cross reactive with the heat shock protein Hsc70.  
 CC p74 is found in a limited number of cell types, but is particularly  
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
 CC cell with an amphoteric detergent, and then passed through an affinity  
 CC column containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 10 AA;  
 SQ 1 A; 3 R; 1 N; 0 D; 0 B; 0 C; 0 Q; 1 E; 0 Z; 0 G; 0 H;  
 SQ 1 I; 2 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 1 Y; 0 V;  
 Found using 'seq1' (seq1.key)

1 renlrialy 10  
 1

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 1 match found in sequence:  
 R95428 : HLA-B2702 84-75-84 palindrome.  
 (from "A-GeneSeq 26")  
 ID R95428 standard; peptide: 20 AA.  
 AC R95428;  
 DE 12-NOV-1996 (first entry)  
 DE HLA-B2702 84-75-84 palindrome.  
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;

KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN WO9513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI: 95-194027/25.  
 PT Compsns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 12; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B2702 84-75-84 palindrome. These sequences can be used to isolate  
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
 CC protein associated with T-cell activation in mammalian T-cells, and is  
 CC also immunologically cross reactive with the heat shock protein Hsc70.  
 CC p74 is found in a limited number of cell types, but is particularly  
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
 CC cell with an amphoteric detergent, and then passed through an affinity  
 CC column containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 20 AA;  
 SQ 2 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 0 G; 0 H;  
 SQ 2 I; 4 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 2 Y; 0 V;  
 Found using 'seq1' (seq1.key)

1 yrlairlnerrenlrialy 20  
 11

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 1 match found in sequence:  
 R95430 : HLA-B2702 84-75/75-84T palindrome.  
 (from "A-GeneSeq 26")  
 ID R95430 standard; peptide: 20 AA.  
 AC R95430;  
 DE 12-NOV-1996 (first entry)  
 DE HLA-B2702 84-75/75-84T palindrome.  
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN WO9513288-A1.  
 PD 18-MAY-1995.  
 PF 10-NOV-1994; U12985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI: 95-194027/25.  
 PT Compsns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 12; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B2702 84-75/75-84T palindrome. These sequences can be used to  
 CC isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface  
 CC membrane protein associated with T-cell activation in mammalian T-cells,  
 CC and is also immunologically cross reactive with the heat shock protein  
 CC Hsc70. p74 is found in a limited number of cell types, but is



CC particularly expressed on B and T cells. p74 can be isolated by lysis of  
 CC a suitable cell with an amphoteric detergent, and then passed through an  
 CC affinity column containing a covalently bound HLA-B2702 palindromic  
 CC peptide. Compositions comprising the extracellular fragment of p74  
 CC combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and  
 CC inhibits cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity.  
 CC Candidate compounds can be screened for their effect on the cytolytic  
 CC activity of T-cells, by combining them with the extracellular portion of  
 CC p74 and determining the amount of binding between the candidate compound  
 CC and p74. Modulation of CTL activity can be inhibited in a cellular  
 CC composition containing T-cells and antigen presenting cells (APCs), by  
 CC adding to the mix the extracellular portion of p74, in an amount  
 CC sufficient to compete with p74 for the binding of the p74 ligand.  
 SQ Sequence 20 AA;  
 SQ 2 A; 5 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 0 G; 0 H;  
 SQ 2 I; 4 L; 0 K; 0 M; 0 F; 0 P; 0 S; 2 T; 0 W; 1 Y; 0 V;  
 Found using 'seq1' (seq1.key)

1 yrlairnretrenlrlr  
 11 20

1 match found in sequence:

R95431 ; HLA-B7.60-84.  
 (from "A-Geneseq 26")  
 ID R95431 standard; peptide; 25 AA.  
 AC R95431; 1996 (first entry)  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B7.60-84.  
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW Cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN W09513288-A1.  
 PD 18-MAY-1995.  
 PR 10-NOV-1994; UI2985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI; 95-194027/25.  
 PT Compsns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 12; 29pp; English.  
 CC R95415, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B7.60-84. These sequences can be used to isolate the protein p74  
 CC from a T-cell lysate. p74 is a T-cell surface membrane protein  
 CC associated with T-cell activation in mammalian T-cells, and is also  
 CC immunologically cross reactive with the heat shock protein Hsc70. p74 is  
 CC found in a limited number of cell types, but is particularly expressed on  
 CC B and T cells. p74 can be isolated by lysis of a suitable cell with an  
 CC amphoteric detergent, and then passed through an affinity column  
 CC containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 25 AA;  
 SQ 2 A; 4 R; 1 N; 2 D; 0 B; 1 C; 2 Q; 2 E; 0 Z; 1 G; 0 H;  
 SQ 1 I; 2 L; 2 K; 0 M; 0 F; 0 P; 1 S; 2 T; 1 W; 1 Y; 0 V;  
 Found using 'seq1' (seq1.key)

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6 gickakagtireslrlrly  
 16 25

1 match found in sequence:

R95415 ; HLA-B7.84-75-84 Palindrome.  
 (from "A-Geneseq 26")  
 ID R95415 standard; peptide; 20 AA.  
 AC R95415;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B7.84-75-84 Palindrome.  
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW Cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN W09513288-A1.  
 PD 18-MAY-1995.  
 PR 10-NOV-1994; UI2985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Clayberger C, Krensky AM;  
 DR WPI; 95-194027/25.  
 PT Compsns. comprising lymphoid surface membrane proteins - which may  
 PT inhibit cytolytic activity and differentiation of CTLs.  
 PS Example; Page 18; 29pp; English.  
 CC R95413, and R95415-R95431 represent palindromes and fragments of  
 CC human-leucocyte-associated antigens. This sequence represents the  
 CC HLA-B7.84-75-84 palindromic peptide. These sequences can be used to isolate  
 CC the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane  
 CC protein associated with T-cell activation in mammalian T-cells, and is  
 CC also immunologically cross reactive with the heat shock protein Hsc70.  
 CC p74 is found in a limited number of cell types, but is particularly  
 CC expressed on B and T cells. p74 can be isolated by lysis of a suitable  
 CC cell with an amphoteric detergent, and then passed through an affinity  
 CC column containing a covalently bound HLA-B2702 palindromic peptide.  
 CC Compositions comprising the extracellular fragment of p74 combined with  
 CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits  
 CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate  
 CC compounds can be screened for their effect on the cytolytic activity of  
 CC T-cells, by combining them with the extracellular portion of p74 and  
 CC determining the amount of binding between the candidate compound and p74.  
 CC Modulation of CTL activity can be inhibited in a cellular composition  
 CC containing T-cells and antigen presenting cells (APCs), by adding to the  
 CC mix the extracellular portion of p74, in an amount sufficient to compete  
 CC with p74 for the binding of the p74 ligand.  
 SQ Sequence 20 AA;  
 SQ 0 A; 6 R; 2 N; 0 D; 0 B; 0 C; 0 Q; 2 E; 0 Z; 2 G; 0 H;  
 SQ 0 I; 4 L; 0 K; 0 M; 0 F; 0 P; 2 S; 0 T; 0 W; 2 Y; 0 V;  
 Found using 'seq1' (seq1.key)  
 1 ygrlnrlserreslrlrly  
 11 20

1 match found in sequence:

R95416 ; HLA-B2702.60-84.  
 (from "A-Geneseq 26")  
 ID R95416 standard; peptide; 25 AA.  
 AC R95416;  
 DT 12-NOV-1996 (first entry)  
 DE HLA-B2702.60-84.  
 KW HLA; p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;  
 KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;  
 KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;  
 KW Cytolysis; antigen presenting cell.  
 OS Synthetic.  
 PN W09513288-A1.  
 PD 18-MAY-1995.  
 PR 10-NOV-1994; UI2985.  
 PR 10-NOV-1993; US-150493.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.

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PI Clayberger C, Krensky AM;
DR WPI: 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 9; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents
CC HLA-B*2702.60-84. These sequences can be used to isolate the protein p74
CC from a T-cell lysate. p74 is a T-cell surface membrane protein
CC associated with T-cell activation in mammalian T-cells, and is also
CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
CC found in a limited number of cell types, but is particularly expressed on
CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
CC amphoteric detergent, and then passed through an affinity column
CC containing a covalently bound HLA-B*2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC this sequence, induces calcium influx, and inhibits cytotoxic T
CC lymphocyte (CTL) differentiation or cytotoxicity. Candidate compounds can
CC be screened for their effect on the cytolytic activity of T-cells, by
CC combining them with the extracellular portion of p74 and determining the
CC amount of binding between the candidate compound and p74. Modulation of
CC CTL activity can be inhibited in a cellular composition containing
CC T-cells and antigen presenting cells (APCs), by adding to the mix the
CC extracellular portion of p74, in an amount sufficient to compete with p74
CC for the binding of the p74 ligand.
SQ Sequence 25 AA;
SQ 3 A; 4 R; 1 N; 2 D; 0 B; 1 C; 2 Q; 2 E; 0 Z; 0 G; 0 H;
SQ 2 I; 2 L; 2 K; 0 M; 0 F; 0 P; 0 S; 2 T; 1 W; 1 Y; 0 V;
Found using 'seq1' (seq1.key)
...
1 match found in sequence:
R95418 : HLA-B*46.60-84.
(from "A-GeneSeq 26")
ID R95418 standard; peptide: 25 AA.
AC R95418;
DE HLA-B*46.60-84.
KW HLA: p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytotoxic; antigen presenting cell.
OS Synthetic.
PN WO9513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; U12985.
PR 10-NOV-1993; US-150493.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI: 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 9; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLA-B*46.60-84. These sequences can be used to isolate the protein p74
CC from a T-cell lysate. p74 is a T-cell surface membrane protein
CC associated with T-cell activation in mammalian T-cells, and is also
CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
CC found in a limited number of cell types, but is particularly expressed on
CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
CC amphoteric detergent, and then passed through an affinity column
CC containing a covalently bound HLA-B*2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B*2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
CC compounds can be screened for their effect on the cytolytic activity of

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CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition
CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.
SQ Sequence 25 AA;
SQ 1 A; 5 R; 1 N; 2 D; 0 B; 0 C; 3 Q; 1 E; 0 Z; 1 G; 0 H;
SQ 0 I; 2 L; 2 K; 0 M; 0 F; 0 P; 1 S; 2 T; 1 W; 2 Y; 1 V;
Found using 'seq1' (seq1.key)
...
1 match found in sequence:
R95419 : HLA-B*62.60-84.
(from "A-GeneSeq 26")
ID R95419 standard; peptide: 25 AA.
AC R95419;
DE HLA-B*62.60-84.
KW HLA: p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytotoxic; antigen presenting cell.
OS Synthetic.
PN WO9513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; U12985.
PR 10-NOV-1993; US-150493.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C, Krensky AM;
DR WPI: 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 9; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLA-B*62.60-84. These sequences can be used to isolate the protein p74
CC from a T-cell lysate. p74 is a T-cell surface membrane protein
CC associated with T-cell activation in mammalian T-cells, and is also
CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
CC found in a limited number of cell types, but is particularly expressed on
CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
CC amphoteric detergent, and then passed through an affinity column
CC containing a covalently bound HLA-B*2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B*2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytotoxicity. Candidate
CC compounds can be screened for their effect on the cytolytic activity of

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R95422 ; HLAB38.6084.
ID (from "A-GenesSeq 26")
AC R95422; standard; peptide; 25 AA.
DT 12-NOV-1996 (first entry)
DE HLAB38.6084.
KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
PN W09513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; U12985.
PI (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Clayberger C. Krensky AM;
DR WPI; 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 9; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLA-B2702.75-84(D). These sequences can be used to isolate the protein
CC p74 from a T-cell lysate. p74 is a T-cell surface membrane protein
CC associated with T-cell activation in mammalian T-cells, and is also
CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
CC found in a limited number of cell types, but is particularly expressed on
CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
CC amphoteric detergent, and then passed through an affinity column
CC containing a covalently bound HLA-B2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
CC compounds can be screened for their effect on the cytolytic activity of
CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition
CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.
SQ Sequence 25 AA;
SQ 1 A; 4 R; 3 N; 1 D; 0 B; 1 C; 2 Q; 1 E; 0 Z; 0 G; 0 H;
SQ 2 I; 2 L; 1 K; 0 M; 0 F; 0 P; 0 S; 4 T; 1 W; 2 Y; 0 V;
Found using 'seq1' (seq1.key)
...
6 qickntqntqrentrialry 25
|-----|
| 16
1 match found in sequence:
R95425 ; HLA-B2702.75-84(D).
ID (from "A-GenesSeq 26")
AC R95425; standard; peptide; 10 AA.
DT 12-NOV-1996 (first entry)
DE HLA-B2702.75-84(D).
KW HLA; p74; alpha-helix; human-leucocyte-associated antigen; inhibitor;
KW T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
KW B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
KW cytolysis; antigen presenting cell.
OS Synthetic.
PN Key Location/Qualifiers
FT /note= "N3D mutation"
FT W09513288-A1.
PD 18-MAY-1995.
PF 10-NOV-1994; U12985.
PI (STRD ) UNIV LELAND STANFORD JUNIOR.

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PI Clayberger C. Krensky AM;
DR WPI; 95-194027/25.
PT Compsns. comprising lymphoid surface membrane proteins - which may
PT inhibit cytolytic activity and differentiation of CTLs.
PS Example; Page 11; 29pp; English.
CC R95413, and R95415-R95431 represent palindromes and fragments of
CC human-leucocyte-associated antigens. This sequence represents the
CC HLA-B2702.75-84(D). These sequences can be used to isolate the protein
CC p74 from a T-cell lysate. p74 is a T-cell surface membrane protein
CC associated with T-cell activation in mammalian T-cells, and is also
CC immunologically cross reactive with the heat shock protein Hsc70. p74 is
CC found in a limited number of cell types, but is particularly expressed on
CC B and T cells. p74 can be isolated by lysis of a suitable cell with an
CC amphoteric detergent, and then passed through an affinity column
CC containing a covalently bound HLA-B2702 palindromic peptide.
CC Compositions comprising the extracellular fragment of p74 combined with
CC HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits
CC cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate
CC compounds can be screened for their effect on the cytolytic activity of
CC T-cells, by combining them with the extracellular portion of p74 and
CC determining the amount of binding between the candidate compound and p74.
CC Modulation of CTL activity can be inhibited in a cellular composition
CC containing T-cells and antigen presenting cells (APCs), by adding to the
CC mix the extracellular portion of p74, in an amount sufficient to compete
CC with p74 for the binding of the p74 ligand.
SQ Sequence 10 AA;
SQ 1 A; 3 R; 0 N; 1 D; 0 B; 0 C; 0 Q; 1 E; 0 Z; 0 G; 0 H;
SQ 2 I; 2 L; 0 K; 0 M; 0 F; 0 P; 0 S; 0 T; 0 W; 1 Y; 0 V;
Found using 'seq1' (seq1.key)
|-----|
| 1
1 match found in sequence:
HLHUB7 ; MHC class I histocompatibility antigen HLA-B7 alpha chain
ID (from "PIR 50")
ENTRY HLHUB7 #type complete
TITLE MHC class I histocompatibility antigen HLA-B7 alpha chain
ORGANISM precursor - human
#formal_name Homo sapiens #common_name man
DATE 31-Jul-1980 #sequence_revision 22-Apr-1995 #text_change
06-Sep-1996
ACCESSIONS B35997; A90435; A93840; A02185
REFERENCE A35997
#authors Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2833-2837
#title Rapid cloning of HLA-A,B CDNA by using the polymerase chain
reaction: frequency and nature of errors produced in
amplification.
#cross-references MUID:90207291
#accession B35997
#molecule_type mRNA
#residues 1-362 #label ENN
##cross-references GB:M32317
#note this allele is designated B*0702 (previously HLA-B*7.2)
REFERENCE A90435
#authors Orr, H.T.; Lopez de Castro, J.A.; Lancet, D.; Strominger,
J.L.
#journal Biochemistry (1979) 18:5711-5720
#title Complete amino acid sequence of a papain-solubilized human
histocompatibility antigen, HLA-B7. 2. Sequence
determination and search for homologies.
#cross-references MUID:80088278
#accession A90435
#molecule_type protein
#residues 25-265, 'E', 267-295 #label ORR
REFERENCE A93840
#authors Tragardh, L.; Rask, L.; Wiman, K.; Fohlman, J.; Peterson,
P.A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1980) 77:1129-1133
#title Complete amino acid sequence of pooled papain-solubilized

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HLA-A, -B, and -C antigens: relatedness to immunoglobulins
and internal homologues.
##cross-references GDB:80145722
#accession A93840
##molecule_type protein
##residues 25-42,'Q','44-47','A','49-53','N','55-68','Q','70-86','Q','88-93,
'H','95-139','TRAI','141-175','A','177-198','R','200-246','N',
248-251,'N','253-297 #label TRA
##experimental_source pooled HLA-A, -B, and -C antigens
##note this sequence represents the predominant amino acid at
each position

GENETICS
#gene GDB:HLA-B
##cross-references GDB:120048
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
KEYWORDS duplication; glycoprotein; heterodimer; transmembrane
protein; transplantation antigen
FEATURE
1-24 #domain signal sequence #status predicted #label SIG\
25-114 #domain alpha-1 #label EX1\
115-206 #domain alpha-2 #label EX2\
220-285 #domain immunoglobulin homology #label IMM\
307-331 #domain transmembrane #status predicted #label TMM\
332-362 #domain intracellular #status predicted #label INT\
110 #binding_site carbohydrate (Asn) (covalent) #status
experimental\
125-188,227-283 #disulfide_bonds #status experimental
SUMMARY #length 362 #molecular_weight 40460 #checksum 8234
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 qiykaqatdreslnrlgynyqseagsh
99 108
|-----|
1 match found in sequence:
HLHU40 ; MHC class I histocompatibility antigen HLA-B40 alpha chain -
(from "PIR 50")
ENTRY
TITLE MHC class I histocompatibility antigen HLA-B40 alpha chain -
human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change
06-Sep-1996
ACCESSIONS A02186
REFERENCE Lopez de Castro, J.A.; Bragado, R.; Strong, D.M.; Strominger,
J.L.
#journal Biochemistry (1983) 22:3961-3969
#title Primary structure of papain-solubilized human
histocompatibility antigen HLA-B40 (-Bw60). An outline of
alloantigenic determinants.
##cross-references MUID:84000412
#accession A02186
##molecule_type protein
##residues 1-270 #label LOP
COMMENT Comparison of a number of class I allelic sequences (-B40 vs. -B7
and -A2 vs. -A28) indicates that the distribution of differences
among the respective alleles (polymorphism) is essentially
restricted to the alpha-1 and alpha-2 domains. The most
conspicuous clustering of variability between the -B40 and -B7
alleles occurs between residues 63-74. This segment and residues
147-156 are possible alloantigenic determinants of these
antigens.

GENETICS
#gene GDB:HLA-B

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##cross-references GDB:120048
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
KEYWORDS duplication; glycoprotein; heterodimer; membrane protein;
transplantation antigen
FEATURE
1-90 #domain alpha-1 #label EX1\
91-181 #domain alpha-2 #label EX2\
185-260 #domain immunoglobulin homology #label IMM\
86 #binding_site carbohydrate (Asn) (covalent) #status
experimental\
101-163,202-258 #disulfide_bonds #status predicted
SUMMARY #length 270 #checksum 4804
SEQUENCE
Found using 'seq1' (seq1.key)
...
65 qiskntqttyreslnrlgynyqseagsh
75 84
|-----|
1 match found in sequence:
HLHU12 ; MHC class I histocompatibility antigen HLA alpha chain
(from "PIR 50")
ENTRY
TITLE MHC class I histocompatibility antigen HLA alpha chain
precursor (clone pHLA 12.4) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change
15-Jun-1996
ACCESSIONS A02189
REFERENCE Malissen, M.; Malissen, B.; Jordan, B.R.
#authors Proc. Natl. Acad. Sci. U.S.A. (1982) 79:893-897
#journal Exon/intron organization and complete nucleotide sequence of
an HLA gene.
##cross-references MUID:82151002
#accession A02189
##molecule_type DNA
##residues 1-359 #label MAL
COMMENT The seven exons correspond approximately to the domain structure of
this chain.
GENETICS
#map_position 6p21.3
#introns 22/1; 112/1; 204/1; 296/1; 335/1; 346/1
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
KEYWORDS duplication; glycoprotein; heterodimer; transmembrane
protein; transplantation antigen
FEATURE
1-21 #domain signal sequence #status predicted #label SIG\
22-359 #product class I histocompatibility antigen HLA alpha
#chain #status predicted #label MAL\
22-304 #domain extracellular #status predicted #label EXT\
22-111 #domain alpha-1 #label EX1\
112-203 #domain alpha-2 #label EX2\
217-282 #domain immunoglobulin homology #label IMM\
305-329 #domain transmembrane #status predicted #label TMM\
335-359 #domain intracellular #status predicted #label INT\
107 #binding_site carbohydrate (Asn) (covalent) #status
predicted\
224-280 #disulfide_bonds #status predicted
SUMMARY #length 359 #molecular_weight 40548 #checksum 2195
SEQUENCE
Found using 'seq1' (seq1.key)
...

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```

86      qickaqagterlnrlryngseggsh
      96
      |-----|
      105
      ...

-----
1 match found in sequence:
HLHUW3 ; MHC class I histocompatibility antigen HLA-Cw3 alpha chain
ENTRY
TITLE      HLHUW3      #type complete
MHC class I histocompatibility antigen HLA-Cw3 alpha chain
precursor - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change
06-Sep-1996
ACCESSIONS  A02190
REFERENCE   A02190
#authors    Sodoyer, R.; Damotte, M.; Delovitch, T.L.; Trucy, J.; Jordan,
            B.R.; Strachan, T.
#journal    EMBO J. (1984) 3:879-885
#title      Complete nucleotide sequence of a gene encoding a functional
            human class I histocompatibility antigen (HLA-Cw3).
#cross-references MUID:84207947
#accession  A02190
#molecule_type DNA
#residues   1-366 #label SOD
GENETICS
#gene       GDB:HLA-C
#cross-references GDB:119311
#map_position 6p21.3-6p21.3
#introns      25/1; 115/1; 207/1; 299/1; 339/1; 350/1; 366/1
CLASSIFICATION #superfamily class I histocompatibility antigen;
                immunoglobulin homology
KEYWORDS       duplication; glycoprotein; heterodimer; transmembrane
                protein; transplantation antigen
FEATURE
1-24          #domain signal sequence #status predicted #label SIG\
25-366        #product class I histocompatibility antigen HLA-Cw3\
                alpha chain #status predicted #label MAT\
25-307        #domain extracellular #status predicted #label EXT\
25-114        #domain alpha-1 #label EX1\
115-206       #domain alpha-2 #label EX2\
220-285       #domain immunoglobulin homology #label IMM\
308-332       #domain transmembrane #status predicted #label TM\
333-366       #domain intracellular #status predicted #label INT\
110           #binding_site carbohydrate (Asn) (covalent) #status
                predicted\
227-283       #disulfide_bonds #status predicted
SUMMARY       #length 366 #molecular-weight 40744 #checksum 4249
SEQUENCE
Found using 'seq1' (seq1.key)
...

89      qxykpaqatdrvslnrlryngseagshi
      99
      |-----|
      108
      ...

-----
1 match found in sequence:
HLHUW4 ; MHC class I histocompatibility antigen HLA-C4 alpha chain -
ENTRY
TITLE      HLHUW4      #type complete
MHC class I histocompatibility antigen HLA-C4 alpha chain -
human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
06-Sep-1996
ACCESSIONS  A24512
REFERENCE   A92500

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#authors      Davidson, W.F.; Kress, M.; Khoury, G.; Jay, G.
#journal      J. Biol. Chem. (1985) 260:13414-13423
#title        Comparison of HLA class I gene sequences. Derivation of
                locus-specific oligonucleotide probes specific for HLA-A,
                HLA-B, and HLA-C genes.
#cross-references MUID:86033791
#accession  A24512
#molecule_type DNA
#residues    1-342 #label DAV
GENETICS
#gene       GDB:HLA-C
#cross-references GDB:119311
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
                immunoglobulin homology
KEYWORDS       glycoprotein; heterodimer; transmembrane protein;
                transplantation antigen
FEATURE
196-261       #domain immunoglobulin homology #label IMM
SUMMARY       #length 342 #molecular-weight 38082 #checksum 7418
SEQUENCE
Found using 'seq1' (seq1.key)
...

65      qkykqaqadrvslrlryngsqsgsht
      75
      |-----|
      84
      ...

-----
1 match found in sequence:
HLHU32 ; MHC class I histocompatibility antigen HLA-A32 alpha chain -
ENTRY
TITLE      HLHU32      #type fragment
MHC class I histocompatibility antigen HLA-A32 alpha chain -
human (fragment)
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
06-Sep-1996
ACCESSIONS  A26088
REFERENCE   A26088
#authors     Wan, A.M.; Ennis, P.; Parham, P.; Holmes, N.
#journal     J. Immunol. (1986) 137:3671-3674
#title       The primary structure of HLA-A32 suggests a region involved
                in formation of the Bw4/Bw6 epitopes.
#cross-references MUID:87058961
#accession  A26088
#molecule_type protein
#residues    1-274 #label WAN
GENETICS
#gene       GDB:HLA-A
#cross-references GDB:119310
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
                immunoglobulin homology
KEYWORDS       glycoprotein; heterodimer; transmembrane protein;
                transplantation antigen
FEATURE
196-261       #domain immunoglobulin homology #label IMM
SUMMARY       #length 274 #checksum 899
SEQUENCE
Found using 'seq1' (seq1.key)
...

65      rnvkhsqtdreslrlryngsqsgsht
      75
      |-----|
      84
      ...

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-----
1 match found in sequence:
HLHUB8 : MHC class I histocompatibility antigen HLA-B*58 alpha chain
      (from "PIR 50")
ENTRY
  TITLE      HLHUB8      #type complete
  MHC class I histocompatibility antigen HLA-B*58 alpha chain
  precursor - human
  #formal_name Homo sapiens #common_name man
  31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
  06-Sep-1996
ACCESSIONS
  A23895
REFERENCE
  #authors    Ways, J.P.; Coppin, H.L.; Parham, P.
  #journal    J. Biol. Chem. (1985) 260:11924-11933
  #title      The complete primary structure of HLA-B*58.
  #cross-references MUID:86008247
  #accession  A23895
  #molecule_type DNA
  #residues   1-362 #label WAY
  #note       the authors translated the codon GCC for residue 349 as
              Ser
COMMENT      This protein is a subtype of the HLA-B*17 family.
GENETICS
  #gene       GDB:HLA-B
  #cross-references GDB:120048
  #map_position 6p21.3-6p21.3
  #introns    25/1; 115/1; 207/1; 299/1; 338/1; 349/1
CLASSIFICATION
  #superfamily class I histocompatibility antigen;
  immunoglobulin homology
KEYWORDS
  duplication; glycoprotein; heterodimer; transmembrane
  protein; transplantation antigen
FEATURE
  1-24      #domain signal sequence #status predicted #label SIG\
  25-362    #product class I histocompatibility antigen HLA-B*58
            alpha chain #status predicted #label MAI\
  25-307    #domain extracellular #status predicted #label EXT\
  25-114    #domain alpha-1 #label EX1\
  115-206   #domain alpha-2 #label EX2\
  220-285   #domain immunoglobulin homology #label IMM\
  308-331   #domain transmembrane #status predicted #label TMM\
  332-362   #domain intracellular #status predicted #label INT\
SUMMARY
  #length 362 #molecular-weight 40321 #checksum 8057
SEQUENCE
  Found using 'seq1' (seq1.key)
...
89      rmkasaqtyrenlrialryngseagshi
      |-----|
      99      108
      .....
-----
1 match found in sequence:
HLMSDB : MHC class I histocompatibility antigen H-2D(b) alpha chain -
      (from "PIR 50")
ENTRY
  TITLE      HLMSDB      #type complete
  MHC class I histocompatibility antigen H-2D(b) alpha chain -
  mouse
  #formal_name Mus musculus #common_name house mouse
  29-Jul-1981 #sequence_revision 14-Nov-1983 #text_change
  04-Dec-1994
ACCESSIONS
  A91747; A92315; A91748; A02200
REFERENCE
  #authors    Reyes, A.A.; Schold, M.; Wallace, R.B.
  #journal    Immunogenetics (1982) 16:1-9
  #title      The complete amino acid sequence of the murine
              transplantation antigen H-2D(b) as deduced by molecular
              cloning
  #cross-references MUID:83005712
  #accession  A91747
  #molecule_type mRNA
...
-----
1 match found in sequence:
A30547 : class I histocompatibility antigen H-2D-b alpha chain - mouse
      (from "PIR 50")
ENTRY
  TITLE      A30547      #type fragment
  class I histocompatibility antigen H-2D-b alpha chain - mouse
  (fragment)
  #formal_name Mus musculus #common_name house mouse
  07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
  12-Apr-1995
ACCESSIONS
  A30547
REFERENCE
  #authors    Duran, L.W.; Horton, R.M.; Birschbach, C.W.; Chang-Miller,
              A.; Pease, L.R.
  #journal    J. Immunol. (1989) 142:288-296
  #title      Structural relationships among the H-2 D-regions of murine
              MHC haplotypes.
  #accession  A30547
  #molecule_type DNA
  #residues   1-206 #label DUR
CLASSIFICATION
  #superfamily class I histocompatibility antigen;
  immunoglobulin homology
...
65      qkagqeqwfrvslrnllyngsaggsht
      |-----|
      75      84
      .....
-----
1 match found in sequence:
A30547 : class I histocompatibility antigen H-2D-b alpha chain - mouse
      (from "PIR 50")
ENTRY
  TITLE      A30547      #type fragment
  class I histocompatibility antigen H-2D-b alpha chain - mouse
  (fragment)
  #formal_name Mus musculus #common_name house mouse
  07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
  12-Apr-1995
ACCESSIONS
  A30547
REFERENCE
  #authors    Duran, L.W.; Horton, R.M.; Birschbach, C.W.; Chang-Miller,
              A.; Pease, L.R.
  #journal    J. Immunol. (1989) 142:288-296
  #title      Structural relationships among the H-2 D-regions of murine
              MHC haplotypes.
  #accession  A30547
  #molecule_type DNA
  #residues   1-206 #label DUR
CLASSIFICATION
  #superfamily class I histocompatibility antigen;
  immunoglobulin homology

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SUMMARY          #length 206 #checksum 9521
SEQUENCE
Found using 'seq1' (seq1.key)
...
89  qkagqeqwfrvslrnllyynqsagsgsht
    |-----|
    99 108
...
-----
1 match found in sequence:
A49411 : human leukocyte antigen, HLA-C (alpha 1 and 2 domains) -
(from "PIR 50")
ENTRY   A49411 #type fragment
TITLE   human leukocyte antigen, HLA-C (alpha 1 and 2 domains) -
        human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE     07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change
        02-Jun-1995
ACCESSIONS A49411
REFERENCE
#authors   Falk, K.; Rotzschke, O.; Grahovac, B.; Schendel, D.;
        Stevanovic, S.; Gnau, V.; Jung, G.; Strominger, J.L.;
        Rammensee, H.G.
#journal   Proc. Natl. Acad. Sci. U.S.A. (1993) 90:12005-12009
#title     Allele-specific peptide ligand motifs of HLA-C molecules.
#cross-references MUID:94089758
#accession A49411
#status    preliminary
#molecule_type protein
#residues  1-182 #label FAL
#cross-references NCBI:P141047
#experimental_source Clr cell line
#note      sequence extracted from NCBI backbone
CLASSIFICATION #superfamily class I histocompatibility antigen;
               immunoglobulin homology
SUMMARY          #length 182 #checksum 3873
SEQUENCE
Found using 'seq1' (seq1.key)
...
65  qkykrqaqadvslrnlryynqsagsgsht
    |-----|
    75 84
...
-----
1 match found in sequence:
A35997 : MHC class I histocompatibility antigen HLA-A25 alpha chain
(from "PIR 50")
ENTRY   A35997 #type complete
TITLE   MHC class I histocompatibility antigen HLA-A25 alpha chain
        precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change
        26-Apr-1996
ACCESSIONS A35997
REFERENCE
#authors   Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P.
#journal   Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2833-2837
#title     Rapid cloning of HLA-A,B cDNA by using the polymerase chain
        reaction: frequency and nature of errors produced in
        amplification.
#cross-references MUID:90207291
#accession A35997
#status    preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues  1-364 #label ENN

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#cross-references GB:M32321
CLASSIFICATION #superfamily class I histocompatibility antigen;
               immunoglobulin homology
FEATURE        219-284
SUMMARY          #domain immunoglobulin homology #label IMM
SEQUENCE          #length 364 #molecular-weight 41147 #checksum 1931
Found using 'seq1' (seq1.key)
...
89  rnvkahsgtdreslrnlryynqsagsgsht
    |-----|
    99 108
...
-----
1 match found in sequence:
S03537 : class I histocompatibility antigen ChLA-B1 alpha chain
(from "PIR 50")
ENTRY   S03537 #type complete
TITLE   class I histocompatibility antigen ChLA-B1 alpha chain
        precursor - chimpanzee
ORGANISM #formal_name Pan troglodytes #common_name chimpanzee
DATE     18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change
        26-Apr-1996
ACCESSIONS S03537
REFERENCE
#authors   Mayer, W.E.; Jonker, M.; Klein, D.; Ivanyi, P.; van Severen,
        G.; Klein, J.
#journal   EMBO J. (1988) 7:2765-2774
#title     Nucleotide sequences of chimpanzee MHC class I alleles:
        evidence for trans-species mode of evolution.
#cross-references MUID:89030641
#accession S03537
#molecule_type mRNA
#residues  1-363 #label MAY
#cross-references EMBL:X13115
CLASSIFICATION #superfamily class I histocompatibility antigen;
               immunoglobulin homology
KEYWORDS      transmembrane protein
FEATURE        1-24
                25-363
                25-298
                220-285
                299-338
                339-363
SUMMARY          #length 363 #molecular-weight 40633 #checksum 1865
SEQUENCE
Found using 'seq1' (seq1.key)
...
89  rnmkasatqdrnlrnlryynqsagsgsht
    |-----|
    99 108
...
-----
1 match found in sequence:
S03538 : class I histocompatibility antigen ChLA-B2 alpha chain
(from "PIR 50")
ENTRY   S03538 #type fragment
TITLE   class I histocompatibility antigen ChLA-B2 alpha chain
        precursor - chimpanzee (fragment)
ORGANISM #formal_name Pan troglodytes #common_name chimpanzee
DATE     18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change
        26-Apr-1996
ACCESSIONS S03538

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REFERENCE      S01171
#authors      Mayer, W.E.; Jonker, M.; Klein, D.; Ivanyi, P.; van Seventer,
               G.; Klein, J.
#journal      EMBO J. (1988) 7:2765-2774
#title        Nucleotide sequences of chimpanzee MHC class I alleles:
               evidence for trans-species mode of evolution.
#cross-references MUID:89030641
#accession    S03538
#molecule_type mRNA
##residues    1-358 #label MAY
##cross-references EMBL:X13116
##note        the four residues preceding 1-Ala shown in Fig. 6 were
               apparently misplaced from the sequence of the CHIA-B1
               protein
##note        the authors translated the codon CCG for residue 125 as
               Ser
CLASSIFICATION #superfamily class I histocompatibility antigen;
               immunoglobulin homology
KEYWORDS       transmembrane protein
FEATURE        1-20
               #domain signal sequence (fragment) #label SIG\
               #product class I histocompatibility antigen alpha chain
               #label MAY\
               #domain extracellular #label EXT\
               #domain immunoglobulin homology #label IMM\
               #domain transmembrane #label TM\
               #domain intracellular #label INT\
               #length 358 #checksum 1496
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...
85  qisktnaqtqreslnrlryynqseagshi
    95
    |-----|
    104
...
1 match found in sequence:
B30345 ; MHC class I histocompatibility antigen HLA-Bw52 precursor -
(from "PIR 50")
ENTRY
TITLE        MHC class I histocompatibility antigen HLA-Bw52 precursor -
             human
ORGANISM      #formal_name Homo sapiens #common_name man
DATE          29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change
26-Apr-1996
ACCESSIONS    B30345
REFERENCE      #authors      Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham,
               P.; Kano, K.; Takiguchi, M.
#journal      J. Immunol. (1989) 142:306-311
#title        HLA-B51 and HLA-Bw52 differ by only two amino acids which are
               in the helical region of the alpha-1 domain.
#cross-references MUID:89080265
#accession    B30345
#status       preliminary
#molecule_type DNA
##residues    1-362 #label HAY
CLASSIFICATION #superfamily class I histocompatibility antigen;
               immunoglobulin homology
FEATURE        220-285
               #domain immunoglobulin homology #label IMM
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...
89  qisktnqtqrenrlrlyynqseagsh
    95
    |-----|
    104
...
1 match found in sequence:
JH0541 ; Class I histocompatibility antigen Gogo-B0103 heavy chain
(from "PIR 50")
ENTRY
TITLE        JH0541 #type complete
               class I histocompatibility antigen Gogo-B0103 heavy chain
               precursor - lowland gorilla
ORGANISM      #formal_name Gorilla gorilla #common_name lowland
               gorilla
DATE          30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
26-Apr-1996
ACCESSIONS    JH0541
REFERENCE      #authors      Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
               J. Exp. Med. (1991) 174:1491-1509
#journal      #title        Gorilla class I major histocompatibility complex alleles:
               comparison to human and chimpanzee class I.
#cross-references MUID:92078860
#accession    JH0541
#molecule_type DNA
##residues    1-362 #label LAW
...

```

```

...
99  108
...
1 match found in sequence:
JH0541 ; Class I histocompatibility antigen Gogo-B0103 heavy chain
(from "PIR 50")
ENTRY
TITLE        JH0541 #type complete
               class I histocompatibility antigen Gogo-B0103 heavy chain
               precursor - lowland gorilla
ORGANISM      #formal_name Gorilla gorilla #common_name lowland
               gorilla
DATE          30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
26-Apr-1996
ACCESSIONS    JH0541
REFERENCE      #authors      Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
               J. Exp. Med. (1991) 174:1491-1509
#journal      #title        Gorilla class I major histocompatibility complex alleles:
               comparison to human and chimpanzee class I.
#cross-references MUID:92078860
#accession    JH0541
#molecule_type DNA
##residues    1-362 #label LAW
...
GENETICS
#introns      25/1; 115/1; 207/1; 299/1; 338/1; 349/1
CLASSIFICATION #superfamily class I histocompatibility antigen;
               immunoglobulin homology
FEATURE        1-24
               #domain signal sequence #label SIG\
               #product class I histocompatibility antigen heavy chain,
               Gogo-B0103 #status predicted #label CLA\
               #domain alpha-1 #label AL1\
               #domain alpha-2 #label AL2\
               #domain alpha-3 #label AL3\
               #domain immunoglobulin homology #label IMM\
               #domain intracellular #label INT
               #length 362 #molecular-weight 40248 #checksum 7416
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...
89  qtskaqadtrenrlrlyynqseagsh
    99
    |-----|
    108
...
1 match found in sequence:
JH0539 ; Class I histocompatibility antigen Gogo-B0101 heavy chain
(from "PIR 50")
ENTRY
TITLE        JH0539 #type complete
               class I histocompatibility antigen Gogo-B0101 heavy chain
               precursor - lowland gorilla
ORGANISM      #formal_name Gorilla gorilla #common_name lowland
               gorilla
DATE          30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
26-Apr-1996
ACCESSIONS    JH0539
REFERENCE      #authors      Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
               J. Exp. Med. (1991) 174:1491-1509
#journal      #title        Gorilla class I major histocompatibility complex alleles:
               comparison to human and chimpanzee class I.
#cross-references MUID:92078860
#accession    JH0539
#molecule_type DNA
##residues    1-362 #label LAW
...

```



24

```

89      qiskntqtyreslnrlygynqseagsh
      |-----|
      99
      108
...
-----
1 match found in sequence:
B37028 ; MHC class I histocompatibility antigen HLA-C precursor (clone
ENTRY (from "PIR 50")
TITLE MHC class I histocompatibility antigen HLA-C precursor (clone
      10) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 14-Feb-1992 #sequence_revision 03-Apr-1992 #text_change
06-Sep-1996
ACCESSIONS B37028
REFERENCE A37028
#authors Clanetti, L.; Testa, U.; Scotto, L.; La Valle, R.; Simeone,
A.; Boccoli, G.; Giannella, G.; Peschle, C.; Boncinelli, E.
#journal Immunogenetics (1989) 29:80-91
#title Three new class I HLA alleles: structure of mRNAs and
alternative mechanisms of processing.
#cross-references MUID:89122144
#accession B37028
#status preliminary
#molecule_type mRNA
#residues 1-366 #label CIA
#cross-references GB:M24097
GENETICS
#gene GDB:HLA-C
#cross-references GDB:119311
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
FEATURE
220-285 #domain immunoglobulin homology #label IMM
SUMMARY #length 366 #molecular-weight 40884 #checksum 6126
SEQUENCE
Found using 'seq1' (seq1.key)
...
89      qkykraqtdrvslnrlygynqseagsh
      |-----|
      99
      108
...
-----
1 match found in sequence:
A45880 ; MHC class I histocompatibility antigen HLA-B35 alpha chain
ENTRY (from "PIR 50")
TITLE MHC class I histocompatibility antigen HLA-B35 alpha chain
      precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change
06-Sep-1996
ACCESSIONS A45880; S32754; S32755
REFERENCE A45880
#authors Ooba T.; Hayashi, H.; Karaki, S.; Tanabe, M.; Kano, K.;
Takiguchi, M.
#journal Immunogenetics (1989) 30:76-80
#title The structure of HLA-B35 suggests that it is derived from
HLA-B*58 by two genetic mechanisms.
#accession A45880
#molecule_type DNA
#residues 1-362 #label OOB
#cross-references GB:M28109; GB:M28110; GB:M28111; GB:M28112;
GB:M28113; GB:M28114; GB:M28115
#note this allele is designated B*3501
...
REFERENCE S32754
Steinle, A.; Reinhardt, C.; Noessner, E.; Uchanska-Ziegler,
B.; Ziegler, A.; Schendel, D.J.
#submission submitted to the EMBL Data Library, April 1993
#description Natural microheterogeneity in HLA-B35 alleles influences
peptide-dependent allorecognition by cytotoxic T cells but
not of a peptide-restricted monoclonal antibody.
#accession S32754
#molecule_type mRNA
#residues 1-179, 'R', 181-362 #label STE
#cross-references EMBL:222651
#note this allele is designated B*3508
#accession S32755
#molecule_type mRNA
#residues 1-179, 'R', 181-362 #label ST2
#cross-references EMBL:222643
GENETICS
#gene GDB:HLA-B
#cross-references GDB:120048
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
FEATURE
1-24 #domain signal sequence #status predicted #label SIG\
220-285 #domain immunoglobulin homology #label IMM
SUMMARY #length 362 #molecular-weight 40455 #checksum 285
SEQUENCE
Found using 'seq1' (seq1.key)
...
89      qifkntqtyreslnrlygynqseagsh
      |-----|
      99
      108
...
-----
1 match found in sequence:
D35997 ; MHC class I histocompatibility antigen HLA-B57 alpha chain
ENTRY (from "PIR 50")
TITLE MHC class I histocompatibility antigen HLA-B57 alpha chain
      precursor - human
ALTERNATE_NAMES HLA-B*57
ORGANISM #formal_name Homo sapiens #common_name man
DATE 16-Nov-1990 #sequence_revision 13-Jan-1993 #text_change
06-Sep-1996
ACCESSIONS D35997; S12622; S16774
REFERENCE A35997
#authors Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2833-2837
#title Rapid cloning of HLA-A,B cDNA by using the polymerase chain
reaction: frequency and nature of errors produced in
amplification.
#cross-references MUID:90207291
#accession D35997
#molecule_type mRNA
#residues 1-364 #label ENN
#cross-references GB:M32318
#note this allele is designated B*5701
REFERENCE S12622
Isamat, M.; Girdlestone, J.; Milstein, C.
#journal Nucleic Acids Res. (1990) 18:6702
#title Nucleotide sequence of an HLA-B*57 gene.
#cross-references MUID:91067476
#accession S12622
#molecule_type DNA
#residues 1-362 #label ISA
#cross-references EMBL:X55711
#note this allele is designated B*5701
REFERENCE S16766
Madrizgal, J.A.; Belich, M.P.; Hildebrand, W.H.; Benjamin,

```

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R.J.; Little, A.M.; Zemmour, J.; Ennis, P.D.; Ward, F.E.;
Petzi-Erler, M.L.; Martelli, R.W.; Du Toit, E.D.; Parham, P.
submitted to the EMBL Data Library, August 1991
#description Molecular definition of HLA-A,B antigens of black
populations: Implications for HLA matching and typing in
transplantation.
#accession S16774
##molecule_type mRNA
##residues 1-137,'N',139,'Y',141-179,'R',181-362 ##label MAD
##cross-references EMBL:X61707
##note this allele is designated B*5702 (formerly Bw57.2)
GENETICS
#gene GDB:HLA-B
##cross-references GDB:120048
#map_position 6p21.3-6p21.3
#introns 25/2; 115/1; 207/1; 338/1; 349/1
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
KEYWORDS duplication; glycoprotein; heterodimer; transmembrane
protein; transplantation antigen
FEATURE
1-24 #domain signal sequence #status predicted #label SIG\
220-285 #domain immunoglobulin homology #label IMM
SUMMARY #length 364 #molecular-weight 40451 #checksum 386
SEQUENCE
Found using 'seq1' (seq1.key)
...

1 match found in sequence:
A45834 ; MHC class I histocompatibility antigen HLA-B53 alpha chain
(from "PIR 50")
ENTRY S24433 #type complete
TITLE MHC class I histocompatibility antigen HLA-B53 alpha chain
precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change
06-Sep-1996
ACCESSIONS A45834
REFERENCE A45834
#authors Hayashi, H.; Ooba, T.; Nakayama, S.; Sekimata, M.; Kano, K.;
Takiguchi, M.
#journal Immunogenetics (1990) 32:195-199
#title Allospecificities between HLA-Bw53 and HLA-B35 are generated
by substitution of the residues associated with HLA-Bw4/Bw6
public epitopes.
#accession A45834
##molecule_type DNA
##residues 1-362 ##label HAV
##cross-references GB:M58636; GB:M33574
##note this allele is designated B*5301
GENETICS
#gene GDB:HLA-B
##cross-references GDB:120048
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
heterodimer; transmembrane protein
KEYWORDS
FEATURE
1-24 #domain signal sequence #status predicted #label SIG\
220-285 #domain immunoglobulin homology #label IMM\
110 #binding_site carbohydrate (Asn) (covalent) #status
predicted
SUMMARY #length 362 #molecular-weight 40495 #checksum 9558
SEQUENCE
Found using 'seq1' (seq1.key)

```

```

...
89 qifkntqtyrenlrirlyngseagsh
108

```

```

...
1 match found in sequence:
S24433 ; class I histocompatibility antigen - human
(from "PIR 50")
ENTRY S24433 #type complete
TITLE class I histocompatibility antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
26-Apr-1996
ACCESSIONS S24433
REFERENCE S24027
#authors Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford,
E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.;
Ghim, S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L.
#journal Nature (1992) 357:329-333
#title New recombinant HLA-B alleles in a tribe of South American
Amerindians indicate rapid evolution of MHC class I loci.
#cross-references MUID:92269956
#accession S24433
##status preliminary
##molecule_type mRNA
##residues 1-354 ##label WAT
CLASSIFICATION #superfamily immunoglobulin homology
FEATURE
212-277 #domain immunoglobulin homology #label IMM
SUMMARY #length 354 #molecular-weight 39493 #checksum 5322
SEQUENCE
Found using 'seq1' (seq1.key)

```

```

...
81 qiskntqtyreslnrlryngseagsh
100

```

```

...
1 match found in sequence:
S24440 ; class I histocompatibility antigen - human
(from "PIR 50")
ENTRY S24440 #type complete
TITLE class I histocompatibility antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
26-Apr-1996
ACCESSIONS S24440
REFERENCE S24027
#authors Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford,
E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.;
Ghim, S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L.
#journal Nature (1992) 357:329-333
#title New recombinant HLA-B alleles in a tribe of South American
Amerindians indicate rapid evolution of MHC class I loci.
#cross-references MUID:92269956
#accession S24440
##status preliminary
##molecule_type mRNA
##residues 1-354 ##label WAT
CLASSIFICATION #superfamily immunoglobulin homology
FEATURE
212-277 #domain immunoglobulin homology #label IMM
SUMMARY #length 354 #molecular-weight 39299 #checksum 5584
SEQUENCE

```

Found using 'seq1' (seq1.key)

```
...
81  qisktntqtdreslnlrgyngseagsh
    |-----|
    91 100
...

```

1 match found in sequence:

```
S24027 ; class I histocompatibility antigen - human
(from "PIR 50")
ENTRY      S24027      #type complete
TITLE      class I histocompatibility antigen - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
26-Apr-1996
ACCESSIONS S24027
REFERENCE  #authors
           Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford,
           E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.;
           Ghim, S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L.
           #journal
           Nature (1992) 357:329-333
           #title
           New recombinant HLA-B alleles in a tribe of South American
           Amerindians indicate rapid evolution of MHC class I loci.
           #cross-references MUID:92269956
           #accession S24027
           #status preliminary
           #molecule_type mRNA
           #residues 1-339 #label WAT
CLASSIFICATION #superfamily immunoglobulin homology
FEATURE
216-281
SUMMARY      #domain immunoglobulin homology #label IMM
SEQUENCE     #length 339 #molecular-weight 38073 #checksum 7431
Found using 'seq1' (seq1.key)
...

```

```
85  qisktntqtdreslnlrgyngseagsh
    |-----|
    95 104
...

```

1 match found in sequence:

```
S24437 ; class I histocompatibility antigen - human
(from "PIR 50")
ENTRY      S24437      #type complete
TITLE      class I histocompatibility antigen - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
26-Apr-1996
ACCESSIONS S24437
REFERENCE  #authors
           Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford,
           E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.;
           Ghim, S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L.
           #journal
           Nature (1992) 357:329-333
           #title
           New recombinant HLA-B alleles in a tribe of South American
           Amerindians indicate rapid evolution of MHC class I loci.
           #cross-references MUID:92269956
           #accession S24437
           #status preliminary
           #molecule_type mRNA
           #residues 1-354 #label WAT
CLASSIFICATION #superfamily immunoglobulin homology
FEATURE
212-277
SUMMARY      #domain immunoglobulin homology #label IMM
SEQUENCE     #length 354 #molecular-weight 39395 #checksum 6619

```

SEQUENCE  
Found using 'seq1' (seq1.key)

```
...
81  qisktntqtdreslnlrgyngseagsh
    |-----|
    91 100
...

```

1 match found in sequence:

```
S24438 ; class I histocompatibility antigen - human
(from "PIR 50")
ENTRY      S24438      #type complete
TITLE      class I histocompatibility antigen - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
26-Apr-1996
ACCESSIONS S24438
REFERENCE  #authors
           Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford,
           E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.;
           Ghim, S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L.
           #journal
           Nature (1992) 357:329-333
           #title
           New recombinant HLA-B alleles in a tribe of South American
           Amerindians indicate rapid evolution of MHC class I loci.
           #cross-references MUID:92269956
           #accession S24438
           #status preliminary
           #molecule_type mRNA
           #residues 1-354 #label WAT
CLASSIFICATION #superfamily immunoglobulin homology
FEATURE
212-277
SUMMARY      #domain immunoglobulin homology #label IMM
SEQUENCE     #length 354 #molecular-weight 39403 #checksum 5245
Found using 'seq1' (seq1.key)
...

```

```
81  qisktntqtdreslnlrgyngseagsh
    |-----|
    91 100
...

```

1 match found in sequence:

```
S24434 ; class I histocompatibility antigen - human
(from "PIR 50")
ENTRY      S24434      #type complete
TITLE      class I histocompatibility antigen - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
26-Apr-1996
ACCESSIONS S24434
REFERENCE  #authors
           Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford,
           E.L.; Levine, C.G.; Garber, T.L.; Dogon, A.L.; Lord, C.I.;
           Ghim, S.H.; Troup, G.M.; Hughes, A.L.; Letvin, N.L.
           #journal
           Nature (1992) 357:329-333
           #title
           New recombinant HLA-B alleles in a tribe of South American
           Amerindians indicate rapid evolution of MHC class I loci.
           #cross-references MUID:92269956
           #accession S24434
           #status preliminary
           #molecule_type mRNA
           #residues 1-362 #label WAT
CLASSIFICATION #superfamily immunoglobulin homology
FEATURE
220-285
SUMMARY      #domain immunoglobulin homology #label IMM

```

SUMMARY #length 362 #molecular-weight 40462 #checksum 9855  
 SEQUENCE  
 Found using 'seq1' (seq1.key)  
 ...

89 qifkntqtyrenlrlryynqseagshi  
 99 108  
 ...

-----  
 1 match found in sequence:  
 S24436 : class I histocompatibility antigen - human  
 (from "PIR 50")  
 ENTRY S24436 #type complete  
 TITLE class I histocompatibility antigen - human  
 #formal\_name Homo sapiens #common\_name man  
 ORGANISM  
 DATE 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change  
 26-Apr-1996  
 S24436  
 S24027  
 #accessions  
 #reference  
 #authors  
 #journal  
 #title  
 #cross-references MUIID:92269956  
 #accession S24436  
 #status preliminary  
 #molecule\_type mRNA  
 #residues 1-354 #label WAT  
 CLASSIFICATION #superfamily immunoglobulin homology  
 FEATURE  
 212-277  
 #domain immunoglobulin homology #label IMM  
 SUMMARY #length 354 #molecular-weight 39558 #checksum 5505  
 SEQUENCE  
 Found using 'seq1' (seq1.key)  
 ...

81 qifkntqtyrenlrlryynqseagshi  
 91 100  
 ...

-----  
 1 match found in sequence:  
 S24435 : class I histocompatibility antigen - human  
 (from "PIR 50")  
 ENTRY S24435 #type complete  
 TITLE class I histocompatibility antigen - human  
 #formal\_name Homo sapiens #common\_name man  
 ORGANISM  
 DATE 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change  
 26-Apr-1996  
 S24435  
 S24027  
 #accessions  
 #reference  
 #authors  
 #journal  
 #title  
 #cross-references MUIID:92269956  
 #accession S24435  
 #status preliminary  
 #molecule\_type mRNA  
 #residues 1-362 #label WAT  
 CLASSIFICATION #superfamily immunoglobulin homology  
 FEATURE

220-285 #domain immunoglobulin homology #label IMM  
 SUMMARY #length 362 #molecular-weight 40396 #checksum 249  
 SEQUENCE  
 Found using 'seq1' (seq1.key)  
 ...

89 qifkntqtyrenlrlryynqseagshi  
 99 108  
 ...

-----  
 1 match found in sequence:  
 S24439 : class I histocompatibility antigen - human  
 (from "PIR 50")  
 ENTRY S24439 #type complete  
 TITLE class I histocompatibility antigen - human  
 #formal\_name Homo sapiens #common\_name man  
 ORGANISM  
 DATE 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change  
 26-Apr-1996  
 S24439  
 S24027  
 #accessions  
 #reference  
 #authors  
 #journal  
 #title  
 #cross-references MUIID:92269956  
 #accession S24439  
 #status preliminary  
 #molecule\_type mRNA  
 #residues 1-274 #label WAT  
 CLASSIFICATION #superfamily immunoglobulin homology  
 FEATURE  
 196-261  
 #domain immunoglobulin homology #label IMM  
 SUMMARY #length 274 #molecular-weight 31614 #checksum 836  
 SEQUENCE  
 Found using 'seq1' (seq1.key)  
 ...

65 qifkntqtdreslnlryynqseagsh  
 75 84  
 ...

-----  
 1 match found in sequence:  
 I37519 : MHC class I histocompatibility antigen HLA-B45 alpha chain  
 (from "PIR 50")  
 ENTRY I37519 #type complete  
 TITLE MHC class I histocompatibility antigen HLA-B45 alpha chain  
 #formal\_name Homo sapiens #common\_name man  
 ORGANISM  
 DATE 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change  
 06-Sep-1996  
 I37519; S16772  
 I37476  
 #accessions  
 #reference  
 #authors  
 #journal  
 #title  
 #cross-references MUIID:93056508  
 #accession I37519  
 #status preliminary; translated from GB/EMBL/DBJ  
 #molecule\_type mRNA  
 #residues 1-362 #label RES

```

(from "PIR 50")
ENTRY
  TITLE
  ORGANISM
  DATE
  ACCESSIONS
  REFERENCE
  #authors
  #journal
  #title
  #cross-references MUID:93056508
  #accession 137522
  #status preliminary; translated from GB/EMBL/DBDJ
  #molecule_type mRNA
  #residues 1-362 #label RES
  #cross-references EMBL:X61708; NID:g32190; CDS_PID:g32191
  #gene GDB:HLA-B
  #cross-references GDB:120048
  #map_position gp21.3-6p21.3
  CLASSIFICATION #superfamily class I histocompatibility antigen;
    immunoglobulin homology
  FEATURE
    220-285 #domain immunoglobulin homology #label IMM
    SUMMARY
    SEQUENCE
    Found using 'seq1' (seq1.key)
  ...

89 qifkntqtdreslnrlrnyngseagsh
99
108
...

-----
1 match found in sequence:
I72113 : histocompatibility antigen HLA-C alpha chain (allele Cw
(from "PIR 50")
ENTRY
  TITLE
  ORGANISM
  DATE
  ACCESSIONS
  REFERENCE
  #authors
  #journal
  #title
  #cross-references MUID:89309827
  #accession I72113
  #status preliminary; translated from GB/EMBL/DBDJ
  #molecule_type DNA
  #residues 1-366 #label RES
  #cross-references GB:M28172; NID:g187828; CDS_PID:g386906
  REFERENCE
  #authors Vilches, C.
  #submission submitted to the EMBL Data Library, January 1993
  #accession S32757
  #molecule_type mRNA
  #residues 1-366 #label VIL
  #cross-references EMBL:X70856
  #note this allele is designated Cw*12022
  GENETICS

```

```
#gene
#cross-references GDB:D6S204
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
FEATURE
220-285 #domain immunoglobulin homology #label IMM
SUMMARY #length 366 #molecular-weight 40885 #checksum 4159
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 qkykrqaqadvrlnrlrgyynqseagsh
99 108
|-----|
...
1 match found in sequence:
A30345 : MHC class I histocompatibility antigen HLA-B51 precursor -
(from 'PIR 50')
ENTRY A30345 #type complete
MHC class I histocompatibility antigen HLA-B51 precursor -
human
#formal_name Homo sapiens #common_name man
29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change
06-Sep-1996
ACCESSIONS A30345; I68746
REFERENCE A30345
#authors Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham,
P.; Kano, K.; Takiguchi, M.
#journal J. Immunol. (1989) 142:306-311
#title HLA-B51 and HLA-B*52 differ by only two amino acids which are
in the helical region of the alpha-1 domain.
#cross-references MUID:89080265
#accession A30345
#status preliminary
#molecule_type mRNA
#residues 1-362 #label HAY
REFERENCE I54457
#authors Pohl, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss,
E.H.
#journal Immunogenetics (1989) 29:297-307
#title Allelic variation in HLA-B and HLA-C sequences and the
evolution of the HLA-B alleles.
#cross-references MUID:89233295
#accession I68746
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-362 #label RES
#cross-references GB:L41087; NID:g735900; CDS_PID:g735902
GENETICS
#gene GDB:HLA-B
#cross-references GDB:120048
#map_position 6p21.3-6p21.3
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
FEATURE
220-285 #domain immunoglobulin homology #label IMM
SUMMARY #length 362 #molecular-weight 40566 #checksum 9719
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 qifktntqtyrenlrialryynqseagsh
99 108
|-----|
```

```
1 match found in sequence:
S25536 : MHC class I histocompatibility antigen - rat
(from 'PIR 50')
ENTRY S25536 #type complete
MHC class I histocompatibility antigen - rat
#formal_name Rattus norvegicus #common_name Norway rat
20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
06-Sep-1996
ACCESSIONS I83469; S25536
REFERENCE I60327
#authors Rothmel, E.; Heine, L.; Wurst, W.; Gunther, E.
#journal Immunogenetics (1993) 38:82-91
#title Characterization of a class IB gene of the rat major
histocompatibility complex.
#cross-references MUID:93246303
#accession I83469
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-353 #label RES
#cross-references EMBL:X67504; NID:g56484; CDS_PID:g56485
GENETICS
#note gene name 11/3R
CLASSIFICATION #superfamily class I histocompatibility antigen;
immunoglobulin homology
SUMMARY #length 353 #molecular-weight 39874 #checksum 7572
SEQUENCE
Found using 'seq1' (seq1.key)
...
86 rragdehmfvrslrnlrgyynqseagsh
96 105
|-----|
...
1 match found in sequence:
I59308 : class I histocompatibility antigen - pygmy chimpanzee
(from 'PIR 50')
ENTRY I59308 #type fragment
class I histocompatibility antigen - pygmy chimpanzee
(fragment)
#formal_name Pan paniscus #common_name pygmy chimpanzee,
bonobo
31-May-1996 #sequence_revision 31-May-1996 #text_change
31-May-1996
ACCESSIONS I59308
REFERENCE I59308
#authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
A.L.; Bontrop, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession I59308
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-354 #label RES
#cross-references EMBL:U05575; NID:g454767; CDS_PID:g454768
SUMMARY #length 354 #checksum 3211
SEQUENCE
Found using 'seq1' (seq1.key)
...
81 qickaqatdrenlrialryynqseagsh
91 100
|-----|
```

```

1 match found in sequence:
I80165 ; class I histocompatibility antigen - pygmy chimpanzee
(from "PIR 50")
ENTRY
TITLE      I80165      #type fragment
class I histocompatibility antigen - pygmy chimpanzee
(fragment)
#formal_name Pan paniscus #common_name pygmy chimpanzee,
bonobo
#accession I80165
#molecule_type mRNA
#status preliminary; translated from GB/EMBL/DBJ
#residues 1-354 #label RES
#cross-references EMBL:U05576; NID:g454771; CDS_PID:g454771
#length 354 #checksum 2433
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

81  qickaqatdreslgnryyngsagsh
91  100
-----|
1 match found in sequence:
I80166 ; class I histocompatibility antigen - pygmy chimpanzee
(from "PIR 50")
ENTRY
TITLE      I80166      #type fragment
class I histocompatibility antigen - pygmy chimpanzee
(fragment)
#formal_name Pan paniscus #common_name pygmy chimpanzee,
bonobo
#accession I80166
#molecule_type mRNA
#status preliminary; translated from GB/EMBL/DBJ
#residues 1-354 #label RES
#cross-references EMBL:U05577; NID:g454771; CDS_PID:g454772
#length 354 #checksum 3433
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

81  qiYkaqatdreslgnryyngsagsh
91  100
-----|
1 match found in sequence:
I80167 ; class I histocompatibility antigen - pygmy chimpanzee
(from "PIR 50")
ENTRY
TITLE      I80167      #type fragment
class I histocompatibility antigen - chimpanzee (fragment)
#formal_name Pan troglodytes #common_name chimpanzee
24-May-1996 #sequence_revision 24-May-1996 #text_change
24-May-1996
ACCESSIONS I80167
REFERENCE I59308
#authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
A.L.; Bontrop, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession I80167
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-354 #label RES
#cross-references EMBL:U05578; NID:g454773; CDS_PID:g454774
#length 354 #checksum 3983
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

81  qickaqatdrenlrlyryngsagsh
91  100
-----|
1 match found in sequence:
I80168 ; class I histocompatibility antigen - chimpanzee (fragment)
(from "PIR 50")
ENTRY
TITLE      I80168      #type fragment
class I histocompatibility antigen - chimpanzee (fragment)
#formal_name Pan troglodytes #common_name chimpanzee
24-May-1996 #sequence_revision 24-May-1996 #text_change
24-May-1996
ACCESSIONS I80168
REFERENCE I59308
#authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
A.L.; Bontrop, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession I80168
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-354 #label RES
#cross-references EMBL:U05579; NID:g454775; CDS_PID:g454776
#length 354 #checksum 5067
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

81  rnvkasagtyrenlrlyryfqsagsh
91  100
-----|
1 match found in sequence:
I80169 ; class I histocompatibility antigen - chimpanzee (fragment)
(from "PIR 50")
ENTRY
TITLE      I80169      #type fragment
class I histocompatibility antigen - chimpanzee (fragment)
#formal_name Pan troglodytes #common_name chimpanzee
24-May-1996 #sequence_revision 24-May-1996 #text_change
24-May-1996

```

```

ENTRY
TITLE      I80167      #type fragment
class I histocompatibility antigen - pygmy chimpanzee
(fragment)
#formal_name Pan paniscus #common_name pygmy chimpanzee,
bonobo
#accession I80167
#molecule_type mRNA
#status preliminary; translated from GB/EMBL/DBJ
#residues 1-354 #label RES
#cross-references EMBL:U05578; NID:g454773; CDS_PID:g454774
#length 354 #checksum 3983
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

81  qickaqatdrenlrlyryngsagsh
91  100
-----|
1 match found in sequence:
I80168 ; class I histocompatibility antigen - chimpanzee (fragment)
(from "PIR 50")
ENTRY
TITLE      I80168      #type fragment
class I histocompatibility antigen - chimpanzee (fragment)
#formal_name Pan troglodytes #common_name chimpanzee
24-May-1996 #sequence_revision 24-May-1996 #text_change
24-May-1996
ACCESSIONS I80168
REFERENCE I59308
#authors McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
A.L.; Bontrop, R.E.; Watkins, D.I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title A uniquely high level of recombination at the HLA-B locus.
#cross-references MUID:94286544
#accession I80168
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-354 #label RES
#cross-references EMBL:U05579; NID:g454775; CDS_PID:g454776
#length 354 #checksum 5067
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

81  rnvkasagtyrenlrlyryfqsagsh
91  100
-----|
1 match found in sequence:
I80169 ; class I histocompatibility antigen - chimpanzee (fragment)
(from "PIR 50")
ENTRY
TITLE      I80169      #type fragment
class I histocompatibility antigen - chimpanzee (fragment)
#formal_name Pan troglodytes #common_name chimpanzee
24-May-1996 #sequence_revision 24-May-1996 #text_change
24-May-1996

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```
ACCESSIONS 180169
REFERENCE   159308
#authors    McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
            A.L.; Bontrop, R.E.; Watkins, D.I.
#journal     Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title       A uniquely high level of recombination at the HLA-B locus.
#cross-references EMBL:U05582; NID:g454781; CDS_PID:g454782
#accession    180169
#status      preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues     1-355 #label RES
#cross-references EMBL:U05580; NID:g454777; CDS_PID:g454778
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

81  rnmkasqtdrenlrilryynqseagsh
    91 100
    |-----|
    1 match found in sequence:
    1 match found in sequence:
    (from "PIR 50")
    ENTRY      180171 #type fragment
    TITLE      class I histocompatibility antigen - chimpanzee (fragment)
    ORGANISM    #formal_name Pan troglodytes #common_name chimpanzee
    DATE        24-May-1996 #sequence_revision 24-May-1996 #text_change
    24-May-1996
ACCESSIONS 180171
REFERENCE   159308
#authors    McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
            A.L.; Bontrop, R.E.; Watkins, D.I.
#journal     Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title       A uniquely high level of recombination at the HLA-B locus.
#cross-references EMBL:U05582; NID:g454781; CDS_PID:g454782
#accession    180171
#status      preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues     1-355 #label RES
#cross-references EMBL:U05582; NID:g454781; CDS_PID:g454782
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

81  rnmkasqtdrenlrilryynqseagsh
    91 100
    |-----|
    1 match found in sequence:
    1 match found in sequence:
    (from "PIR 50")
    ENTRY      180175 #type fragment
    TITLE      class I histocompatibility antigen - chimpanzee (fragment)
    ORGANISM    #formal_name Pan troglodytes #common_name chimpanzee
    DATE        24-May-1996 #sequence_revision 24-May-1996 #text_change
    24-May-1996
ACCESSIONS 180175
REFERENCE   159308
#authors    McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes,
            A.L.; Bontrop, R.E.; Watkins, D.I.
#journal     Proc. Natl. Acad. Sci. U.S.A. (1994) 91:5893-5897
#title       A uniquely high level of recombination at the HLA-B locus.
#cross-references EMBL:U05582; NID:g454781; CDS_PID:g454782
```

```
#accession 180175 preliminary; translated from GB/EMBL/DBJ
#status     preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues   1-137 #label RES
#cross-references EMBL:U05586; NID:g454789; CDS_PID:g454790
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

30  qiykaqaqtdrvslgnlryynqseagsh
    40 49
    |-----|
    1 match found in sequence:
    1 match found in sequence:
    (from "PIR 50")
    ENTRY      136957 #type complete
    TITLE      MHC Class II chain - chimpanzee
    ORGANISM    #formal_name Pan troglodytes #common_name chimpanzee
    DATE        02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
    13-Sep-1996
ACCESSIONS 136957
REFERENCE   136956
#authors    Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal     J. Immunol. (1989) 142:3937-3950
#title       Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215
#accession    136957
#status      preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues     1-363 #label RES
#cross-references GB:M24045; NID:g176814; CDS_PID:g176815
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

89  rnvkasqtdrenlrilryynqseagsh
    99 108
    |-----|
    1 match found in sequence:
    1 match found in sequence:
    (from "PIR 50")
    ENTRY      136956 #type fragment
    TITLE      MHC Class II chain - chimpanzee (fragment)
    ORGANISM    #formal_name Pan troglodytes #common_name chimpanzee
    DATE        02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
    13-Sep-1996
ACCESSIONS 136956
REFERENCE   136956
#authors    Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal     J. Immunol. (1989) 142:3937-3950
#title       Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215
#accession    136956
#status      preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues     1-308 #label RES
#cross-references GB:M24044; NID:g176812; CDS_PID:g176813
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
```

```

...
35 qisktnaqtyreslnrlrgyynqseagshi
   45
   |-----|
   54
...
1 match found in sequence:
I36958 ; MHC ChIA chain - chimpanzee (fragment)
ENTRY (from "PIR 50")
TITLE MHC ChIA chain - chimpanzee (fragment)
ORGANISM #formal_name Pan troglodytes #common_name chimpanzee
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
13-Sep-1996
ACCESSIONS I36958
REFERENCE I36956
#authors Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal J. Immunol. (1989) 142:3937-3950
#title Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215
#accession I36958
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-313 #label RES
#cross-references GB:M24046; NID:g176816; CDS_PID:g176817
SUMMARY #length 313 #checksum 5311
SEQUENCE
Found using 'seq1' (seq1.key)
...
36 qkykraqadrvslrlrgyynqsdgsht
   46
   |-----|
   55
...
1 match found in sequence:
I68701 ; cell surface antigen - human (fragment)
ENTRY (from "PIR 50")
TITLE cell surface antigen - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
15-Jun-1996
ACCESSIONS I68701
REFERENCE I54412
#authors Arnot, D.; Lillie, J.W.; Auffray, C.; Kappes, D.; Strominger, J.L.
#journal Immunogenetics (1984) 20:237-252
#title Inter-locus and intra-allelic polymorphisms of HLA class I antigen gene mRNA.
#cross-references MUID:84287690
#accession I68701
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-300 #label RES
#cross-references GB:M27540; NID:g187733; CDS_PID:g386890
SUMMARY #length 300 #checksum 294
SEQUENCE
Found using 'seq1' (seq1.key)
...
27 qiykahagtdreslnrlrgyynqseagshi
   37
   |-----|
   46

```

```

...
1 match found in sequence:
I62045 ; gene HLA B-1517 protein - human
ENTRY (from "PIR 50")
TITLE gene HLA B-1517 protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
13-Sep-1996
ACCESSIONS I62045
REFERENCE I38421
#authors Hilдебранд, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.; Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.; Bias, W.B.; Parham, P.
#journal Tissue Antigens (1994) 43:209-218
#title HLA-B*15: a widespread and diverse family of HLA-B alleles.
#cross-references MUID:94367483
#accession I62045
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-362 #label RES
#cross-references EMBL:U01848; NID:g402676; CDS_PID:g402677
GENETICS
#note gene name HLA B-1517
SUMMARY #length 362 #molecular-weight 40417 #checksum 7730
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 rnmkasaqtyreslnrlrgyynqseagshi
   99
   |-----|
  108
...
1 match found in sequence:
I54298 ; gene HLA-B protein - human
ENTRY (from "PIR 50")
TITLE gene HLA-B protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
ACCESSIONS I54298
REFERENCE I54298
#authors Chertkoff, L.P.; Herrera, M.; Fainboim, L.; Satz, M.L. Hum. Immunol. (1991) 31:153-158
#journal Complete nucleotide sequence of a genomic clone encoding HLA-B*35 isolated from a Caucasian individual of Hispanic origin. Identification of a new variant of HLA-B*35.
#cross-references MUID:91365651
#accession I54298
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-362 #label RES
#cross-references GB:M63454; NID:g187856; CDS_PID:g403145
GENETICS
#note 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
#introns gene name HLA-B
SUMMARY #length 362 #molecular-weight 40564 #checksum 567
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 qifktnqtyreslnrlrgyynqseagshi
   99
   |-----|
  108

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```
-----
1 match found in sequence:
I56034 ; gene HLA-C protein - human
ENTRY (from "PIR 50") I56034 #type complete
TITLE gene HLA-C protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I56034
REFERENCE Takiguchi, M.; Nishimura, I.; Hayashi, H.; Karaki, S.;
#authors Kariyone, A.; Kano, K.
#journal J. Immunol. (1989) 143:1372-1378
#title The structure and expression of genes encoding serologically
#undetectable HLA-C locus antigens.
#cross-references MUID:89309827
#accession I56034
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-366 #label RES
#cross-references GB:M28171; NID:g187826; CDS_PID:g385905
SUMMARY #length 366 #molecular-weight 40855 #checksum 5205
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 qkykrqatdrvslrnyngseagsh
99 108
-----
1 match found in sequence:
I38437 ; HLA B-40011 - human
ENTRY (from "PIR 50") I38437 #type complete
TITLE HLA B-40011 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS I38437
REFERENCE Ways, J.W.; Lawlor, D.A.; Wan, A.M.; Parham, P.
#authors Immunogenetics (1987) 25:323-328
#journal A Transposable Epitope of HLA-B7, B40 Molecules.
#title #cross-references MUID:87192942
#accession I38437
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-362 #label RES
#cross-references EMBL:U03698; NID:g425708; CDS_PID:g425709
SUMMARY #length 362 #molecular-weight 40432 #checksum 8017
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 qiskntqtvyreslrrnyngseagsh
99 108
-----
1 match found in sequence:
I54493 ; HLA-A protein - human
ENTRY (from "PIR 50") I54493 #type complete
TITLE HLA-A protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 08-May-1995 #sequence_revision 21-Jul-1995 #text_change
ACCESSIONS I54493
REFERENCE Herrero, M.J.
#authors
```

```
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS I54493
REFERENCE Little, A.M.; Madrigal, J.A.; Parham, P.
#authors Immunogenetics (1992) 35:41-45
#journal Molecular definition of an elusive third HLA-A9 molecule:
#title HLA-A9.3
#cross-references MUID:92104637
#accession I54493
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-365 #label RES
#cross-references GB:M64741; NID:g187615; CDS_PID:g187616
SUMMARY #length 365 #molecular-weight 40831 #checksum 2547
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 gkvkahsqtdrenlralryngseagsh
99 108
-----
1 match found in sequence:
I54416 ; HLA-AW24 protein - human
ENTRY (from "PIR 50") I54416 #type complete
TITLE HLA-AW24 protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS I54416
REFERENCE N'Guyen, C.; Sodoyer, R.; Trucy, J.; Strachan, T.; Jordan,
#authors B.R.
#journal Immunogenetics (1985) 21:479-489
#title The HLA-AW24 gene: sequence, surroundings and comparison with
#the HLA-A2 and HLA-A3 genes.
#cross-references MUID:85206128
#accession I54416
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-365 #label RES
#cross-references GB:M15497; NID:g187644; CDS_PID:g386877
SUMMARY #length 365 #molecular-weight 40644 #checksum 1573
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 gkvkahsqtdrenlralryngseagsh
99 108
-----
1 match found in sequence:
S52486 ; HLA-B protein alpha chain - human
ENTRY (from "PIR 50") S52486 #type complete
TITLE HLA-B protein alpha chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 08-May-1995 #sequence_revision 21-Jul-1995 #text_change
ACCESSIONS S52486
REFERENCE Herrero, M.J.
#authors
```

```
#submission submitted to the EMBL Data Library, February 1995
#accession S52486
##status preliminary
##molecule_type mRNA
##residues 1-362 ##label HER
##cross-references EMBL:X84725
CLASSIFICATION #superfamily immunoglobulin homology
FEATURE
220-285 #domain immunoglobulin homology #label IMM
SEQUENCE
#length 362 #molecular-weight 40592 #checksum 651
Found using 'seq1' (seq1.key)
```

```
...
89 giskntqtyreslnrlrgyynqseagsh
99
108
```

```
-----
1 match found in sequence:
I62044 ; HLA-B*1514 - human
(from "PIR 50")
ENTRY I62044 #type complete
TITLE HLA-B*1514 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS I62044
REFERENCE I38421
#authors Hildebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.;
Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
Bisio, W.B.; Parham, P.
#journal Tissue Antigens (1994) 43:209-218
#title HLA-B*1514: a widespread and diverse family of HLA-B alleles.
#cross-references MUID:94367483
#accession I62044
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-362 ##label RES
##cross-references GB:L19937; NID:g493167; CDS_PID:g493168
GENETICS
#note gene name HLA-B
SUMMARY #length 362 #molecular-weight 40289 #checksum 9607
SEQUENCE
Found using 'seq1' (seq1.key)
```

```
...
89 giskntqtyreslnrlrgyynqseagsh
99
108
```

```
-----
1 match found in sequence:
I56130 ; HLA-B*5401 - human
(from "PIR 50")
ENTRY I56130 #type complete
TITLE HLA-B*5401 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I56130
REFERENCE I56130
#authors Hildebrand, W.H.; Madrigal, J.A.; Little, A.M.; Parham, P.
#journal J. Immunol. (1992) 148:1155-1162
#title HLA-B*22: a family of molecules with identity to HLA-B7 in
the alpha 1-helix.
#cross-references MUID:92148136
```

```
#accession I56130
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-362 ##label RES
##cross-references GB:M77774; NID:g184116; CDS_PID:g184117
SUMMARY #length 362 #molecular-weight 40380 #checksum 8309
SEQUENCE
Found using 'seq1' (seq1.key)
```

```
...
89 gikykaqtdreslnrlrgyynqseagsh
99
108
```

```
-----
1 match found in sequence:
I72752 ; HLA-B*5501 - human
(from "PIR 50")
ENTRY I72752 #type complete
TITLE HLA-B*5501 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I72752
REFERENCE I56130
#authors Hildebrand, W.H.; Madrigal, J.A.; Little, A.M.; Parham, P.
#journal J. Immunol. (1992) 148:1155-1162
#title HLA-B*22: a family of molecules with identity to HLA-B7 in
the alpha 1-helix.
#cross-references MUID:92148136
#accession I72752
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-362 ##label RES
##cross-references GB:M7778; NID:g184118; CDS_PID:g184119
SUMMARY #length 362 #molecular-weight 40496 #checksum 7953
SEQUENCE
Found using 'seq1' (seq1.key)
```

```
...
89 gikykaqtdreslnrlrgyynqseagsh
99
108
```

```
-----
1 match found in sequence:
I72753 ; HLA-B*5502 - human
(from "PIR 50")
ENTRY I72753 #type complete
TITLE HLA-B*5502 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I72753
REFERENCE I56130
#authors Hildebrand, W.H.; Madrigal, J.A.; Little, A.M.; Parham, P.
#journal J. Immunol. (1992) 148:1155-1162
#title HLA-B*22: a family of molecules with identity to HLA-B7 in
the alpha 1-helix.
#cross-references MUID:92148136
#accession I72753
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-362 ##label RES
##cross-references GB:M7777; NID:g184120; CDS_PID:g184121
SUMMARY #length 362 #molecular-weight 40466 #checksum 8038
SEQUENCE
```

Found using 'seq1' (seq1.key)

```
...
-----|-----|
89  qiylkaqatdreslnrlgynyqseagsh
    (from "PIR 50")
    99 108
```

```
...
-----|-----|
1 match found in sequence:
I72754 ; HLA-B*5601 - human
ENTRY   I72754      #type complete
TITLE   HLA-B*5601 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE    02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS
REFERENCE I72754
#authors Hildebrand, W.H.; Madrigal, J.A.; Little, A.M.; Parham, P.
#journal J. Immunol. (1992) 148:1155-1162
#title   HLA-B*22: a family of molecules with identity to HLA-B7 in
          the alpha 1-helix.
#cross-references MUID:92148136
#accession I72754
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-362 ##label RES
##cross-references GB:M7776; NID:g184122; CDS_PID:g184123
SUMMARY  #length 362 #molecular-weight 40478 #checksum 7910
SEQUENCE
Found using 'seq1' (seq1.key)
```

```
...
-----|-----|
89  qiylkaqatdreslnrlgynyqseagsh
    (from "PIR 50")
    99 108
```

```
...
-----|-----|
1 match found in sequence:
I72755 ; HLA-B*5602 - human
ENTRY   I72755      #type complete
TITLE   HLA-B*5602 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE    02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS
REFERENCE I72755
#authors Hildebrand, W.H.; Madrigal, J.A.; Little, A.M.; Parham, P.
#journal J. Immunol. (1992) 148:1155-1162
#title   HLA-B*22: a family of molecules with identity to HLA-B7 in
          the alpha 1-helix.
#cross-references MUID:92148136
#accession I72755
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-362 ##label RES
##cross-references GB:M7775; NID:g184124; CDS_PID:g184125
SUMMARY  #length 362 #molecular-weight 40460 #checksum 7841
SEQUENCE
Found using 'seq1' (seq1.key)
```

```
...
-----|-----|
89  qiylkaqatdreslnrlgynyqseagsh
    (from "PIR 50")
    99 108
```

```
...
-----|-----|
1 match found in sequence:
I59645 ; HLA-B-6701 - human
ENTRY   I59645      #type complete
TITLE   HLA-B-6701 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE    02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS
REFERENCE I59645
#authors Little, A.M.; Domena, J.D.; Hildebrand, W.H.; Shen, S.Y.;
          Barber, L.D.; Marsh, S.G.; Bias, W.B.; Parham, P.
#journal Tissue Antigens (1994) 43:38-43
#title   HLA-B*67: a member of the HLA-B*6 family that expresses the
          ME1 epitope.
#cross-references MUID:94294981
#accession I59645
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-362 ##label RES
##cross-references GB:I17005; NID:g292147; CDS_PID:g488426
SUMMARY  #length 362 #molecular-weight 40342 #checksum 9311
SEQUENCE
Found using 'seq1' (seq1.key)
```

```
...
-----|-----|
89  qiylkaqatdreslnrlgynyqseagsh
    (from "PIR 50")
    99 108
```

```
...
-----|-----|
1 match found in sequence:
I37521 ; HLA-B*57.2 antigen - human
ENTRY   I37521      #type complete
TITLE   HLA-B*57.2 antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE    02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS
REFERENCE I37521
#authors Madrigal, J.A.; Beilich, M.P.; Hildebrand, W.H.; Benjamin,
          R.J.; Little, A.M.; Zemmour, J.; Ennis, P.D.; Ward, F.E.;
          Petzl-Erler, M.L.; Du Toit, E.D.; Parham, P.
#journal J. Immunol. (1992) 149:3411-3415
#title   Distinctive HLA-A,B antigens of black populations formed by
          interallelic conversion.
#cross-references MUID:93056508
#accession I37521
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-362 ##label RES
##cross-references EMBL:X61707; NID:g32186; CDS_PID:g32187
SUMMARY  #length 362 #molecular-weight 40342 #checksum 7369
SEQUENCE
Found using 'seq1' (seq1.key)
```

```
...
-----|-----|
89  rnmkasadyrenlralryynqseagshi
    (from "PIR 50")
    99 108
```

```

1 match found in sequence:
I54430 ; HLA-Cw1 heavy chain - human
ENTRY (from "PIR 50")
TITLE I54430 #type complete
ORGANISM HLA-Cw1 heavy chain - human
DATE #formal_name Homo sapiens #common_name man
07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS I54430
REFERENCE I54430
#authors Gussow, D.; Rein, R.S.; Meijer, I.; de Hoog, W.; Seemann, G.H.; Hochstenbach, F.M.; Ploegh, H.L.
#journal Immunogenetics (1987) 25:313-322
#title Isolation, expression, and the primary structure of HLA-Cw1 and HLA-Cw2 genes: evolutionary aspects [published erratum appears in Immunogenetics 1988;27(2):158].
#cross-references MUID:87192941
#accession I54430
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-366 #label RES
#cross-references GB:M16272; NID:g187913; CDS_PID:g386912
SUMMARY #length 366 #molecular-weight 40936 #checksum 5559
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qkykrqatdrvslrnlrgyngseagsht
99
108
|-----|
1 match found in sequence:
I54505 ; lymphocyte antigen - human
ENTRY (from "PIR 50")
TITLE I54505 #type complete
ORGANISM lymphocyte antigen - human
DATE #formal_name Homo sapiens #common_name man
07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS I54505
REFERENCE I54505
#authors Kato, N.; Karaki, S.; Kashiwase, K.; Muller, C.; Akaza, T.; Juji, T.; Kano, K.; Takiguchi, M.
#journal Immunogenetics (1993) 37:212-216
#title Molecular analysis of HLA-B39 subtypes.
#cross-references MUID:93131294
#accession I54505
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-362 #label RES
#cross-references GB:M94052; NID:g184163; CDS_PID:g184164
SUMMARY #length 362 #molecular-weight 40328 #checksum 9858
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qickntqtdreslrlrgyngseagsht
99
108
|-----|
1 match found in sequence:
I56149 ; lymphocyte antigen - human
ENTRY (from "PIR 50")
TITLE I56149 #type complete
ORGANISM lymphocyte antigen - human
DATE #formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change

```

```

ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I56149
REFERENCE I56149
#authors Hildebrand, W.H.; Madrigal, J.A.; Bellich, M.P.; Zemmour, J.; Ward, F.E.; Williams, R.C.; Parham, P.
#journal J. Immunol. (1992) 149:3563-3568
#title Serologic cross-reactivities poorly reflect allelic relationships in the HLA-B*2 and HLA-B*21 groups. Dominant epitopes of the alpha 2 helix.
#cross-references MUID:93056529
#accession I56149
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-362 #label RES
#cross-references GB:M84694; NID:g188474; CDS_PID:g188475
SUMMARY #length 362 #molecular-weight 40519 #checksum 616
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qiskntqtyreslrlrgyngseagsht
99
108
|-----|
1 match found in sequence:
I59622 ; lymphocyte antigen - human
ENTRY (from "PIR 50")
TITLE I59622 #type complete
ORGANISM lymphocyte antigen - human
DATE #formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I59622
REFERENCE I59622
#authors Zemmour, J.; Gumperz, J.E.; Hildebrand, W.H.; Ward, F.E.; Marsh, S.G.; Williams, R.C.; Parham, P.
#journal Tissue Antigens (1992) 39:249-257
#title The molecular basis for reactivity of anti-Cw1 and anti-Cw3 alloantisera with HLA-B*46 haplotypes.
#cross-references MUID:93031775
#accession I59622
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-366 #label RES
#cross-references GB:M84171; NID:g187862; CDS_PID:g187863
GENETICS
#note gene name HLA-C
SUMMARY #length 366 #molecular-weight 40950 #checksum 5590
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qkykrqatdrvslrnlrgyngseagsht
99
108
|-----|
1 match found in sequence:
I59651 ; lymphocyte antigen - human
ENTRY (from "PIR 50")
TITLE I59651 #type complete
ORGANISM lymphocyte antigen - human
DATE #formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change

```

```
02-Jul-1996
ACCESSIONS 159651
REFERENCE 159651
#authors Arnett, K.L.; Adams, E.J.; Domena, J.D.; Parham, P.
#journal Tissue Antigens (1994) 44:318-321
#title Structure of a novel subtype of B7 (B*0705) isolated from a Chinese individual.
#cross-references MUID:95184211
#accession 159651
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-362 #label RES
#cross-references GB:I33922; NID:g520834; CDS_PID:g520835
SUMMARY #length 362 #molecular-weight 40473 #checksum 8201
SEQUENCE
Found using 'seq1' (seq1.key)

...

89 qlykaqgtdreslnrlrgyynqseagsh
99 108
|-----|

1 match found in sequence:
159655 : lymphocyte antigen - human
(from "PIR 50")
ENTRY I59655 #type complete
TITLE lymphocyte antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I59655
REFERENCE Adams, E.J.; Little, A.
#authors Tissue Antigens (1995) 46:204-205
#journal Identification of a novel HLA-B allele (B*4008) in a patient with leukemia.
#title
#accession 159655
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-362 #label RES
#cross-references GB:I41353; NID:gl041064; CDS_PID:gl041065
GENETICS
#note gene name HLA-B*4008
SUMMARY #length 362 #molecular-weight 40550 #checksum 417
SEQUENCE
Found using 'seq1' (seq1.key)

...

89 qifktntqtyreslnrlrgyynqseagsh
99 108
|-----|

1 match found in sequence:
159655 : lymphocyte antigen - human
(from "PIR 50")
ENTRY I59655 #type complete
TITLE lymphocyte antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS I59655
REFERENCE Bellich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.; Petzl-Erler, M.L.; Parham, P.
#authors Nature (1992) 357:326-329
#journal Unusual HLA-B alleles in two tribes of Brazilian Indians.
#title
#cross-references MUID:92269955
#accession I59655
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-362 #label RES
#cross-references GB:M84381; NID:g187711; CDS_PID:g187712
GENETICS
#note gene name HLA-B
SUMMARY #length 362 #molecular-weight 40514 #checksum 187
SEQUENCE
Found using 'seq1' (seq1.key)

...

89 qifktntqtyreslnrlrgyynqseagshi
99 108
|-----|

1 match found in sequence:
161905 : lymphocyte antigen - human
(from "PIR 50")
ENTRY I61905 #type complete
TITLE lymphocyte antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS I61905
REFERENCE Bellich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.; Petzl-Erler, M.L.; Parham, P.
#authors Nature (1992) 357:326-329
#journal Unusual HLA-B alleles in two tribes of Brazilian Indians.
#title
#cross-references MUID:92269955
#accession I61905
```

```
#title Unusual HLA-B alleles in two tribes of Brazilian Indians.
#cross-references MUID:92269955
#accession 161903
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-362 #label RES
#cross-references GB:M84380; NID:g187707; CDS_PID:g187708
GENETICS
#note gene name HLA-B
SUMMARY #length 362 #molecular-weight 40362 #checksum 286
SEQUENCE
Found using 'seq1' (seq1.key)

...

89 qfktntqtyreslnrlrgyynqseagsh
99 108
|-----|

1 match found in sequence:
161904 : lymphocyte antigen - human
(from "PIR 50")
ENTRY I61904 #type complete
TITLE lymphocyte antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS I61904
REFERENCE Bellich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.; Petzl-Erler, M.L.; Parham, P.
#authors Nature (1992) 357:326-329
#journal Unusual HLA-B alleles in two tribes of Brazilian Indians.
#title
#cross-references MUID:92269955
#accession I61904
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-362 #label RES
#cross-references GB:M84381; NID:g187711; CDS_PID:g187712
GENETICS
#note gene name HLA-B
SUMMARY #length 362 #molecular-weight 40514 #checksum 187
SEQUENCE
Found using 'seq1' (seq1.key)

...

89 qfktntqtyreslnrlrgyynqseagshi
99 108
|-----|

1 match found in sequence:
161905 : lymphocyte antigen - human
(from "PIR 50")
ENTRY I61905 #type complete
TITLE lymphocyte antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS I61905
REFERENCE Bellich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.; Petzl-Erler, M.L.; Parham, P.
#authors Nature (1992) 357:326-329
#journal Unusual HLA-B alleles in two tribes of Brazilian Indians.
#title
#cross-references MUID:92269955
#accession I61905
```

```

##status      preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues    1-362 ##label RES
##cross-references GB:M84383; NID:g187715; CDS_PID:g187716
GENETICS
#note
SUMMARY      gene name HLA-B
SEQUENCE     #length 362 #molecular-weight 40430 #checksum 193
Found using 'seq1' (seq1.key)
...
89  qiskntqtyreslnrlrgyynqseagsh
    |-----|
    99 108
...
1 match found in sequence:
I61906 : lymphocyte antigen - human
ENTRY   I61906 #type complete
TITLE   lymphocyte antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS
REFERENCE I61906
#authors  Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.;
           Williams, R.C.; Luz, R.; Petz1-Erlor, M.L.; Parham, P.
#journal  Nature (1992) 357:326-329
#title    Unusual HLA-B alleles in two tribes of Brazilian Indians.
#cross-references MUID:92269955
#accession I61906
##status  preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-362 ##label RES
##cross-references GB:M84384; NID:g187717; CDS_PID:g187718
GENETICS
#note
SUMMARY      gene name HLA-B
SEQUENCE     #length 362 #molecular-weight 40600 #checksum 393
Found using 'seq1' (seq1.key)
...
89  qiskntqtyreslnrlrgyynqseagshi
    |-----|
    99 108
...
1 match found in sequence:
I61907 : lymphocyte antigen - human
ENTRY   I61907 #type complete
TITLE   lymphocyte antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS
REFERENCE I61907
#authors  Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.;
           Williams, R.C.; Luz, R.; Petz1-Erlor, M.L.; Parham, P.
#journal  Nature (1992) 357:326-329
#title    Unusual HLA-B alleles in two tribes of Brazilian Indians.
#cross-references MUID:92269955
#accession I61907
##status  preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-362 ##label RES

```

```

##cross-references GB:M84385; NID:g187719; CDS_PID:g187720
GENETICS
#note
SUMMARY      gene name HLA-B
SEQUENCE     #length 362 #molecular-weight 40374 #checksum 351
Found using 'seq1' (seq1.key)
...
89  qifkntqtyreslnrlrgyynqseagsh
    |-----|
    99 108
...
1 match found in sequence:
I68850 : lymphocyte antigen - human
ENTRY   I68850 #type complete
TITLE   lymphocyte antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS
REFERENCE I68850
#authors  Kato, N.; Karaki, S.; Kashiwase, K.; Muller, C.; Akaza, T.;
           Juji, T.; Kano, K.; Takiguchi, M.
#journal  Immunogenetics (1993) 37:212-216
#title    Molecular analysis of HLA-B39 subtypes.
#cross-references MUID:93131294
#accession I68850
##status  preliminary; translated from GB/EMBL/DBDJ
##molecule_type DNA
##residues 1-362 ##label RES
##cross-references GB:M94053; NID:g184165; CDS_PID:g184166
SUMMARY      #length 362 #molecular-weight 40327 #checksum 132
SEQUENCE
Found using 'seq1' (seq1.key)
...
89  qiskntqtdreslnrlrgyynqseagsh
    |-----|
    99 108
...
1 match found in sequence:
I81231 : lymphocyte antigen - human
ENTRY   I81231 #type complete
TITLE   lymphocyte antigen - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS
REFERENCE I81231
#authors  Zemmour, J.; Gumperz, J.E.; Hildebrand, W.H.; Ward, F.E.;
           Marsh, S.G.; Williams, R.C.; Parham, P.
#journal  Tissue Antigens (1992) 39:249-257
#title    The molecular basis for reactivity of anti-Cw1 and anti-Cw3
           . alloantisera with HLA-B46 haplotypes.
##cross-references MUID:93031775
#accession I81231
##status  preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-366 ##label RES
##cross-references GB:M84172; NID:g187864; CDS_PID:g187865
GENETICS
#note
SUMMARY      gene name HLA-C
           #length 366 #molecular-weight 40784 #checksum 5046

```



## SEQUENCE

Found using 'seq1' (seq1.key)

...

89 qkykrqatdrvslnrlrgyynqseagsh  
99 108

...

-----

1 match found in sequence:

I81232 ; lymphocyte antigen - human  
(from "PIR 50")  
ENTRY I81232 #type complete  
TITLE lymphocyte antigen - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change  
ACCESSIONS I81232  
REFERENCE I59622  
#authors Zemmour, J.; Gumperz, J.E.; Hildebrand, W.H.; Ward, F.E.;  
Marsh, S.G.; Williams, R.C.; Parham, P.  
#journal Tissue Antigens (1992) 39:249-257  
#title The molecular basis for reactivity of anti-Cw1 and anti-Cw3  
alloantisera with HLA-B46 haplotypes.  
#cross-references MUID:93031775  
#accession I81232 preliminary; translated from GB/EMBL/DBJ  
#status  
#molecule\_type mRNA  
#residues 1-366 #label RES  
#cross-references GB:M84174; NID:g187868; CDS\_PID:g187869  
GENETICS  
#note gene name HLA-C  
SUMMARY #length 366 #molecular-weight 40772 #checksum 5003  
SEQUENCE  
Found using 'seq1' (seq1.key)

...

89 qkykrqatdrvslnrlrgyynqseagsh  
99 108

...

-----

1 match found in sequence:

I81233 ; lymphocyte antigen - human  
(from "PIR 50")  
ENTRY I81233 #type complete  
TITLE lymphocyte antigen - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change  
ACCESSIONS I81233  
REFERENCE I59631  
#authors Theller, G.; Pando, M.; Delfino, J.M.; Takiguchi, M.; Satz,  
M.L.  
#journal Tissue Antigens (1993) 41:143-147  
#title Isolation and characterization of two new functional subtypes  
of HLA-B35.  
#cross-references MUID:93303752  
#accession I81233 preliminary; translated from GB/EMBL/DBJ  
#status  
#molecule\_type mRNA  
#residues 1-362 #label RES  
#cross-references GB:L04695; NID:g187892; CDS\_PID:g187893  
GENETICS  
#note gene name HLA-B  
SUMMARY #length 362 #molecular-weight 40497 #checksum 885  
SEQUENCE

Found using 'seq1' (seq1.key)

...

89 qifkntqtqreslnrlrgyynqseagsh  
99 108

...

-----

1 match found in sequence:

I81239 ; lymphocyte antigen - human  
(from "PIR 50")  
ENTRY I81239 #type complete  
TITLE lymphocyte antigen - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change  
ACCESSIONS I81239  
REFERENCE I59645  
#authors Little, A.M.; Domena, J.D.; Hildebrand, W.H.; Shen, S.Y.;  
Barber, L.D.; Marsh, S.G.; Bias, W.B.; Parham, P.  
#journal Tissue Antigens (1994) 43:38-43  
#title HLA-B\*67: a member of the HLA-B16 family that expresses the  
ME1 epitope.  
#cross-references MUID:94294981  
#accession I81239 preliminary; translated from GB/EMBL/DBJ  
#status  
#molecule\_type DNA  
#residues 1-362 #label RES  
#cross-references GB:L41628; NID:g773174; CDS\_PID:g773175  
GENETICS  
#note gene name HLA-B\*40012  
SUMMARY #length 362 #molecular-weight 40432 #checksum 8017  
SEQUENCE  
Found using 'seq1' (seq1.key)

...

89 qiskntqtqreslnrlrgyynqseagsh  
99 108

...

-----

1 match found in sequence:

I84488 ; lymphocyte antigen - human  
(from "PIR 50")  
ENTRY I84488 #type complete  
TITLE lymphocyte antigen - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change  
ACCESSIONS I84488  
REFERENCE I38464  
#authors Adams, E.J.; Martinez-Naves, E.; Arnett, K.L.; Little, A.M.;  
Ryan, D.B.; Parham, P.  
#journal Tissue Antigens (1995) 45:18-26  
#title HLA-B16 antigens: sequence of the ST-16 antigen, further  
definition of two B38 subtypes and evidence for convergent  
evolution of B\*3902.  
#cross-references MUID:95242308  
#accession I84488 preliminary; translated from GB/EMBL/DBJ  
#status  
#molecule\_type mRNA  
#residues 1-362 #label RES  
#cross-references GB:L36318; NID:g793946; CDS\_PID:g793947  
GENETICS  
#note gene name HLA-B-3905  
SUMMARY #length 362 #molecular-weight 40376 #checksum 719  
SEQUENCE

Found using 'seq1' (seq1.key)

```
...
89  qickntqtyreslnrlrgyngseagsh
    |-----|
    99  108
...
```

```
-----
1 match found in sequence:
I84490 : lymphocyte antigen - human
(from "PIR 50")
ENTRY      I84490      #type complete
TITLE      lymphocyte antigen - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS  I84490
REFERENCE   I38518
#authors    Browning, M.J.; Madrigal, J.A.; Krausa, P.; Kowalski, H.;
              Allsopp, C.E.; Little, A.M.; Turner, S.; Adams, E.J.;
              Arnett, K.L.; Bodmer, W.F.; Bodmer, J.G.; Parham, P.
#journal     Tissue Antigens (1995) 45:177-187
#title       The HLA-A,B,C genotype of the class I negative cell line
              Daudi reveals novel HLA-A and -B alleles.
#cross-references MUID:95282145
#accession   I84490
#status      preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues    1-362 #label RES
#cross-references GB:I33923; NID:g520836; CDS_PID:g520837
GENETICS
#note        gene name HLA-A10-B38
SUMMARY      #length 362 #molecular-weight 40355 #checksum 8277
SEQUENCE
Found using 'seq1' (seq1.key)
...
```

```
89  rmkasaqtyrenlrlaryngseagsh
    |-----|
    99  108
...
```

```
-----
1 match found in sequence:
I59654 : major histocompatibility complex class I - human
(from "PIR 50")
ENTRY      I59654      #type complete
TITLE      major histocompatibility complex class I - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS  I59654
REFERENCE   I59654
#authors    Lienert, K.; McCluskey, J.; Bennett, G.; Fowler, C.; Russ, G.
#journal     Tissue Antigens (1995) 45:12-17
#title       HLA class I variation in Australian aborigines:
              characterization of allele B*1521.
#cross-references MUID:95242307
#accession   I59654
#status      preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues    1-362 #label RES
#cross-references GB:I32862; NID:g487817; CDS_PID:g487818
GENETICS
#note        gene name HLA-B
SUMMARY      #length 362 #molecular-weight 40354 #checksum 9646
SEQUENCE
Found using 'seq1' (seq1.key)
...
```

```
...
89  qickntqtyreslnrlrgyngseagsh
    |-----|
    99  108
...
-----
1 match found in sequence:
I37120 : MCH class I HLA-B*5104 - human
(from "PIR 50")
ENTRY      I37120      #type complete
TITLE      MCH class I HLA-B*5104 - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
ACCESSIONS  I37120
REFERENCE   I37120
#authors    Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.;
              Williams, R.C.; Luz, R.; Petzi-Erler, M.L.; Parham, P.
#journal     Nature (1992) 357:326-329
#title       Unusual HLA-B alleles in two tribes of Brazilian Indians.
#cross-references MUID:92269955
#accession   I37120
#status      preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues    1-362 #label RES
#cross-references EMBL:Z15143; NID:g28234; CDS_PID:g28235
SUMMARY      #length 362 #molecular-weight 40560 #checksum 9591
SEQUENCE
Found using 'seq1' (seq1.key)
...
```

```
89  qifkntqtyrenlrlaryngseagsh
    |-----|
    99  108
...
```

```
-----
1 match found in sequence:
I79640 : MHC cell surface antigen - human (fragment)
(from "PIR 50")
ENTRY      I79640      #type fragment
TITLE      MHC cell surface antigen - human (fragment)
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS  I79640
REFERENCE   I59188
#authors    Bronson, S.K.; Pei, J.; Taillon-Miller, P.; Chorney, M.J.;
              Geraghty, D.E.; Chaplin, D.D.
#journal     Proc. Natl. Acad. Sci. U.S.A. (1991) 88:1676-1680
#title       Isolation and characterization of yeast artificial chromosome
              clones linking the HLA-B and HLA-C loci.
#cross-references MUID:91156671
#accession   I79640
#status      preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues    1-181 #label RES
#cross-references GB:M59865; NID:g187802; CDS_PID:g187803
GENETICS
#introns     90/1
#note        gene name HLA-C
SUMMARY      #length 181 #checksum 2853
SEQUENCE
Found using 'seq1' (seq1.key)
...
```

```
64 qkykrqagtdrvslrnlrgyynqseahtl
74
83
|-----|
1 match found in sequence:
159188 : MHC cell surface glycoprotein - human (fragment)
(from "PIR 50")
ENTRY I59188 #type fragment
TITLE MHC cell surface glycoprotein - human (fragment)
#formal_name Homo sapiens #common_name man
ORGANISM 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
DATE 02-Jul-1996
ACCESSIONS I59188
REFERENCE I59188
#authors Bronson, S.K.; Pei, J.; Taillon-Miller, P.; Chorney, M.J.;
Geraghty, D.E.; Chaplin, D.D.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:1676-1680
#title Isolation and characterization of yeast artificial chromosome
clones linking the HLA-B and HLA-C loci.
#cross-references MUID:91156671
#accession I59188
#status preliminary; translated from GB/EMBL/DBBJ
#molecule_type DNA
#residues 1-181 #label RES
#cross-references GB:M59841; NID:gl87697; CDS_PID:gl87698
GENETICS
#introns 90/1
#note gene name HLA-B
SUMMARY #length 181 #checksum 2981
SEQUENCE
Found using 'seq1' (seq1.key)
...

64 qifktntqtdreslrlrgyynqseagsh
74
83
|-----|
1 match found in sequence:
179639 : MHC cell surface glycoprotein - human (fragment)
(from "PIR 50")
ENTRY I79639 #type fragment
TITLE MHC cell surface glycoprotein - human (fragment)
#formal_name Homo sapiens #common_name man
ORGANISM 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
DATE 02-Aug-1996
ACCESSIONS I79639
REFERENCE I79639
#authors Bronson, S.K.; Pei, J.; Taillon-Miller, P.; Chorney, M.J.;
Geraghty, D.E.; Chaplin, D.D.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:1676-1680
#title Isolation and characterization of yeast artificial chromosome
clones linking the HLA-B and HLA-C loci.
#cross-references MUID:91156671
#accession I79639
#status preliminary; translated from GB/EMBL/DBBJ
#molecule_type DNA
#residues 1-181 #label RES
#cross-references GB:M59840; NID:gl87758; CDS_PID:gl87759
GENETICS
#introns 90/1
#note gene name HLA-B
SUMMARY #length 181 #checksum 3163
SEQUENCE
Found using 'seq1' (seq1.key)
...

64 qickntqtdreslrlrgyynqseagsh
74
83
|-----|
1 match found in sequence:
138464 : MHC class I antigen - human
(from "PIR 50")
ENTRY I38464 #type complete
TITLE MHC class I antigen - human
#formal_name Homo sapiens #common_name man
ORGANISM 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
DATE 06-Sep-1996
ACCESSIONS I38464
REFERENCE I38464
#authors Adams, E.J.; Martinez-Naves, E.; Arnett, K.L.; Little, A.M.;
Tyan, D.B.; Parham, P.
#journal Tissue Antigens (1995) 45:18-26
#title HLA-B*16 antigens: sequence of the ST-16 antigen, further
definition of two B38 subtypes and evidence for convergent
evolution of B*3902.
#cross-references MUID:95242308
#accession I38464
#status preliminary; translated from GB/EMBL/DBBJ
#molecule_type mRNA
#residues 1-362 #label RES
#cross-references EMBL:U04243; NID:g458659; CDS_PID:g458660
GENETICS
#note gene name HLA-B
SUMMARY #length 362 #molecular-weight 40327 #checksum 132
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qiskntqtdreslrlrgyynqseagsh
99
108
|-----|
1 match found in sequence:
138860 : MHC class I antigen - human (fragment)
(from "PIR 50")
ENTRY I38860 #type fragment
TITLE MHC class I antigen - human (fragment)
#formal_name Homo sapiens #common_name man
ORGANISM 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
DATE 15-Jun-1996
ACCESSIONS I38860
REFERENCE I38860
#authors Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.;
Rickards, O.; De Stefano, G.; Watkins, D.I.
#journal Immunogenetics (1995) 42:19-27
#title HLA-B alleles of the Cayapa of Ecuador: new B39 and B15
alleles.
#cross-references MUID:95317819
#accession I38860
#status preliminary; translated from GB/EMBL/DBBJ
#molecule_type DNA
#residues 1-137 #label RES
#cross-references EMBL:U14756; NID:g930328; CDS_PID:g930329
SUMMARY #length 137 #checksum 5553
SEQUENCE
Found using 'seq1' (seq1.key)
...

|-----|
```



```

I38507 ; MHC class I histocompatibility antigen - human
(from "PIR 50")
ENTRY      I38507      #type complete
TITLE      MHC class I histocompatibility antigen - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS I38507
REFERENCE  #authors      Cereb, N.; Choi, J.W.; Lee, S.; Maye, P.; Kong, Y.; Yang, S.Y.
#journal   Tissue Antigens (1994) 44:193-195
#title     Identification of two new HLA-C alleles, Cw*1203 and Cw*1402,
            from the sequence analysis of seven HLA homozygous cell
            lines carrying HLA-C blank.
#cross-references MUID:95141286
#accession I38507      preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-366 #label RES
#cross-references EMBL:U06695; NID:g469540; CDS_PID:g469541
GENETICS
#note      gene name HLA-Cw
SUMMARY    #length 366 #molecular-weight 40915 #checksum 4194
SEQUENCE
Found using 'seq1' (seq1.key)

...

89  qkykrqaqadrslrnlrgyngseagsht
    |-----|
    99      108
...

1 match found in sequence:
I38508 ; MHC class I histocompatibility antigen - human
(from "PIR 50")
ENTRY      I38508      #type complete
TITLE      MHC class I histocompatibility antigen - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS I38508
REFERENCE  #authors      Cereb, N.; Choi, J.W.; Lee, S.; Maye, P.; Kong, Y.; Yang, S.Y.
#journal   Tissue Antigens (1994) 44:193-195
#title     Identification of two new HLA-C alleles, Cw*1203 and Cw*1402,
            from the sequence analysis of seven HLA homozygous cell
            lines carrying HLA-C blank.
#cross-references MUID:95141286
#accession I38508      preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-366 #label RES
#cross-references EMBL:U06696; NID:g469542; CDS_PID:g469543
GENETICS
#note      gene name HLA-Cw
SUMMARY    #length 366 #molecular-weight 40915 #checksum 4194
SEQUENCE
Found using 'seq1' (seq1.key)

...

89  qkykrqaqadrslrnlrgyngseagsht
    |-----|
    99      108

```

```

1 match found in sequence:
I38509 ; MHC class I histocompatibility antigen - human (fragment)
(from "PIR 50")
ENTRY      I38509      #type fragment
TITLE      MHC class I histocompatibility antigen - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
ACCESSIONS I38509
REFERENCE  #authors      Cereb, N.; Choi, J.W.; Riu, K.Z.; Yang, S.Y.
#journal   Tissue Antigens (1994) 44:271-273
#title     HLA-B*5105, a newly identified B51 IEF variant.
#cross-references MUID:95176331
#accession I38509      preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-273 #label RES
#cross-references EMBL:U06697; NID:g469544; CDS_PID:g469545
GENETICS
#note      gene name HLA-B
SUMMARY    #length 273 #checksum 6533
SEQUENCE
Found using 'seq1' (seq1.key)

...

64  qifkntqtyrenlrnlrgyngseagsht
    |-----|
    74      83
...

1 match found in sequence:
I56065 ; MHC class I HLA-B - human
(from "PIR 50")
ENTRY      I56065      #type complete
TITLE      MHC class I HLA-B - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I56065
REFERENCE  #authors      Sekimata, M.; Hiraiwa, M.; Andrien, M.; Dupont, E.; Karaki, S.; Yamamoto, J.; Kano, K.; Takiguchi, M.
#journal   J. Immunol. (1990) 144:3228-3233
#title     Allodeterminants and evolution of a novel HLA-B5 CREG
            antigen, HLA-B SNA.
#cross-references MUID:90217537
#accession I56065      preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues  1-362 #label RES
#cross-references GB:M33573; NID:gi187745; CDS_PID:gi187746
SUMMARY    #length 362 #molecular-weight 40478 #checksum 9585
SEQUENCE
Found using 'seq1' (seq1.key)

...

89  qifkntqtdreslnlrnlrgyngseagsht
    |-----|
    99      108
...

1 match found in sequence:
I37135 ; MHC class I HLA-Cw*0803 - human (fragment)
(from "PIR 50")
ENTRY      I37135      #type fragment
TITLE      MHC class I HLA-Cw*0803 - human (fragment)

```

```

ORGANISM #formal_name Homo sapiens #common_name man
DATE 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
ACCESSIONS I37135
REFERENCE I37120
#authors Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.;
Williams, R.C.; Luz, R.; Petzl-Erler, M.L.; Parham, P.
#journal Nature (1992) 357:326-329
#title Unusual HLA-B alleles in two tribes of Brazilian Indians.
#cross-references MUID:92269955
#accession I37135
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-366 #label RES
#cross-references EMBL:Z15144; NID:g28356; CDS_PID:g28357
SUMMARY #length 366 #checksum 5311
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qkykrqatdrslrnlrgyngseagsh
99
108
...
-----
1 match found in sequence:
I68747 ; MHC class I lymphocyte antigen - human (fragment)
(from "PIR 50")
ENTRY I68747 #type fragment
TITLE MHC class I lymphocyte antigen - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS I68747
REFERENCE I54457
#authors Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss,
E.H.
#journal Immunogenetics (1989) 29:297-307
#title Allelic variation in HLA-B and HLA-C sequences and the
evolution of the HLA-B alleles.
#cross-references MUID:89233295
#accession I68747
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-350 #label RES
#cross-references GB:M28204; NID:g576472; CDS_PID:g576473
SUMMARY #length 350 #checksum 636
SEQUENCE
Found using 'seq1' (seq1.key)
...

77 qifktntqdrslrnlrgyngseagsh
87
96
...
-----
1 match found in sequence:
I68748 ; MHC class I lymphocyte antigen - human (fragment)
(from "PIR 50")
ENTRY I68748 #type fragment
TITLE MHC class I lymphocyte antigen - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS I68748
REFERENCE I54457
#authors Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss,
E.H.
#journal Immunogenetics (1989) 29:297-307
#title Allelic variation in HLA-B and HLA-C sequences and the
evolution of the HLA-B alleles.
#cross-references MUID:89233295
#accession I68748
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-290 #label RES
#cross-references GB:M28207; NID:g576478; CDS_PID:g576479
SUMMARY #length 290 #checksum 415
SEQUENCE
Found using 'seq1' (seq1.key)
...

13 qnykrqqaqdrslrnlrgyngseagsh
23
32
...
-----
1 match found in sequence:
I56133 ; MHC class I protein - human
(from "PIR 50")
ENTRY I56133 #type complete
TITLE MHC class I protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I56133
REFERENCE I56133
#authors Zemmour, J.; Little, A.M.; Schendel, D.J.; Parham, P.
#journal J. Immunol. (1992) 148:1941-1948
#title The HLA-A,B 'negative' mutant cell line C1R expresses a novel
HLA-B*35 allele, which also has a point mutation in the
translation initiation codon.
#cross-references MUID:92176661

```

```

E.H.
Immunogenetics (1989) 29:297-307
#journal Allelic variation in HLA-B and HLA-C sequences and the
#title evolution of the HLA-B alleles.
#cross-references MUID:89233295
#accession I68748
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-358 #label RES
#cross-references GB:M28203; NID:g576474; CDS_PID:g576475
SUMMARY #length 358 #checksum 2000
SEQUENCE
Found using 'seq1' (seq1.key)
...

85 qiskntqtreslrlrgyngseagsh
95
104
...
-----
1 match found in sequence:
I68750 ; MHC class I lymphocyte antigen - human (fragment)
(from "PIR 50")
ENTRY I68750 #type fragment
TITLE MHC class I lymphocyte antigen - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS I68750
REFERENCE I54457
#authors Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss,
E.H.
#journal Immunogenetics (1989) 29:297-307
#title Allelic variation in HLA-B and HLA-C sequences and the
evolution of the HLA-B alleles.
#cross-references MUID:89233295
#accession I68750
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-290 #label RES
#cross-references GB:M28207; NID:g576478; CDS_PID:g576479
SUMMARY #length 290 #checksum 415
SEQUENCE
Found using 'seq1' (seq1.key)
...

13 qnykrqqaqdrslrnlrgyngseagsh
23
32
...
-----
1 match found in sequence:
I56133 ; MHC class I protein - human
(from "PIR 50")
ENTRY I56133 #type complete
TITLE MHC class I protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I56133
REFERENCE I56133
#authors Zemmour, J.; Little, A.M.; Schendel, D.J.; Parham, P.
#journal J. Immunol. (1992) 148:1941-1948
#title The HLA-A,B 'negative' mutant cell line C1R expresses a novel
HLA-B*35 allele, which also has a point mutation in the
translation initiation codon.
#cross-references MUID:92176661

```

```

#accession I56133
##status preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-362 #label RES
##cross-references GB:M81798; NID:g187858; CDS_PID:g187859
SUMMARY #length 362 #molecular-weight 40515 #checksum 9947
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qifkntqttyreslnrlrgyngseagsh
108
...

-----
1 match found in sequence:
I62041; MHC HLA-B71 - human (fragment)
(from "PIR 50")
ENTRY I62041 #type complete
TITLE MHC HLA B71 - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS I54308
REFERENCE I54308
#authors Rodriguez, S.G.; Johnson, A.H.; Hurley, C.K.
#journal Hum. Immunol. (1993) 37:192-194
#title Molecular characterization of HLA-B71 from an African
#cross-references MUID:94064392
#accession I54308
##status preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-350 #label RES
##cross-references GB:L07950; NID:g307236; CDS_PID:g307237
GENETICS
#note gene name HLA-B
SUMMARY #length 350 #checksum 7005
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qifkntqttyreslnrlrgyngseagsh
108
...

-----
1 match found in sequence:
I62041; MHC HLA-B cell surface glycoprotein - human
(from "PIR 50")
ENTRY I62041 #type complete
TITLE MHC HLA-B cell surface glycoprotein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS I62041
REFERENCE I38421
#authors Hildebrand, W.H.; Domene, J.D.; Shen, S.Y.; Lau, M.;
Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
Bias, W.B.; Parham, P.
#journal Tissue Antigens (1994) 43:209-218
#title HLA-B15: a widespread and diverse family of HLA-B alleles.
#cross-references MUID:94367483
#accession I62041
##status preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-362 #label RES
##cross-references GB:L11603; NID:g493164; CDS_PID:g493165

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##cross-references GB:L11666; NID:g493160; CDS_PID:g493161
GENETICS
#note gene name HLA-B
SUMMARY #length 362 #molecular-weight 40433 #checksum 9515
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qifkntqttyreslnrlrgyngseagsh
108
...

-----
1 match found in sequence:
I62042; MHC HLA-B cell surface glycoprotein - human
(from "PIR 50")
ENTRY I62042 #type complete
TITLE MHC HLA-B cell surface glycoprotein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS I62042
REFERENCE I38421
#authors Hildebrand, W.H.; Domene, J.D.; Shen, S.Y.; Lau, M.;
Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
Bias, W.B.; Parham, P.
#journal Tissue Antigens (1994) 43:209-218
#title HLA-B15: a widespread and diverse family of HLA-B alleles.
#cross-references MUID:94367483
#accession I62042
##status preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-362 #label RES
##cross-references GB:L11604; NID:g493162; CDS_PID:g493163
GENETICS
#note gene name HLA-B
SUMMARY #length 362 #molecular-weight 40449 #checksum 161
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qifkntqttyreslnrlrgyngseagsh
108
...

-----
1 match found in sequence:
I62043; MHC HLA-B cell surface glycoprotein - human
(from "PIR 50")
ENTRY I62043 #type complete
TITLE MHC HLA-B cell surface glycoprotein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSIONS I62043
REFERENCE I38421
#authors Hildebrand, W.H.; Domene, J.D.; Shen, S.Y.; Lau, M.;
Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
Bias, W.B.; Parham, P.
#journal Tissue Antigens (1994) 43:209-218
#title HLA-B15: a widespread and diverse family of HLA-B alleles.
#cross-references MUID:94367483
#accession I62043
##status preliminary; translated from GB/EMBL/DBDJ
##molecule_type mRNA
##residues 1-362 #label RES
##cross-references GB:L11603; NID:g493164; CDS_PID:g493165

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```

GENETICS
#note
SUMMARY
#length 362 #molecular-weight 40245 #checksum 9348
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qisktntqtyreslnlrgyynqseqsht
108
-----|
1 match found in sequence:
I61859 ; MHC HLA-B14 chain - human
(from "PIR 50")
ENTRY
I61859 #type complete
TITLE MHC HLA-B14 chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
ACCESSIONS
REFERENCE I61859
#authors Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal J. Immunol. (1989) 142:3937-3950
#title Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215
#accession I61859
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-362 #label RES
#cross-references GB:M24040; NID:g187807; CDS_PID:g386898
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qifkntqtyrenlrialryynqseqsht
108
-----|
1 match found in sequence:
I61859 ; MHC HLA-B14 chain - human
(from "PIR 50")
ENTRY
I61859 #type complete
TITLE MHC HLA-B14 chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
ACCESSIONS
REFERENCE I61859
#authors Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal J. Immunol. (1989) 142:3937-3950
#title Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215
#accession I61859
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-362 #label RES
#cross-references GB:M24040; NID:g187807; CDS_PID:g386898
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

```

```

...
89 qicknttdreslnlrgyynqseqsht
108
-----|
1 match found in sequence:
I61860 ; MHC HLA-B18 chain - human
(from "PIR 50")
ENTRY
I61860 #type complete
TITLE MHC HLA-B18 chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
ACCESSIONS
REFERENCE I61860
#authors Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal J. Immunol. (1989) 142:3937-3950
#title Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215
#accession I61860
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-362 #label RES
#cross-references GB:M24039; NID:g187809; CDS_PID:g386899
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qiskntqtyreslnlrgyynqseqsht
108
-----|
1 match found in sequence:
I54463 ; MHC HLA-B38 chain - human (fragment)
(from "PIR 50")
ENTRY
I54463 #type fragment
TITLE MHC HLA-B38 chain - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
07-Jun-1996
ACCESSIONS
REFERENCE I54463
#authors Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.;
Weiss, E.; Schmidt, H.
#journal Immunogenetics (1989) 30:200-207
#title Genetic and serological heterogeneity of the supertypic HLA-B
#cross-references MUID:89379286
#accession I54463
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-274 #label RES
#cross-references GB:M29864; NID:g187674; CDS_PID:g187675
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

65 qickntqtyrenlrialryynqseqsht
75
-----|

```



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-----
1 match found in sequence:
168774 : MHC HLA-B39 chain - human (fragment)
ENTRY (from "PIR 50")
TITLE MHC HLA-B39 chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS 168774
REFERENCE #authors
#journal
#title
#cross-references MUID:89379286
#accession 168774
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-274 #label RES
#cross-references GB:M29865; NID:gl87676; CDS_PID:gl87677
SUMMARY #length 274 #checksum 1017
SEQUENCE
Found using 'seq1' (seq1.key)
...

65 qickntqtdreslnrlygynqseagsh
75
84
|-----|
1 match found in sequence:
154314 : MHC HLA-B39N - human
ENTRY (from "PIR 50")
TITLE MHC HLA-B39N - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS 154314
REFERENCE #authors
#journal
#title
#cross-references MUID:95189597
#accession 154314
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-362 #label RES
#cross-references GB:L22649; NID:g437369; CDS_PID:g437370
GENETICS
#note
#length 362 #molecular-weight 40344 #checksum 8904
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qickntqtdreslnrlygynqseagsh
99
108
|-----|
1 match found in sequence:
161864 : MHC HLA-Bw41 chain - human
ENTRY (from "PIR 50")
TITLE MHC HLA-Bw41 chain - human
```

```
-----
1 match found in sequence:
154418 : MHC HLA-B7 heavy chain precursor - human
ENTRY (from "PIR 50")
TITLE MHC HLA-B7 heavy chain precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change
ACCESSIONS 154418
REFERENCE #authors
#journal
#title
#cross-references MUID:85287366
#accession 154418
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-361 #label RES
#cross-references GB:M16102; NID:gl87693; CDS_PID:g307217
SUMMARY #length 361 #molecular-weight 40366 #checksum 8200
SEQUENCE
Found using 'seq1' (seq1.key)
...

88 qikykaqatdreslnrlygynqseagsh
98
107
|-----|
1 match found in sequence:
184431 : MHC HLA-B8 chain - human
ENTRY (from "PIR 50")
TITLE MHC HLA-B8 chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS 184431
REFERENCE #authors
#journal
#title
#cross-references MUID:89235215
#accession 184431
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-362 #label RES
#cross-references GB:M24036; NID:gl84169; CDS_PID:g386775
SUMMARY #length 362 #molecular-weight 40331 #checksum 7954
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qifktntqtdreslnrlygynqseagsh
99
108
|-----|
1 match found in sequence:
161864 : MHC HLA-Bw41 chain - human
ENTRY (from "PIR 50")
TITLE MHC HLA-Bw41 chain - human
```

```

ORGANISM      #formal_name Homo sapiens #common_name man
DATE          02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
              02-Jul-1996
ACCESSIONS    I61864
REFERENCE     I36956
#authors      Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal      J. Immunol. (1989) 142:3937-3950
#title        Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215
#accession    I61864
##status      preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues    1-362 ##label RES
##cross-references GB:M24035; NID:g187820; CDS_PID:g386903
SUMMARY       #length 362 #molecular-weight 40539 #checksum 9199
SEQUENCE
Found using 'seq1' (seq1.key)
...
89      qsktntqtdreslnrlrgyynqseqsht
          99
          |-----|
          108
...
1 match found in sequence:
I61865 ; MHC HLA-B*42 chain - human
(from "PIR 50")
ENTRY     I61865      #type complete
TITLE     MHC HLA-B*42 chain - human
ORGANISM  #formal_name Homo sapiens #common_name man
DATE      02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSION I61865
REFERENCE I36956
#authors  Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal  J. Immunol. (1989) 142:3937-3950
#title    Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215
#accession I61865
##status      preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues    1-362 ##label RES
##cross-references GB:M24034; NID:g187822; CDS_PID:g386904
SUMMARY       #length 362 #molecular-weight 40333 #checksum 8952
SEQUENCE
Found using 'seq1' (seq1.key)
...
89      qlykaqatdreslnrlrgyynqseqsht
          99
          |-----|
          108
...
1 match found in sequence:
I61863 ; MHC HLA-B*46 - human
(from "PIR 50")
ENTRY     I61863      #type complete
TITLE     MHC HLA-B*46 - human
ORGANISM  #formal_name Homo sapiens #common_name man
DATE      02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSION I61863
REFERENCE I36956
#authors  Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal  J. Immunol. (1989) 142:3937-3950
#title    Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215

```

```

#accession    I61863
##status      preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues    1-362 ##label RES
##cross-references GB:M24033; NID:g187818; CDS_PID:g307227
SUMMARY       #length 362 #molecular-weight 40440 #checksum 9144
SEQUENCE
Found using 'seq1' (seq1.key)
...
89      qkykrqatdreslnrlrgyynqseqsht
          99
          |-----|
          108
...
1 match found in sequence:
I61862 ; MHC HLA-B*65 chain - human
(from "PIR 50")
ENTRY     I61862      #type complete
TITLE     MHC HLA-B*65 chain - human
ORGANISM  #formal_name Homo sapiens #common_name man
DATE      02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSION I61862
REFERENCE I36956
#authors  Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
#journal  J. Immunol. (1989) 142:3937-3950
#title    Diversity and diversification of HLA-A,B,C alleles.
#cross-references MUID:89235215
#accession I61862
##status      preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues    1-362 ##label RES
##cross-references GB:M24032; NID:g187816; CDS_PID:g386902
SUMMARY       #length 362 #molecular-weight 40342 #checksum 8952
SEQUENCE
Found using 'seq1' (seq1.key)
...
89      qickntqtdreslnrlrgyynqseqsht
          99
          |-----|
          108
...
1 match found in sequence:
I84486 ; transmembrane glycoprotein - human
(from "PIR 50")
ENTRY     I84486      #type complete
TITLE     transmembrane glycoprotein - human
ORGANISM  #formal_name Homo sapiens #common_name man
DATE      02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
ACCESSION I84486
REFERENCE I38421
#authors  Hildebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.;
          Terasaki, P.I.; Bunce, M.; Marsh, S.G.; Guttridge, M.G.;
          Bias, W.B.; Parham, P.
#journal  Tissue Antigens (1994) 43:209-218
#title    HLA-B*51: a widespread and diverse family of HLA-B alleles.
#cross-references MUID:94367483
#accession I84486
##status      preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues    1-362 ##label RES
##cross-references GB:L15005; NID:g493154; CDS_PID:g493155
GENETICS
#note       gene name HLA-B*1513

```

```
SUMMARY          #length 362  #molecular-weight 40378  #checksum 9463
SEQUENCE
Found using 'seq1' (seq1.key)
...

89  qiskntdtqyrenlxrlalryynqseagshi
    |-----|
    99 108
...

1 match found in sequence:
155665 : H-2D cell surface glycoprotein - mouse (fragment)
(from "PIR 50")
ENTRY      I55665      #type fragment
TITLE      H-2D cell surface glycoprotein - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
DATE      26-Jul-1996
ACCESSIONS I55665
REFERENCE  I55665
#authors   Hemmi, S.; Gelliebter, J.; Zeff, R.A.; Melvold, R.W.;
           Nathenson, S.G.
#journal   J. Exp. Med. (1988) 168:2319-2335
#title     Three spontaneous H-2D-b mutants are generated by genetic
           micro-recombination (gene conversion) events: Impact on the
           H-2-restricted immune responsiveness.
#cross-references MUID:89067835
#accession I55665
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-337 ##label RES
#cross-references GB:M37680; NID:g293733; CDS_PID:g293734
GENETICS
#introns   90/1; 182/1; 274/1; 313/1; 324/1; 337/1
#note      gene name H-2D
#length    337  #checksum 9859
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

64  qkqkqeqqfvrslrnllyynqsgsht
    |-----|
    74  83
...

1 match found in sequence:
170693 : H-2D cell surface glycoprotein - mouse (fragment)
(from "PIR 50")
ENTRY      I70693      #type fragment
TITLE      H-2D cell surface glycoprotein - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
DATE      02-Aug-1996
ACCESSIONS I70693
REFERENCE  I55665
#authors   Hemmi, S.; Gelliebter, J.; Zeff, R.A.; Melvold, R.W.;
           Nathenson, S.G.
#journal   J. Exp. Med. (1988) 168:2319-2335
#title     Three spontaneous H-2D-b mutants are generated by genetic
           micro-recombination (gene conversion) events: Impact on the
           H-2-restricted immune responsiveness.
#cross-references MUID:89067835
#accession I70693
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-337 ##label RES
#cross-references GB:M37681; NID:g293735; CDS_PID:g293736
```

```
GENETICS
#introns   90/1; 182/1; 274/1; 313/1; 324/1; 337/1
#note      gene name H-2D
#length    337  #checksum 9564
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

64  qkqkqeqqfvrslrnllyynqsgsht
    |-----|
    74  83
...

1 match found in sequence:
155961 : MHC class I H2D-P protein - mouse
(from "PIR 50")
ENTRY      I55961      #type complete
TITLE      MHC class I H2D-P protein - mouse
#formal_name Mus musculus #common_name house mouse
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
DATE      26-Jul-1996
ACCESSIONS I55961
REFERENCE  I55961
#authors   Schepart, B.S.; Takahashi, H.; Cozad, K.M.; Murray, R.;
           Orato, K.; Appella, E.; Frelinger, J.A.
#journal   J. Immunol. (1986) 136:3489-3495
#title     The nucleotide sequence and comparative analysis of the H2D-P
           class I H-2 gene.
#cross-references MUID:86169714
#accession I55961
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues  1-368 ##label RES
#cross-references GB:M12381; NID:g199418; CDS_PID:g387454
GENETICS
#introns   22/1; 112/1; 204/1; 296/1; 335/1; 346/1; 359/1
#note      gene name H-2D
#length    368  #molecular-weight 41342  #checksum 7387
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...

86  qnakdheqsfvrslrnllyynqsgsht
    |-----|
    96 105
...

1 match found in sequence:
157814 : MHC class I-alpha - mouse
(from "PIR 50")
ENTRY      I57814      #type complete
TITLE      MHC class I-alpha - mouse
#formal_name Mus musculus #common_name house mouse
02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
DATE      02-Aug-1996
ACCESSIONS I57814
REFERENCE  I57814
#authors   Hildebrand, W.H.; Horton, R.M.; Pease, L.R.; Martinko, J.M.
#journal   Mol. Immunol. (1992) 29:61-69
#title     Nucleotide sequence analysis of H-2D(f) and the spontaneous
           in vivo H-2D(fm2) mutation.
#cross-references MUID:92114891
#accession I57814
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues  1-365 ##label RES
#cross-references GB:M86502; NID:g199306; CDS_PID:g199307
GENETICS
```

```

#note
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 qkagqeqwfrvnlrllgynqsgsht
108
|-----|
1 match found in sequence:
I56002 ; MHC H-2D-b protein - mouse
(from "PIR 50")
ENTRY
I56002 #type complete
TITLE MHC H-2D-b protein - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
23-Aug-1996
ACCESSIONS
REFERENCE I56002; I48323
#authors
Watts, S.; Vogel, J.M.; Harriman, W.D.; Itoh, T.; Stauss,
H.J.; Goodenow, R.S.
#journal
J. Immunol. (1987) 139:3878-3885
#title
DNA sequence analysis of the C3H H-2Kk and H-2Dk loci.
Evolutionary relationships to H-2 genes from four other
mouse strains.
#cross-references MUID:88060499
#accession
I56002
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-362 #label RES
#cross-references GB:M18523; NID:g199413; CDS_PID:g387452
REFERENCE I48323
#authors
Joly, E.; Oldstone, M.B.
#journal
Immunogenetics (1991) 34:62-65
#title
Manufacture of a functional cDNA for the H-2Db molecule using
a retroviral shuttle vector.
#cross-references MUID:91310091
#accession
I48323
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-362 #label RE2
#cross-references EMBL:X52490; NID:g50671; CDS_PID:g50672
GENETICS
#introns 25/1; 115/1; 207/1; 299/1; 338/1; 349/1; 362/1
#note
gene name D(b) gene
#length 362 #molecular-weight 40836 #checksum 8991
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...
89 qkagqeqwfrvnlrllgynqsgsht
108
|-----|
1 match found in sequence:
I54531 ; MHC class I protein - rat (fragment)
(from "PIR 50")
ENTRY
I54531 #type fragment
TITLE MHC class I protein - rat (fragment)
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
02-Aug-1996
ACCESSIONS
REFERENCE I54531

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#authors
Salgar, S.K.; Sawai, H.; Kunz, H.W.; Gill, T.J.
#journal
Immunogenetics (1994) 39:447
#title
Cloning and expression of the rat class I MHC gene RT1.AL.
#cross-references MUID:94245290
#accession
I54531
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-370 #label RES
#cross-references GB:L26224; NID:g710562; CDS_PID:g710563
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...
92 qkagqeqwfrvnlrllgynqsgsht
102
|-----|
1 match found in sequence:
I54554 ; MHC class I RT1.Aw3 protein - rat
(from "PIR 50")
ENTRY
I54554 #type complete
TITLE MHC class I RT1.Aw3 protein - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
02-Aug-1996
ACCESSIONS
REFERENCE I54554
#authors
Salgar, S.K.; Kunz, H.W.; Gill, T.J.
#journal
Immunogenetics (1995) 42:244-253
#title
Nucleotide sequence and structural analysis of the rat RT1.Eu
and RT1.Aw31 genes, and of genes related to RT1.O and
RT1.C.
#cross-references MUID:95402978
#accession
I54554
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-360 #label RES
#cross-references GB:L40363; NID:g992566; CDS_PID:g992567
SUMMARY
SEQUENCE
Found using 'seq1' (seq1.key)
...
79 qkagqeqwfrvnlrllgynqsgsht
98
|-----|
1 match found in sequence:
I68771 ; MHC RT16 protein - rat (fragment)
(from "PIR 50")
ENTRY
I68771 #type fragment
TITLE MHC RT16 protein - rat (fragment)
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
02-Aug-1996
ACCESSIONS
REFERENCE I68771
#authors
Mauxion, F.; Sobczak, J.; Kress, M.
#journal
Immunogenetics (1989) 29:397-401
#title
Characterization of five distinct cDNA clones encoding for
class I RT1 antigens.
#cross-references MUID:89277428
#accession
I68771
#status preliminary; translated from GB/EMBL/DBJ

```

```

##molecule_type mRNA
##residues 1-296 #label RES
##cross-references GB:M24023; NID:g2054449; CDS_PID:g205449
SUMMARY #length 296 #checksum 9381
SEQUENCE
Found using 'seq1' (seq1.key)
...

15 qkagneqnyrvslrnlrgyngseagsh
25 34
|-----|
1 match found in sequence:
S07113 ; class I histocompatibility antigen Ch39 alpha chain -
ENTRY (from "PIR 50")
TITLE class I histocompatibility antigen Ch39 alpha chain -
ORGANISM chimpanzee
#formal_name Pan troglodytes #common_name chimpanzee
DATE 01-Dec-1993 #sequence_revision 01-Dec-1993 #text_change
ACCESSIONS S07113
REFERENCE S06424
#authors Lawlor, D.A.; Ward, F.E.; Ennis, P.D.; Jackson, A.P.; Parham,
P.
#journal Nature (1988) 335:268-271
#title HLA-A and B polymorphisms predate the divergence of humans
and chimpanzees.
#cross-references MUID:88319000
#accession S07113
#status preliminary
##residues 1-363 #label LAW
SUMMARY #length 363 #molecular-weight 40540 #checksum 610
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 rnvksaqtdrenlrnlrgyngseagsh
99 108
|-----|
1 match found in sequence:
S06001 ; HLA-B*0703, a B7 variant
ENTRY (from "PIR 50")
TITLE HLA-B*0703 (class I) protein - human
ORGANISM Homo sapiens
#formal_name Homo sapiens #common_name man
DATE 20-Jul-1996 #sequence_revision 20-Jul-1996 #text_change
ACCESSIONS S06001
REFERENCE S06001
#authors Bergmans, A.M.C.; Tijssen, H.; Lardy, N.; Reekers, P.
#journal Hum. Immunol. (1993) 38:159-162
#title Complete nucleotide sequence of HLA-B*0703, a B7 variant
(B*0703).
#accession S06001
#status preliminary
##residues 1-362 #label BER
##cross-references EMBL:X64454
SUMMARY #length 362 #molecular-weight 40529 #checksum 9704
SEQUENCE
Found using 'seq1' (seq1.key)
...

89 qiykntqtdreslrnlrgyngseagsh
99 108
|-----|
1 match found in sequence:
S03687 ; Class I histocompatibility antigen H-2DP alpha chain - Mouse
ENTRY (from "PIR 50")
TITLE Class I histocompatibility antigen H-2DP alpha chain - Mouse
(fragment)
ORGANISM Mus musculus #common_name house mouse
DATE 21-Nov-1993 #sequence_revision 21-Nov-1993 #text_change
ACCESSIONS S03687
REFERENCE S03687
#authors Murray, R.; Pederson, K.; Prosser, H.; Muller, D.; Hutchison
III, C.A.; Frelinger, J.A.
#journal Nucleic Acids Res. (1988) 16:9761-9773
#title Random oligonucleotide mutagenesis: application to a large
protein coding sequence of a major histocompatibility
complex class I gene, H-2DP.
#cross-references MUID:89041564
#accession S03687
#status preliminary
##residues 1-90 #label MUR
SUMMARY #length 90 #checksum 1722
SEQUENCE
Found using 'seq1' (seq1.key)
...

65 qnakdheqsfvslrnlrgyngskg
75 84
|-----|
1 match found in sequence:
1A02_PANTR ; CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-5 ALPHA CHAIN PRECURSOR
ENTRY (from "Swiss-Prot 34")
ID 1A02_PANTR STANDARD; PRT; 362 AA.
AC P16210;
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-5 ALPHA CHAIN PRECURSOR.
OS PAN TROGLODYTES (CHIMPANZEE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90201944.
RA LAWLOR D.A.; WARREN E.; WARD F.E.; PARHAM P.;
RL IMMUNOL. REV. 113:147-185(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
DR EMBL; M30679; G176825; -.
DR HSSP; P03989; 1HSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
A-5 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
CYTOPLASMIC TAIL.

```

FT DISULFID 125 188 BY SIMILARITY.  
 FT DISULFID 227 283 BY SIMILARITY.  
 FT CARBOHYD 110 110 BY SIMILARITY.  
 SQ SEQUENCE 362 AA; 40487 MW; 9/E6CE8A CRC32;  
 Found using 'seq1' (seq1.key)

...

89 qisktnaqtyreslnrlgynyqseagsh  
 99 108

...

1 match found in sequence:  
 1A23\_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) ALPHA CHAIN  
 (from "Swiss-Prot 34")  
 ID 1A23\_HUMAN STANDARD; PRT; 365 AA.  
 AC P30447;  
 DT 01-APR-1993 (REL. 25, CREATED)  
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) ALPHA CHAIN  
 DE PRECURSOR.  
 GN HLAA.

OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]

RP SEQUENCE FROM N.A. (A\*2301).  
 RX MEDLINE: 92104637.

RA LITTLE A.-M., MADRIGAL J.A., PARHAM P.;  
 RL IMMUNOGENETICS 35:41-45(1992).

CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 THE IMMUNE SYSTEM.

CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 MICROGLOBULIN).

CC -!- POLYMORPHISM: THE ONLY ALLELE OF A-23 KNOWN IS A\*2301 WHICH IS  
 SHOWN HERE.  
 DR EMBL; M64742; G187618; -.  
 DR HSP; P01892; LHG.

DR MIM; 142800; -.

DR PROSITE: PS00290; IG\_MHC.

KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.

FT SIGNAL 1 24

FT CHAIN 25 365 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 ALPHA CHAIN A-23(A9).  
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.  
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.  
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.  
 FT DOMAIN 299 308 CONNECTING PEPTIDE.

FT TRANSMEM 309 332 CYTOPLASMIC TAIL.

FT DOMAIN 333 365 BY SIMILARITY.

FT CARBOHYD 110 110 BY SIMILARITY.

FT DISULFID 125 188 BY SIMILARITY.

FT DISULFID 227 283 BY SIMILARITY.

SQ SEQUENCE 365 AA; 40732 MW; B1C21094 CRC32;

Found using 'seq1' (seq1.key)

...

89 gkvkhsqtdrenlrlyryngseagsh  
 99 108

...

1 match found in sequence:  
 1A24\_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) ALPHA CHAIN  
 (from "Swiss-Prot 34")  
 ID 1A24\_HUMAN STANDARD; PRT; 365 AA.

AC P05534; P30448; P30449;  
 DT 01-NOV-1988 (REL. 09, CREATED)  
 DT 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) ALPHA CHAIN  
 DE PRECURSOR (AW-24).  
 GN HLAA.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]

RP SEQUENCE FROM N.A. (A\*2401).  
 RX MEDLINE: 85206128.

RA N'GUYEN C., SODOYER R., TRUCY J., STRACHAN T., JORDAN B.R.;

RL IMMUNOGENETICS 21:479-489(1985).

RN [2]

RP REVISIONS (A\*2401).  
 RA JORDAN B.R.;

RL SUBMITTED (XXX-1988) TO EMBL/GENBANK/DBJ DATA BANKS.

RN [3]

RP SEQUENCE FROM N.A. (A\*2402/A\*2403).  
 RX MEDLINE: 92104637.

RA LITTLE A.-M., MADRIGAL J.A., PARHAM P.;

RL IMMUNOGENETICS 35:41-45(1992).

RN [4]

RP SEQUENCE FROM N.A. (A\*2402).  
 RX MEDLINE: 92269955.

RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,

RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;

RL NATURE 357:326-329(1992).

RN [5]

RP SEQUENCE OF 26-206 FROM N.A.

RA GAO X., MCCLUSKEY J.;

RL SUBMITTED (JAN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.

CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 THE IMMUNE SYSTEM.

CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 MICROGLOBULIN).

CC -!- POLYMORPHISM: THE FOLLOWING ALLELES OF A-24 ARE KNOWN: A\*2401,  
 A\*2401 AND A\*2403. THE SEQUENCE SHOWN IS THAT OF A\*2401.

DR EMBL; M15497; G386877; -.

DR EMBL; M64740; G187614; -.

DR EMBL; M64741; G187616; -.

DR EMBL; U19733; G624267; -.

DR EMBL; U18987; G624267; JOINED.

DR HSP; P01892; LHG.

DR MIM; 142800; -.

DR PROSITE: PS00290; IG\_MHC.

KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; POLYMORPHISM.

FT SIGNAL 1 24

FT CHAIN 25 365 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 ALPHA CHAIN A-24(A9).

FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.

FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.

FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.

FT DOMAIN 299 308 CONNECTING PEPTIDE.

FT TRANSMEM 309 332 CYTOPLASMIC TAIL.

FT DOMAIN 333 365 BY SIMILARITY.

FT CARBOHYD 110 110 BY SIMILARITY.

FT DISULFID 125 188 BY SIMILARITY.

FT DISULFID 227 283 BY SIMILARITY.

FT VARIANT 5 5 G -> A (IN A\*2402 AND A\*2403).

FT VARIANT 180 180 Q -> W (IN REF. 5).

FT VARIANT 190 191 DG -> EW (IN A\*2403).

FT VARIANT 206 206 A -> T (IN A\*2402, A\*2403 AND REF. 5).

SQ SEQUENCE 365 AA; 40644 MW; DE23D06E CRC32;

Found using 'seq1' (seq1.key)

...

89 gkvkhsqtdrenlrlyryngseagsh  
 99 108

```

...
-----
1 match found in sequence:
1A25_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-25(A-10) ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1A25_HUMAN STANDARD; PRT; 365 AA.
AC P18462;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-25(A-10) ALPHA CHAIN
DE PRECURSOR.
DE HLA.
GN HLA.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
[1]
RN SEQUENCE FROM N.A. (A*2501).
RX ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -!- POLYMORPHISM: THE ONLY ALLELE OF A-25 KNOWN IS A*2501 WHICH IS
CC SHOWN HERE.
DR EMBL; M32321; G307225; -.
DR PIR; A35997; A35997.
DR HSP; P01891; 1HSB.
DR MIN; 142800; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 365
FT FT
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN A-25(A-10).
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT DOMAIN 309 332
FT DOMAIN 333 365
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT CYTOPLASMIC TAIL.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
SQ SEQUENCE 365 AA; 41218 MW; 131A8F20 CRC32;
Found using 'seq1' (seq1.key)
...
89 rnvkhsqtdreslrlyynqsgsht
|-----|
99 108
...
-----
1 match found in sequence:
1A32_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-32(AW-19) ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1A32_HUMAN STANDARD; PRT; 365 AA.
AC P10314;
DT 01-MAR-1989 (REL. 10, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-32(AW-19) ALPHA CHAIN
DE PRECURSOR.
DE HLA.
GN HLA.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
[1]
RN SEQUENCE FROM N.A. (A*2501).
RX ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -!- POLYMORPHISM: THE ONLY ALLELE OF A-25 KNOWN IS A*2501 WHICH IS
CC SHOWN HERE.
DR EMBL; M32321; G307225; -.
DR PIR; A35997; A35997.
DR HSP; P01891; 1HSB.
DR MIN; 142800; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 365
FT FT
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN A-25(A-10).
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT DOMAIN 309 332
FT DOMAIN 333 365
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT CYTOPLASMIC TAIL.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
SQ SEQUENCE 365 AA; 41218 MW; 131A8F20 CRC32;
Found using 'seq1' (seq1.key)
...
89 rnvkhsqtdreslrlyynqsgsht
|-----|
99 108
...
-----
1 match found in sequence:
1A32_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-32(AW-19) ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1A32_HUMAN STANDARD; PRT; 365 AA.
AC P10314;
DT 01-MAR-1989 (REL. 10, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-32(AW-19) ALPHA CHAIN
DE PRECURSOR.
DE HLA.
GN HLA.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
[1]
RN SEQUENCE FROM N.A. (A*2501).
RX ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -!- POLYMORPHISM: THE ONLY ALLELE OF A-25 KNOWN IS A*2501 WHICH IS
CC SHOWN HERE.
DR EMBL; M32321; G307225; -.
DR PIR; A35997; A35997.
DR HSP; P01891; 1HSB.
DR MIN; 142800; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 365
FT FT
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN A-25(A-10).
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT DOMAIN 309 332
FT DOMAIN 333 365
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT CYTOPLASMIC TAIL.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
SQ SEQUENCE 365 AA; 41218 MW; 131A8F20 CRC32;
Found using 'seq1' (seq1.key)
...
89 rnvkhsqtdreslrlyynqsgsht
|-----|
99 108
...
-----
1 match found in sequence:
1B01_GORGO; CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECUR
(from "Swiss-Prot 34")
ID 1B01_GORGO STANDARD; PRT; 362 AA.
AC P30379;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECURSOR.
DE GORILLA GORILLA (LOWLAND GORILLA).
DE OS
DE EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
DE EUTHERIA; PRIMATES.
[1]
RN SEQUENCE FROM N.A.
RX LAWLER D.A., WARREN E., TAYLOR P., PARHAM P.;
RL J. EXP. MED. 174:1491-1509(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC EMBL; X60255; G22866; -.
DR PIR; J05339; J05339.
DR HSP; P03989; 1HSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT CLASS I HISTOCOMPATIBILITY ANTIGEN,

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RN SEQUENCE FROM N.A. (A*3201).
RP DOMENA J.D.;
RL SUBMITTED (DEC-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
[2]
RN SEQUENCE OF 25-298 FROM N.A. (A*3201).
RX MEDLINE; 87058961.
RA WAN A.M., ENNIS P., PARHAM P., HOLMES N.;
RL J. IMMUNOL. 137:3671-3674(1986)
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -!- POLYMORPHISM: THE ONLY ALLELE OF A-32 KNOWN IS A*3201 WHICH IS
CC SHOWN HERE.
DR EMBL; U03907; G432996; -.
DR PIR; A26088; HLH032.
DR HSP; P01892; 1HHG.
DR MIN; 142800; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 365
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN A-32(AW-19).
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT DOMAIN 309 332
FT TRANSMEM 333 365
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT CYTOPLASMIC TAIL.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
SQ SEQUENCE 365 AA; 41048 MW; 71FA71A9 CRC32;
Found using 'seq1' (seq1.key)
...
89 rnvkhsqtdreslrlyynqsgsht
|-----|
99 108
...
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1 match found in sequence:
1B01_GORGO; CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECUR
(from "Swiss-Prot 34")
ID 1B01_GORGO STANDARD; PRT; 362 AA.
AC P30379;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECURSOR.
DE GORILLA GORILLA (LOWLAND GORILLA).
DE OS
DE EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
DE EUTHERIA; PRIMATES.
[1]
RN SEQUENCE FROM N.A.
RX LAWLER D.A., WARREN E., TAYLOR P., PARHAM P.;
RL J. EXP. MED. 174:1491-1509(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC EMBL; X60255; G22866; -.
DR PIR; J05339; J05339.
DR HSP; P03989; 1HSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT CLASS I HISTOCOMPATIBILITY ANTIGEN,

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FT DOMAIN 25 114 GOGO-B0101 ALPHA CHAIN.
FT DOMAIN 113 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40170 MW; 2E33E2B8 CRC32;
Found using 'seq1' (seq1.key)
...

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89 qtskaqactdrenlrialryynqseqsht
99 108
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1 match found in sequence:
1B01_PANTR ; CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR
(from "Swiss-Prot 34")

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ID 1B01_PANTR STANDARD; PRT; 359 AA.
AC P13750;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR
DE (FRAGMENT).
OS PAN TROGLODYTES (CHIMPANZEE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89030641.
RA MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,
RA KLEIN J.;
RL EMBO J. 7:2765-2774(1988).
RN [2]
RP REVISIONS.
RA MAYER W.;
RL SUBMITTED (FEB-1989) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
DR EMBL; X13115; G755776; -.
DR PIR; S03537; S03537.
DR HSSP; P03989; IHSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT NON_TER 1 1
FT SIGNAL <1 20
FT CHAIN 21 359

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CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
B-1 ALPHA CHAIN.
FT DOMAIN 21 110 EXTRACELLULAR ALPHA-1.
FT DOMAIN 111 202 EXTRACELLULAR ALPHA-2.
FT DOMAIN 203 294 EXTRACELLULAR ALPHA-3.
FT DOMAIN 295 305 CONNECTING PEPTIDE.
FT TRANSMEM 306 329
FT DOMAIN 330 359 CYTOPLASMIC TAIL.
FT DISULFID 121 184 BY SIMILARITY.
FT DISULFID 223 279 BY SIMILARITY.
FT CARBOHYD 106 106 BY SIMILARITY.
SQ SEQUENCE 359 AA; 40173 MW; 5395FFC9 CRC32;
Found using 'seq1' (seq1.key)
...

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85 rmkkaactdrenlrialryynqseqsht
99 104
...
1 match found in sequence:
1B02_GORG0 ; CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECUR
(from "Swiss-Prot 34")
ID 1B02_GORG0 STANDARD; PRT; 362 AA.
AC P30380;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECURSOR.
OS GORILLA GORILLA (LOWLAND GORILLA).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92078860.
RA LAWLER D.A., WARREN E., TAYLOR P., PARHAM P.;
RL J. EXP. MED. 174:1491-1509(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
DR EMBL; X60693; G22868; -.
DR PIR; JH0540; JH0540.
DR HSSP; P03989; IHSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 BY SIMILARITY.
FT CLASS I HISTOCOMPATIBILITY ANTIGEN,
GOGO-B0102 ALPHA CHAIN.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40204 MW; 3CF119AD CRC32;
Found using 'seq1' (seq1.key)
...

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89 qtskaqactdrenlrialryynqseqsht
99 108
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1 match found in sequence:
1B02_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-7 B*0702 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B02_HUMAN STANDARD; PRT; 362 AA.
AC P01889;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-7 B*0702 ALPHA CHAIN
DE PRECURSOR (B7.2).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90207291.

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RA ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
[2]
RX SEQUENCE FROM N.A.
RA MEDLINE; 90315860.
RA PARHAM P., BENJAMIN R.J., CHEN B.P., CLAYBERGER C., ENNIS P.D.,
RA KRENSKY A.M., LAWLER D.A., LITTMAN D.R., NORMENT A.M., ORR H.T.,
RA SALTER R.D., ZEMMOUR J.;
RL COLD SPRING HARB. SYMP. QUANT. BIOL. 54:529-543(1989).
[3]
RX SEQUENCE FROM N.A.
RA MEDLINE; 85287366.
RA SOOD A.K., PAN J., BIRO P.A., PEREIRA D., SRIVASTAVA R., REDDY V.B.,
RA DUCEMAN B.W., WEISSMAN S.M.;
RL IMMUNOGENETICS 22:101-121(1985).
[4]
RX SEQUENCE FROM N.A.
RA ELLEXSON M.E., ZHANG L., HILDEBRAND W.H.;
RL SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
[5]
RX SEQUENCE OF 25-295.
RA ORR H.T., LOPEZ DE CASTRO J.A., LANCET D., STROMINGER J.L.;
RL BIOCHEMISTRY 18:5711-5720(1979).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M32317; G307221; -.
DR EMBL; M16102; G307217; ALT_SEQ.
DR EMBL; U29057; G1213467; -.
DR PIR; A02185; HLHUB7.
DR PIR; B35997; B35997.
DR HSSP; P03989; ILSA.
DR MIM; I42830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN B-7 B*0702.
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 309
FT TRANSMEM 310 333
FT DOMAIN 334 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT CONFLICT 15 18
FT CONFLICT 266 266
FT CONFLICT 268 268
FT CONFLICT 297 297
FT CONFLICT 314 315
SQ SEQUENCE 362 AA; 40460 MW; 87B2ED84 CRC32;
Found using 'seq1' (seq1.key)
...
89 qlykaqaqtreslnlrgyynqseagsh
|-----|
99 108
...
1 match found in sequence:
1B02_PANTR ; CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-2 ALPHA CHAIN PRECURSOR
(from "Swiss-Prot 34")
ID 1B02_PANTR STANDARD; PRT; 362 AA.
AC P13751;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)

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DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-2 ALPHA CHAIN PRECURSOR.
OS PAN TROGLODYTES (CHIMPANZEE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 89030641.
RA MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,
RA KLEIN J.;
RL EMBL J. 7:2765-2774(1988).
[2]
RN REVISIONS.
RA MAYER W.;
RL SUBMITTED (FEB-1989) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; X13116; G38209; -.
DR PIR; S03538; S03538.
DR HSSP; P03989; ILSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT B-2 ALPHA CHAIN.
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
SQ SEQUENCE 362 AA; 40488 MW; 4BF65A6C CRC32;
Found using 'seq1' (seq1.key)
...
89 qisktnaqtreslnlrgyynqseagsh
|-----|
99 108
...
1 match found in sequence:
1B03_GORGO ; CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0103 ALPHA CHAIN PRECUR
(from "Swiss-Prot 34")
ID 1B03_GORGO STANDARD; PRT; 362 AA.
AC P30381;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0103 ALPHA CHAIN PRECURSOR.
OS GORILLA GORILLA GORILLA (LOWLAND GORILLA).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 92078860.
RA LAWLER D.A., WARREN E., TAYLOR P., PARHAM P.;
RL J. EXP. MED. 174:1491-1509(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; X60254; G22870; -.
DR PIR; JH0541; JH0541.
DR HSSP; P03989; ILSA.
DR PROSITE; PS00290; IG_MHC.

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KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24 BY SIMILARITY.
FT CHAIN 25 362 CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT GOGO-B0103 ALPHA CHAIN.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40248 MW; FEA6A941 CRC32;
Found using 'seq1' (seq1.key)

...

89 qtskacqatdrenlrnryynqseqsht
|-----|
99 108

...

1 match found in sequence:
1B04.HUMAN : HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-8 B*0801 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B04_HUMAN STANDARD; PRT; 362 AA.
AC P30460;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-8 B*0801 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89235215.
RA PARHAM P.; LAWLER D.A.; LOMEN C.E.; ENNIS P.D.;
RL J. IMMUNOL. 142:3937-3950(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
CC EMBL; M24036; G386775; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN B-8 B*0801.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 309 CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT DOMAIN 334 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40331 MW; 1467B8EB CRC32;
Found using 'seq1' (seq1.key)

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89 qifktntdreslnrlyynqseqsht
|-----|
99 108

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1 match found in sequence:
1B07.HUMAN : HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-14 B*1401 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B07_HUMAN STANDARD; PRT; 362 AA.
AC P30462;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-14 B*1401 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89235215.
RA PARHAM P.; LAWLER D.A.; LOMEN C.E.; ENNIS P.D.;
RL J. IMMUNOL. 142:3937-3950(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
CC EMBL; M24040; G386898; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN B-14 B*1401.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 309 CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT DOMAIN 334 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40358 MW; 9BED8199 CRC32;
Found using 'seq1' (seq1.key)

...

89 qifktntdreslnrlyynqseqsht
|-----|
99 108

...

1 match found in sequence:
1B08.HUMAN : HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-65(B-14) B*1402 ALPHA
(from "Swiss-Prot 34")
ID 1B08_HUMAN STANDARD; PRT; 362 AA.
AC P30463;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-65(B-14) B*1402 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89235215.

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1 match found in sequence:  
 1B12 HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B\*62 B\*1504 ALPHA CHAIN  
 (from "Swiss-Prot 34")  
 ID 1B12 HUMAN STANDARD: PRT: 362 AA.

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AC P30513;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-62 B*1504 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX MEDLINE; 92269956.
RA WATKINS D.I., MCADAM S.N., LIU X., STANG C.R., MILFORD E.L.,
RA LEVINE C.G., GABER T.L., DOGON A.L., LORD C.I., GHIM S.H.,
RA TROOP G.M., HUGHES A.L., LETVIN N.L.;
RL NATURE 357:329-333(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M84382; G187714; -.
DR PIR; S24433; S24433.
DR HSP; P03989; ILSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN B-62 B*1504.
FT EXTRACELLULAR ALPHA-1.
FT EXTRACELLULAR ALPHA-2.
FT EXTRACELLULAR ALPHA-3.
FT CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT DOMAIN 334 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT BY SIMILARITY.
SQ SEQUENCE 362 AA; 40406 MW; E80FC24C CRC32;
Found using 'seq1' (seq1.key)

...

89 qiskntqttyreslnrlgynyqseqsht
108
...

1 match found in sequence:
1B13_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B13_HUMAN STANDARD; PRT; 362 AA.
AC P30466;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX MEDLINE; 89235215.
RA PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
RA IMMUNOL. 142:3937-3950(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M84382; G187714; -.
DR PIR; S24433; S24433.
DR HSP; P03989; ILSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN B-62 B*1504.
FT EXTRACELLULAR ALPHA-1.
FT EXTRACELLULAR ALPHA-2.
FT EXTRACELLULAR ALPHA-3.
FT CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT DOMAIN 334 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT BY SIMILARITY.
SQ SEQUENCE 362 AA; 40406 MW; E80FC24C CRC32;
Found using 'seq1' (seq1.key)

...

89 qiskntqttyreslnrlgynyqseqsht
108
...

1 match found in sequence:
1B13_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B13_HUMAN STANDARD; PRT; 362 AA.
AC P30466;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX MEDLINE; 89235215.
RA PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
RA IMMUNOL. 142:3937-3950(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M84382; G187714; -.
DR PIR; S24433; S24433.
DR HSP; P03989; ILSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN B-62 B*1504.
FT EXTRACELLULAR ALPHA-1.
FT EXTRACELLULAR ALPHA-2.
FT EXTRACELLULAR ALPHA-3.
FT CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT DOMAIN 334 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT BY SIMILARITY.
SQ SEQUENCE 362 AA; 40406 MW; E80FC24C CRC32;
Found using 'seq1' (seq1.key)

...

89 qiskntqttyreslnrlgynyqseqsht
108
...

1 match found in sequence:
1B15_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B15_HUMAN STANDARD; PRT; 362 AA.
AC P10317;
DT 01-MAR-1989 (REL. 10, CREATED)
DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN
DE PRECURSOR (B-27K) (B27.2).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX MEDLINE; 86220133.
RA SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;
RA EMBO J. 5:547-552(1986).
RN [2]
RX SEQUENCE FROM N.A.
RA PARHAM P., ARNETT K.L., ADAMS E.J.;
RA SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RX SEQUENCE OF 86-107 AND 171-181.
RA VEGA M.A., EZQUERRA A., ROJO S., APARICIO P., BRAGADO R.,
RA LOPEZ DE CASTRO J.A.;
RA PROC. NATL. ACAD. SCI. U.S.A. 82:7394-7398(1985).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; X03664; G871296; -.
DR EMBL; X03667; G871296; JOINED.
DR EMBL; L38504; G896271; -.
DR PIR; B25092; HLHUBK.
DR HSP; P03989; ILSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN B-27 B*2702.

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FT DOMAIN 25 114 ALPHA CHAIN B-27 B*2702.
FT FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT FT DOMAIN 309 332 CONNECTING PEPTIDE.
FT FT TRANSMEM 333 362 CYTOPLASMIC TAIL.
FT FT DOMAIN 110 110 BY SIMILARITY.
FT FT CARBOHYD 125 188 BY SIMILARITY.
FT FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40397 MW; 9798F0EB CRC32;
Found using 'seq1' (seq1.key)

...

89 qickakaqtdrenlrialyynqseqsht
99 108
-----|
1 match found in sequence:
1B21_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3501 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B21_HUMAN STANDARD; PRT; 362 AA.
AC P30685;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3501 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89339610.
RA Ooba T., HAYASHI H., KARAKI S., TANABE M., KANO K., TAKIGUCHI M.;
RL IMMUNOGENETICS 30:76-80(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M28115; G187673; JOINED.
DR EMBL; M28109; G187673; JOINED.
DR EMBL; M28110; G187673; JOINED.
DR EMBL; M28111; G187673; JOINED.
DR EMBL; M28112; G187673; JOINED.
DR EMBL; M28113; G187673; JOINED.
DR EMBL; M28114; G187673; JOINED.
DR PIR; A45880; A45880.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT FT DOMAIN 25 114 ALPHA CHAIN B-35 B*3501.
FT FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT FT CARBOHYD 110 110 BY SIMILARITY.
FT FT DISULFID 125 188 BY SIMILARITY.
FT FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40455 MW; AEC1C675 CRC32;
Found using 'seq1' (seq1.key)

...

89 qickakaqtdrenlrialyynqseqsht
99 108
-----|
1 match found in sequence:
1B21_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3501 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B21_HUMAN STANDARD; PRT; 362 AA.
AC P30685;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3501 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89339610.
RA Ooba T., HAYASHI H., KARAKI S., TANABE M., KANO K., TAKIGUCHI M.;
RL IMMUNOGENETICS 30:76-80(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M28115; G187673; JOINED.
DR EMBL; M28109; G187673; JOINED.
DR EMBL; M28110; G187673; JOINED.
DR EMBL; M28111; G187673; JOINED.
DR EMBL; M28112; G187673; JOINED.
DR EMBL; M28113; G187673; JOINED.
DR EMBL; M28114; G187673; JOINED.
DR PIR; A45880; A45880.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT FT DOMAIN 25 114 ALPHA CHAIN B-35 B*3501.
FT FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT FT CARBOHYD 110 110 BY SIMILARITY.
FT FT DISULFID 125 188 BY SIMILARITY.
FT FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40455 MW; AEC1C675 CRC32;
Found using 'seq1' (seq1.key)

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89 qifkntqtqreslnlrgyynqseqgshi
99 108
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1 match found in sequence:
1B22_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3502 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B22_HUMAN STANDARD; PRT; 362 AA.
AC P30468;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3502 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91365651.
RA CHERTKOFF L.P., HERRERA M., FAINBOIM L., SATZ M.L.;
RL HUM. IMMUNOL. 31:153-158(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M63454; G403145; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT FT DOMAIN 25 114 ALPHA CHAIN B-35 B*3502.
FT FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT FT CARBOHYD 110 110 BY SIMILARITY.
FT FT DISULFID 125 188 BY SIMILARITY.
FT FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40564 MW; D7B5C3C9 CRC32;
Found using 'seq1' (seq1.key)

...

89 qifkntqtqreslnlrgyynqseqgshi
99 108
-----|
1 match found in sequence:
1B23_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3503 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B23_HUMAN STANDARD; PRT; 362 AA.
AC P30469;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3503 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

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OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92176661.
RA ZEMMOUR J., LITTLE A.M., SCHENDEL D.J., PARHAM P.;
RL J. IMMUNOL. 148:1194-1948(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M81798; G187859; -.
DR HSP; P03989; IHSA.
DR MIN; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN B-35 B*3503.
FT DOMAIN 25 114
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206
FT EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298
FT EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308
FT CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT CYTOPLASMIC TAIL.
FT DOMAIN 333 362
FT BY SIMILARITY.
FT CARBOHYD 110 110
FT BY SIMILARITY.
FT DISULFID 125 188
FT BY SIMILARITY.
FT DISULFID 227 283
FT BY SIMILARITY.
SQ SEQUENCE 362 AA; 40515 MW; 4222D30A CRC32;
Found using 'seq1' (seq1.key)
...

89 gikfntqtqyreslnrlrgynqseagshi
99 108
...

1 match found in sequence:
1B24_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3504 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B24_HUMAN STANDARD; PRT; 354 AA.
AC P30470;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3504 ALPHA CHAIN
DE PRECURSOR (FRAGMENT).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92269956.
RA WATKINS D.I., MCADAM S.N., LIU X., STANG C.R., MILFORD E.L.,
RA LEVINE C.G., GABER T.L., DOON C.I., GHIM S.H.,
RA TROUP G.M., HUGHES A.L., LETVIN N.L.;
RL NATURE 357:329-333(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M86403; -. NOT_ANNOTATED_CDS.
DR HSP; P03989; IHSA.
DR MIN; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT NON_TER 1 1
FT SIGNAL <1 16
FT CHAIN 17 354 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN B-35 B*3504.

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FT DOMAIN 17 106
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 107 198
FT EXTRACELLULAR ALPHA-2.
FT DOMAIN 199 290
FT EXTRACELLULAR ALPHA-3.
FT DOMAIN 291 300
FT CONNECTING PEPTIDE.
FT TRANSMEM 301 324
FT CYTOPLASMIC TAIL.
FT DOMAIN 325 354
FT BY SIMILARITY.
FT CARBOHYD 102 102
FT BY SIMILARITY.
FT DISULFID 117 180
FT BY SIMILARITY.
FT DISULFID 219 275
FT BY SIMILARITY.
SQ SEQUENCE 354 AA; 39617 MW; 6564795A CRC32;
Found using 'seq1' (seq1.key)
...

81 gikfntqtqyreslnrlrgynqseagshi
99 100
...

1 match found in sequence:
1B25_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3505 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B25_HUMAN STANDARD; PRT; 362 AA.
AC P30471;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3505 ALPHA CHAIN
DE PRECURSOR (B35-G).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92269955.
RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
RL NATURE 357:326-329(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M84385; G187720; -.
DR HSP; P03989; IHSA.
DR MIN; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN B-35 B*3505.
FT DOMAIN 25 114
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206
FT EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298
FT EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308
FT CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT CYTOPLASMIC TAIL.
FT DOMAIN 333 362
FT BY SIMILARITY.
FT CARBOHYD 110 110
FT BY SIMILARITY.
FT DISULFID 125 188
FT BY SIMILARITY.
FT DISULFID 227 283
FT BY SIMILARITY.
SQ SEQUENCE 362 AA; 40374 MW; B404A7FA CRC32;
Found using 'seq1' (seq1.key)
...

89 gikfntqtqyreslnrlrgynqseagshi
99 108
...

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CC  -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC  THE IMMUNE SYSTEM.
CC  -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC  MICROGLOBULIN).
DR  EMBL; L04695; G187893; -.
DR  HSSP; P03989; IHSA.
DR  MIM; 142830; -.
DR  PROSITE; PS00290; IG_MHC.
KW  MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT  SIGNAL 1 24
FT  CHAIN 25 362
FT  DOMAIN 25 114
FT  DOMAIN 115 206
FT  DOMAIN 207 298
FT  DOMAIN 299 308
FT  DOMAIN 309 332
FT  DOMAIN 333 362
FT  CARBOHYD 110 110
FT  DISULFID 125 188
FT  DISULFID 227 283
SQ  SEQUENCE 362 AA; 40497 MW; 9F979909 CRC32;
Found using 'seq1' (seq1.key)
...
89 qifkntgtqreslnrlrgynqseagshi
|-----|
99 108
...
1 match found in sequence:
1B28_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3508 ALPHA CHAIN
(from 'Swiss-Prot 34")
ID 1B28_HUMAN STANDARD; PRT; 362 AA.
AC P30474;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3508 ALPHA CHAIN
DE PRECURSOR.
DE GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93303752.
RA THEILER G., PANDO M., DELFINO J.M., TAKIGUCHI M., SATZ M.L.;
RL TISSUE ANTIGENS 41:143-147(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94186367.
RA STEINLE A., REINHARDT C., NOESSNER E., UCHANSKA-ZIEGLER B.,
RA ZIEGLER A., SCHENDEL D.J.;
RL HUM. IMMUNOL. 38:261-269(1993).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR  EMBL; L04696; G184216; -.
DR  EMBL; Z22651; G297143; -.
DR  PIR; S32754; S32754.
DR  PIR; S32755; S32755.
DR  HSSP; P03989; IHSA.
DR  MIM; 142830; -.
DR  PROSITE; PS00290; IG_MHC.
KW  MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT  SIGNAL 1 24
FT  CHAIN 25 362
FT  DOMAIN 25 114
FT  DOMAIN 115 206
FT  DOMAIN 207 298
FT  DOMAIN 299 308
FT  DOMAIN 309 332
FT  DOMAIN 333 362
FT  CARBOHYD 110 110
FT  DISULFID 125 188
FT  DISULFID 227 283
SQ  SEQUENCE 362 AA; 40497 MW; 9F979909 CRC32;
Found using 'seq1' (seq1.key)
...

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FT DOMAIN      25      114      EXTRACELLULAR ALPHA-1.
FT DOMAIN     115      206      EXTRACELLULAR ALPHA-2.
FT DOMAIN     207      298      EXTRACELLULAR ALPHA-3.
FT DOMAIN     299      308      CONNECTING PEPTIDE.
FT TRANSMEM   309      332
FT DOMAIN     333      362      CYTOPLASMIC TAIL.
FT CARBOHYD   110      110      BY SIMILARITY.
FT DISULFID   125      188      BY SIMILARITY.
FT DISULFID   227      283      BY SIMILARITY.
SQ SEQUENCE   362 AA; 40498 MW; E067BD80 CRC32;
Found using 'seq1' (seq1.key)

...

89      qfktntqtyreslnrlgynqseagshl
          |-----|
          99      108

...

1 match found in sequence:
1B31_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-39 B*3901 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B31_HUMAN STANDARD; PRT; 362 AA.
AC P30475;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-39 B*3901 ALPHA CHAIN
DE PRECURSOR (B39.1).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93131294.
RA KATO N., KARAKI S., KASHIWASE K., MUELLER C., AKAZA T., JUJI T.,
RA KANO K., TAKIGUCHI M.;
RL IMMUNOGENETICS 37:212-216(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95242308.
RA ADAMS E.J., MARTINEZ-NAVES E., ARNETT K.L., LITTLE A.M.,
RA TYAN D.B., PARHAM P.;
RL TISSUE ANTIGENS 45:18-26(1995).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M94053; G184166; -
DR EMBL; U04243; G458660; -
DR HSSP; P03989; ILSA.
DR MIM; 142830; -
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL      1      24
FT CHAIN       25      362      HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN      25      114      ALPHA CHAIN B-39 B*3901.
FT DOMAIN     115      206      EXTRACELLULAR ALPHA-1.
FT DOMAIN     207      298      EXTRACELLULAR ALPHA-2.
FT DOMAIN     299      308      EXTRACELLULAR ALPHA-3.
FT TRANSMEM   309      332      CONNECTING PEPTIDE.
FT DOMAIN     333      362      CYTOPLASMIC TAIL.
FT CARBOHYD   110      110      BY SIMILARITY.
FT DISULFID   125      188      BY SIMILARITY.
FT DISULFID   227      283      BY SIMILARITY.
SQ SEQUENCE   362 AA; 40328 MW; F1DE607E CRC32;
Found using 'seq1' (seq1.key)

...

89      qfktntqtdreslnrlgynqseagsh
          |-----|
          99      108

...

1 match found in sequence:
1B31_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-39 B*3901 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B31_HUMAN STANDARD; PRT; 362 AA.
AC P30475;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-39 B*3901 ALPHA CHAIN
DE PRECURSOR (B39.1).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93131294.
RA KATO N., KARAKI S., KASHIWASE K., MUELLER C., AKAZA T., JUJI T.,
RA KANO K., TAKIGUCHI M.;
RL IMMUNOGENETICS 37:212-216(1993).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M94052; G184164; -
DR EMBL; M94051; G184168; -
DR HSSP; P03989; ILSA.
DR MIM; 142830; -
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL      1      24
FT CHAIN       25      362      HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN      25      114      ALPHA CHAIN B-39 B*3901.
FT DOMAIN     115      206      EXTRACELLULAR ALPHA-1.
FT DOMAIN     207      298      EXTRACELLULAR ALPHA-2.
FT DOMAIN     299      308      EXTRACELLULAR ALPHA-3.
FT TRANSMEM   309      332      CONNECTING PEPTIDE.
FT DOMAIN     333      362      CYTOPLASMIC TAIL.
FT CARBOHYD   110      110      BY SIMILARITY.
FT DISULFID   125      188      BY SIMILARITY.
FT DISULFID   227      283      BY SIMILARITY.
SQ SEQUENCE   362 AA; 40328 MW; F1DE607E CRC32;
Found using 'seq1' (seq1.key)

...

89      qfktntqtdreslnrlgynqseagsh
          |-----|
          99      108

...

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1 match found in sequence:
1B32_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-39 B*3902 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B32_HUMAN STANDARD; PRT; 362 AA.
AC P30476;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-39 B*3902 ALPHA CHAIN
DE PRECURSOR (B39.2).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93131294.
RA KATO N., KARAKI S., KASHIWASE K., MUELLER C., AKAZA T., JUJI T.,
RA KANO K., TAKIGUCHI M.;
RL IMMUNOGENETICS 37:212-216(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95242308.
RA ADAMS E.J., MARTINEZ-NAVES E., ARNETT K.L., LITTLE A.M.,
RA TYAN D.B., PARHAM P.;
RL TISSUE ANTIGENS 45:18-26(1995).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M94053; G184166; -
DR EMBL; U04243; G458660; -
DR HSSP; P03989; ILSA.
DR MIM; 142830; -
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL      1      24
FT CHAIN       25      362      HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN      25      114      ALPHA CHAIN B-39 B*3902.
FT DOMAIN     115      206      EXTRACELLULAR ALPHA-1.
FT DOMAIN     207      298      EXTRACELLULAR ALPHA-2.
FT DOMAIN     299      308      EXTRACELLULAR ALPHA-3.
FT TRANSMEM   309      332      CONNECTING PEPTIDE.
FT DOMAIN     333      362      CYTOPLASMIC TAIL.
FT CARBOHYD   110      110      BY SIMILARITY.
FT DISULFID   125      188      BY SIMILARITY.
FT DISULFID   227      283      BY SIMILARITY.
SQ SEQUENCE   362 AA; 40327 MW; D0E420A1 CRC32;
Found using 'seq1' (seq1.key)

...

89      qfktntqtdreslnrlgynqseagsh
          |-----|
          99      108

...

1 match found in sequence:
1B33_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-60(B-40) B*4001 ALPHA
(from "Swiss-Prot 34")
ID 1B33_HUMAN STANDARD; PRT; 270 AA.
AC P01890;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-60(B-40) B*4001 ALPHA CHAIN
DE (FRAGMENT).
GN HLAB.

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OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE.
RX MEDLINE: 84000412.
RA LOPEZ DE CASTRO J.A., BRAGADO R., STRONG D.M., STROMINGER J.L.;
RL BIOCHEMISTRY 22:3961-3969(1983).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
    THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
    MICROGLOBULIN).
CC PIR; A02186; HLH040.
DR HSSP; P03989; 1HSA.
DR MIM; 142830.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; GLYCOPROTEIN.
FT DOMAIN 1 90 EXTRACELLULAR ALPHA-1.
FT DOMAIN 91 181 EXTRACELLULAR ALPHA-2.
FT DOMAIN 182 >270 EXTRACELLULAR ALPHA-3.
FT CARBOHYD 86 86
FT DISULFID 101 153
FT DISULFID 202 258
FT NON_TER 270 270
SQ SEQUENCE 270 AA; 31205 MW; BFE44EFF CRC32;
Found using 'seq1' (seq1.key)

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65 qiskntqtqreslnlrgyynqseagsht
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    75 84

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1 match found in sequence:
1B34_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4002 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B34_HUMAN STANDARD; PRT; 362 AA.
AC Q04826;
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4002 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93127148.
RA DOMENA J.D., JOHNSTON-DOW L., PARHAM P.;
RL TISSUE ANTIGENS 40:254-256(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
    THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
    MICROGLOBULIN).
CC EMBL; L09736; G187679; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142830.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
    ALPHA CHAIN B-40 B*4002.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332 CYTOPLASMIC TAIL.
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40600 MW; EIFE537C CRC32;
Found using 'seq1' (seq1.key)

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FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40505 MW; C2A00916 CRC32;
Found using 'seq1' (seq1.key)

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89 qiskntqtqreslnlrgyynqseagsht
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    99 108

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1 match found in sequence:
1B35_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4003 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B35_HUMAN STANDARD; PRT; 362 AA.
AC P30477;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4003 ALPHA CHAIN
DE PRECURSOR (B40-G1).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92269955.
RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
    WILLIAMS R.C., LUZ R., PEYTL-ERLER M.L., PARHAM P.;
RL NATURE 357:326-329(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
    THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
    MICROGLOBULIN).
CC EMBL; M84384; G187718; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
    ALPHA CHAIN B-40 B*4003.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332 CYTOPLASMIC TAIL.
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40600 MW; EIFE537C CRC32;
Found using 'seq1' (seq1.key)

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89 qiskntqtqreslnlrgyynqseagsht
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    99 108

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1 match found in sequence:
1B36_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B*4004 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B36_HUMAN STANDARD; PRT; 362 AA.
AC P30478;

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DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B*4004 ALPHA CHAIN
DE PRECURSOR (B40-G2).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92269955.
RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
RL NATURE 357:326-329(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M84383; G187716; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN B*4004.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 308 CONNECTING PEPTIDE.
FT TRANSMEM 309 332
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40430 MW; 3797AB68 CRC32;
Found using 'seq1' (seq1.key)
...

89 qiskntqtyreslnrgynqseagst
|-----|
99 108

1 match found in sequence:
1B38_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-41 B*4101 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B38_HUMAN STANDARD; PRT; 362 AA.
AC P30479;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-41 B*4101 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89235215.
RA PARHAM P., LAWLER D.A., LOMEN C.E., ENNIS P.D.;
RL J. IMMUNOL. 142:3937-3950(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M24034; G386904; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN BW-41 B*4101.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 309 CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT DOMAIN 334 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40333 MW; 795A36FD CRC32;
Found using 'seq1' (seq1.key)
...

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DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN BW-41 B*4101.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 309 CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT DOMAIN 334 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40539 MW; A292D60A CRC32;
Found using 'seq1' (seq1.key)
...

89 qiskntqtyreslnrgynqseagst
|-----|
99 108

1 match found in sequence:
1B39_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-42 B*4201 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B39_HUMAN STANDARD; PRT; 362 AA.
AC P30480;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-42 B*4201 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89235215.
RA PARHAM P., LAWLER D.A., LOMEN C.E., ENNIS P.D.;
RL J. IMMUNOL. 142:3937-3950(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M24034; G386904; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN BW-42 B*4201.
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 309 CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT DOMAIN 334 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40333 MW; 795A36FD CRC32;
Found using 'seq1' (seq1.key)
...

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89      qiYkaqagtdreslnrlrgyynqseagsh
      99
      108
...
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1 match found in sequence:
1B43_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-45(B-12) B*4501 ALPHA
(from "Swiss-Prot 34")
ID 1B43_HUMAN STANDARD; PRT; 362 AA.
AC P30483;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-45(B-12) B*4501 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93056508.
RA MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
RA LITTLE A.M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
RA MARTELL R.W., DU TOIT E.D., PARHAM P.;
RL J. IMMUNOL. 149:3411-3415(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93056508.
RA MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
RA LITTLE A.M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
RA MARTELL R.W., DU TOIT E.D., PARHAM P.;
RL J. IMMUNOL. 149:3411-3415(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; X61710; G32183; -.
DR PIR; S16772; S16772.
DR HSSP; P03989; ILSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 309
FT TRANSMEM 310 333
FT DOMAIN 334 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT SEQUENCE 362 AA; 40414 MW; 9B9A5539 CRC32;
Found using 'seq1' (seq1.key)
...
89      giskntqtdreslnrlrgyynqseagsh
      99
      108
...
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1 match found in sequence:
1B44_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-46 B*4601 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B44_HUMAN STANDARD; PRT; 362 AA.
AC P30484;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-46 B*4601 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).

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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89235215.
RA PARHAM P., LAWLOW D.A., LOMEN C.E., ENNIS P.D.;
RL J. IMMUNOL. 142:3937-3950(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M24033; G307227; -.
DR HSSP; P03989; ILSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 309
FT TRANSMEM 310 333
FT DOMAIN 334 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT SEQUENCE 362 AA; 40440 MW; EC587DD3 CRC32;
Found using 'seq1' (seq1.key)
...
89      qkykrqagtdreslnrlrgyynqseagsh
      99
      108
...
-----
1 match found in sequence:
1B46_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-48 B*4801 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B46_HUMAN STANDARD; PRT; 362 AA.
AC P30486;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-48 B*4801 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92269955.
RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
RL NATURE 357:326-329(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M84380; G187708; -.
DR HSSP; P03989; ILSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 309
FT TRANSMEM 310 333
FT DOMAIN 334 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT SEQUENCE 362 AA; 40440 MW; EC587DD3 CRC32;
Found using 'seq1' (seq1.key)
...

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FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.
FT DOMAIN 299 309 CONNECTING PEPTIDE.
FT TRANSMEM 310 333
FT DOMAIN 334 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40362 MW; 081D8291 CRC32;
Found using 'seq1' (seq1.key)

...

89 gskstntqyreslnrlgyynqseqsgh
99
108
}-----|
1 match found in sequence:
1B47_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA C
(from "Swiss-Prot 34")
ID 1B47_HUMAN STANDARD; PRT; 362 AA.
AC P30487;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93056529.
RA HILDEBRAND W.H., MADRIGAL J.A., BELICH M.P., ZEMMOUR J., WARD F.E.,
RA WILLIAMS R.C., PARHAM P.;
RL J. IMMUNOL. 149:3563-3568(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M24037; G407191; -.
DR HSSP; P03989; LHSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN B-49(B-21) B*4901.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 309 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 310 333 CONNECTING PEPTIDE.
FT DOMAIN 334 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40581 MW; E996F82F CRC32;
Found using 'seq1' (seq1.key)

...

89 gskstntqyreslnrlgyynqseqsgh
99
108
}-----|
1 match found in sequence:
1B49_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CH
(from "Swiss-Prot 34")
ID 1B49_HUMAN STANDARD; PRT; 362 AA.
AC P18464;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

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...

99 108
}-----|
1 match found in sequence:
1B48_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-50(B-21) B*5001 ALPHA
(from "Swiss-Prot 34")
ID 1B48_HUMAN STANDARD; PRT; 362 AA.
AC P30488;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-50(B-21) B*5001 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93056508.
RA MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
RA LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
RA MARTELL R.W., DU TOIT E.D., PARHAM P.;
RL J. IMMUNOL. 149:3411-3415(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; X61706; G32185; -.
DR PIR; S16773; S16773.
DR HSSP; P03989; LHSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN BW-50(B-21) B*5001.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 309 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 310 333 CONNECTING PEPTIDE.
FT DOMAIN 334 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40541 MW; 6C8B4A34 CRC32;
Found using 'seq1' (seq1.key)

...

89 gskstntqyreslnrlgyynqseqsgh
99
108
}-----|
1 match found in sequence:
1B49_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CH
(from "Swiss-Prot 34")
ID 1B49_HUMAN STANDARD; PRT; 362 AA.
AC P18464;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

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...
89 qifkntqtyrenlrialryngqseagshi
99
108
-----
1 match found in sequence:
1B55_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-54 (BW-22) B*5401 ALPHA
(from "Swiss-Prot 34")
ID 1B55_HUMAN STANDARD; PRT; 362 AA.
AC P30492;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-54 (BW-22) B*5401 ALPHA
DE CHAIN PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92148136.
RA HILDEBRAND W.H., MADRIGAL J.A., LITTLE A.-M., PARHAM P.;
RL J. IMMUNOL. 148:1155-1162(1992).
CC -I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
EMBL: M77774; G184117; -
DR HSP; P03989; ILSA.
DR MIM: 142830; -
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN BW-54 (BW-22) B*5401.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
SQ SEQUENCE 362 AA; 40521 MW; 3B436FE8 CRC32;
Found using 'seq1' (seq1.key)
...
89 qiykaqaqtdreslnrlrgyngqseagsh
99
108
-----
1 match found in sequence:
1B56_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-55 (BW-22) B*5501 ALPHA
(from "Swiss-Prot 34")
ID 1B56_HUMAN STANDARD; PRT; 362 AA.
AC P30493;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-55 (BW-22) B*5501 ALPHA
DE CHAIN PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92148136.
RA HILDEBRAND W.H., MADRIGAL J.A., LITTLE A.-M., PARHAM P.;
RL J. IMMUNOL. 148:1155-1162(1992).
CC -I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
EMBL: M77774; G184117; -
DR HSP; P03989; ILSA.
DR MIM: 142830; -
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN BW-55 (BW-22) B*5501.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
SQ SEQUENCE 362 AA; 40495 MW; 2BDC746E CRC32;
Found using 'seq1' (seq1.key)
...

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DR PIR; B30548; B30548.
DR HSP; P03989; ILSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT FT
FT FT
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40521 MW; 3B436FE8 CRC32;
Found using 'seq1' (seq1.key)

...

89 qiskntqtyrenlrialryngqseagsh
99
108
-----|
1 match found in sequence:
1B55_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 (B*5301 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1B54_HUMAN STANDARD; PRT; 362 AA.
AC P30491;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 (B*5301 ALPHA CHAIN
DE DE
DE CHAIN PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92148136.
RA HILDEBRAND W.H., MADRIGAL J.A., LITTLE A.-M., PARHAM P.;
RL J. IMMUNOL. 148:1155-1162(1992).
CC -I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
EMBL; M77774; G184117; -.
DR HSP; P03989; ILSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT FT
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40495 MW; 2BDC746E CRC32;
Found using 'seq1' (seq1.key)

...

89 qiykaqaqtdreslnrlrgyngqseagsh
99
108
-----|
1 match found in sequence:
1B56_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-55 (B*5501 ALPHA
(from "Swiss-Prot 34")
ID 1B56_HUMAN STANDARD; PRT; 362 AA.
AC P30493;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-55 (B*5501 ALPHA
DE DE
DE CHAIN PRECURSOR.
GN HLAB.

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      115    206    EXTRACELLULAR ALPHA-2.
      207    298    EXTRACELLULAR ALPHA-3.
      299    308    CONNECTING PEPTIDE.
      309    332    CYTOPLASMIC TAIL.
      333    362    BY SIMILARITY.
      110    110    BY SIMILARITY.
      125    188    BY SIMILARITY.
      227    283    BY SIMILARITY.
SQ SEQUENCE 362 AA; 40466 MW; D5BF98F0 CRC32;
Found using 'seq1' (seq1.key)

.....
89      qiykaqatdreslnlrngynqseagsh
          99      108
          |-----|
          -----
1 match found in sequence:
1B58 HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-56(BW-22) B*5601 ALPHA
(from "SwIss-Prot 34")
ID   1B58_HUMAN        STANDARD;             PRT;   362 AA.
AC   P30495;
DT   01-APR-1993 (REL. 25, CREATED)
DI   01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DD   01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE   HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-56(BW-22) B*5601 ALPHA
DE   CHAIN PRECURSOR.
GN   HLA-B.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92148136.
RA   HILDEBRAND W.H., MADRIGAL J.A., LITTLE A.-M., PARHAM P.;
RL   J. IMMUNOL. 148:1155-1162(1992).
CC   C -I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC   THE IMMUNE SYSTEM.
CC   C -I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC   MICROGLOBULIN).
EMBL; M77776; G184123; -.
DR   HSP: P03989; IHSA.
DR   MIN: 142830; -.
DR   PROSITE; PS00290; IG_MHC.
KW   MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL           1       24
FT   CHAIN            25      362
                                     HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT   DOMAIN            25      114     ALPHA CHAIN BW-56(BW-22) B*5601.
FT   DOMAIN            115     206     EXTRACELLULAR ALPHA-1.
FT   DOMAIN            207     298     EXTRACELLULAR ALPHA-2.
FT   DOMAIN            299     308     EXTRACELLULAR ALPHA-3.
FT   TRANSMEM          309     332     CONNECTING PEPTIDE.
FT   DOMAIN            333     362     CYTOPLASMIC TAIL.
FT   CARBOHYD          110     110     BY SIMILARITY.
FT   DISULFID          125     188     BY SIMILARITY.
FT   DISULFID          227     283     BY SIMILARITY.
SQ SEQUENCE 362 AA; 40478 MW; C91D06CC CRC32;
Found using 'seq1' (seq1.key)

.....
89      qiykaqatdreslnlrngynqseagsh
          99      108
          |-----|
          -----
1 match found in sequence:

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1B59_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-56(BW-22) B*5602 ALPHA
(from "Swiss-Prot 34")
ID 1B59_HUMAN STANDARD; PRT; 362 AA.
AC P30456;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-56(BW-22) B*5602 ALPHA
DE CHAIN PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92148136.
RA HILDEBRAND W.H., MADRIGAL J.A., LITTLE A.-M., PARHAM P.;
RL J. IMMUNOL. 148:1155-1162(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL: M7775; G184125; -.
DR HSSP: P03989; 1HSA.
DR MIM: 142830; -.
DR PROSITE: PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN BW-56(BW-22) B*5602.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40460 MW; 64608CFE CRC32;
Found using 'seq1' (seq1.key)
...

89 qiylkaqtdreslnrlryynqseagsh
99
108
-----!-----
1 match found in sequence:
1B60_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5701 ALPHA
(from "Swiss-Prot 34")
ID 1B60_HUMAN STANDARD; PRT; 362 AA.
AC P18465;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5701 ALPHA
DE CHAIN PRECURSOR (BW57.1).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90207291.
RA ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91067476.

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RA ISAMAT M., GIRDLESTONE J., MILSTEIN C.;
RL NUCLEIC ACIDS RES. 18:6702-6702(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL: M32318; G307222; -.
DR EMBL: X55711; G32181; -.
DR PIR: S12622; S12622.
DR PIR: D35997; D35997.
DR HSSP: P03989; 1HSA.
DR MIM: 142830; -.
DR PROSITE: PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN B-57(B-17) B*5701.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 BY SIMILARITY.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40224 MW; D91DF8DD CRC32;
Found using 'seq1' (seq1.key)
...

89 rmkasaqtyrenrlryynqseagshi
99
108
-----!-----
1 match found in sequence:
1B61_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5702 ALPHA C
(from "Swiss-Prot 34")
ID 1B61_HUMAN STANDARD; PRT; 362 AA.
AC P30497;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5702 ALPHA CHAIN
DE PRECURSOR (BW57.2).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93056508.
RA MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
RA LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
RA MARTELL R.W., DU TOIT E.D., PARHAM P.;
RL J. IMMUNOL. 149:3411-3415(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL: X61707; G32187; -.
DR PIR: S16774; S16774.
DR HSSP: P03989; 1HSA.
DR MIM: 142830; -.
DR PROSITE: PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN B-57(B-17) B*5702.

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OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX MEDLINE; 89215297.
RA ELLIS S.A., STRACHAN T., PALMER M.S., MCMICHAEL A.J.;
RL J. IMMUNOL. 142:3281-3285(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M26429; G307239; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142840; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN CW-1 CW*0101.
FT DOMAIN 25 114
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 333
FT CYTOPLASMIC TAIL.
FT DOMAIN 334 366
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
FT BY SIMILARITY.
SQ SEQUENCE 366 AA; 40964 MW; 922CF5E4 CRC32;
Found using 'seq1' (seq1.key)
...
89 qkynrqatdrvslrnlrgyynqseagsh
99 108
...
-----
1 match found in sequence:
1C01_PANTR; CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, C ALPHA CHAIN PRECURSOR.
(from "Swiss-Prot 34")
ID 1C01_PANTR STANDARD; PRT; 366 AA.
AC P30686;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, C ALPHA CHAIN PRECURSOR.
OS PAN TROGLODYTES (CHIMPANZEE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE; 92391104.
RA KATO T., ESUMI M., YAMASHITA S., ABE K., SHIKATA T.;
RL VIROLOGY 190:856-860(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; D11383; E56339; ALT_INIT.
DR HSSP; P03989; 1HSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366
FT CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT C ALPHA CHAIN.
FT DOMAIN 25 114
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT CONNECTING PEPTIDE.

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FT TRANSMEM 309 332
FT DOMAIN 333 366
FT DISULFID 125 192
FT DISULFID 227 283
FT CARBOHYD 110 110
FT BY SIMILARITY.
SQ SEQUENCE 366 AA; 40842 MW; 98538EE9 CRC32;
Found using 'seq1' (seq1.key)
...
89 qkykrqatdrvslrnlrgyynqseagsh
99 108
...
-----
1 match found in sequence:
1C02_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-1 CW*0102 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1C02_HUMAN STANDARD; PRT; 366 AA.
AC P30500;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-1 CW*0102 ALPHA CHAIN
DE PRECURSOR (CW1.2).
GN HLAC.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE; 93031775.
RA ZEMMOUR J., GUMPERTZ J.E., HILDEBRAND W.H., WARD F.E., MARSH S.G.,
RA WILLIAMS R.C., FARHAM P.;
RL TISSUE ANTIGENS 39:249-257(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M84171; G187863; -.
DR HSSP; P03989; 1HSA.
DR MIM; 142840; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366
FT HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT ALPHA CHAIN CW-1 CW*0102.
FT DOMAIN 25 114
FT EXTRACELLULAR ALPHA-1.
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 333
FT CYTOPLASMIC TAIL.
FT DOMAIN 334 366
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
FT BY SIMILARITY.
SQ SEQUENCE 366 AA; 40950 MW; A19B2984 CRC32;
Found using 'seq1' (seq1.key)
...
89 qkykrqatdrvslrnlrgyynqseagsh
99 108
...
-----
1 match found in sequence:
1C05_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-3 CW*0301 ALPHA CHAIN
(from "Swiss-Prot 34")

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ID 1C05_HUMAN STANDARD; PRT; 366 AA.
AC P04222;
DT 20-MAR-1987 (REL. 04, CREATED)
DT 20-MAR-1987 (REL. 04, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-3 CW*0301 ALPHA CHAIN
DE PRECURSOR (CW3.1).
GN HLAC.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84207947.
RA SODOYER R., DAMOTTE M., DELOVITCH T.L., TRUCY J., JORDAN B.R.,
RA STRACHAN T.;
RL EMBO J. 3:879-885(1984).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; X00495; G642239; -.
DR PIR; A02190; HLHW3.
DR HSP; P03989; ILSA.
DR MIM; 142840; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 333
FT DOMAIN 334 366
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
FT CARBOHYD 366 AA; 40744 MW; 53795742 CRC32;
SQ SEQUENCE 366 AA; 40744 MW; 53795742 CRC32;
Found using 'seq1' (seq1.key)
...

89 qkykpaqtdrslrnlrgyynqseqagshi
99 108
...

1 match found in sequence:
1C06_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-3 CW*0302 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1C06_HUMAN STANDARD; PRT; 366 AA.
AC P30503;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-3 CW*0302 ALPHA CHAIN
DE PRECURSOR (CW3.2).
GN HLAC.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93031775.
RA ZEMMOUR J., GUMPERZ J.E., HILDEBRAND W.H., WARD F.E., MARSH S.G.,
RA WILLIAMS R.C., PARHAM P.;
RL TISSUE ANTIGENS 39:249-257(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M84174; G187869; -.
DR HSP; P03989; ILSA.
DR MIM; 142840; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 333
FT DOMAIN 334 366
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
FT CARBOHYD 366 AA; 40772 MW; A59EF965 CRC32;
SQ SEQUENCE 366 AA; 40772 MW; A59EF965 CRC32;
Found using 'seq1' (seq1.key)
...

89 qkykpaqtdrslrnlrgyynqseqagshi
99 108
...

1 match found in sequence:
1C12_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW*0801 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1C12_HUMAN STANDARD; PRT; 366 AA.
AC P30505;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW*0801 ALPHA CHAIN
DE PRECURSOR (CW8.1).
GN HLAC.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93031775.
RA ZEMMOUR J., GUMPERZ J.E., HILDEBRAND W.H., WARD F.E., MARSH S.G.,
RA WILLIAMS R.C., PARHAM P.;
RL TISSUE ANTIGENS 39:249-257(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M84174; G187869; -.
DR HSP; P03989; ILSA.
DR MIM; 142840; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 333
FT DOMAIN 334 366
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
FT CARBOHYD 366 AA; 40772 MW; A59EF965 CRC32;
SQ SEQUENCE 366 AA; 40772 MW; A59EF965 CRC32;
Found using 'seq1' (seq1.key)
...

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CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M84172; G187865; -.
DR HSP; P03989; ILSA.
DR MIM; 142840; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 333
FT DOMAIN 334 366
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
FT CARBOHYD 366 AA; 40784 MW; C1B041C6 CRC32;
SQ SEQUENCE 366 AA; 40784 MW; C1B041C6 CRC32;
Found using 'seq1' (seq1.key)
...

89 qkykpaqtdrslrnlrgyynqseqagshi
99 108
...

1 match found in sequence:
1C12_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW*0801 ALPHA CHAIN
(from "Swiss-Prot 34")
ID 1C12_HUMAN STANDARD; PRT; 366 AA.
AC P30505;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW*0801 ALPHA CHAIN
DE PRECURSOR (CW8.1).
GN HLAC.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93031775.
RA ZEMMOUR J., GUMPERZ J.E., HILDEBRAND W.H., WARD F.E., MARSH S.G.,
RA WILLIAMS R.C., PARHAM P.;
RL TISSUE ANTIGENS 39:249-257(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M84174; G187869; -.
DR HSP; P03989; ILSA.
DR MIM; 142840; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 333
FT DOMAIN 334 366
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
FT CARBOHYD 366 AA; 40772 MW; A59EF965 CRC32;
SQ SEQUENCE 366 AA; 40772 MW; A59EF965 CRC32;
Found using 'seq1' (seq1.key)
...

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Found using 'seq1' (seq1.key)

```
...
89 qkykrqatdrvslrnlrgyngseagsh
99 |-----|
108
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1 match found in sequence:  
1C13\_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW\*0802 ALPHA CHAIN  
(from "Swiss-Prot 34")

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ID 1C13_HUMAN STANDARD; PRT; 366 AA.
AC P30506;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW*0802 ALPHA CHAIN
DE PRECURSOR (CW8.2).
GN HLAC.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX MEDLINE: 93031775.
RA ZEMMOUR J., GUMPERZ J.E., HILDEBRAND W.H., WARD F.E., MARSH S.G.,
RA WILLIAMS R.C., PARHAM P.;
RL TISSUE ANTIGENS 39:249-257(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC EMBL; M84173; G187867; -.
DR DR HSSP; P03989; ILSA.
DR MIM; 142840; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN CW-8 CW*0802.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 333 CONNECTING PEPTIDE.
FT DOMAIN 334 366 CYTOPLASMIC TAIL.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.
SQ SEQUENCE 366 AA; 40871 MW; 450BD038 CRC32;
Found using 'seq1' (seq1.key)
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...
89 qkykrqatdrvslrnlrgyngseagsh
99 |-----|
108
```

1 match found in sequence:  
1C14\_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW\*0803 ALPHA CHAIN  
(from "Swiss-Prot 34")

```
ID 1C14_HUMAN STANDARD; PRT; 366 AA.
AC P30507;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW*0803 ALPHA CHAIN
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DE PRECURSOR.
GN HLAC.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX MEDLINE: 92269955.
RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
RA WILLIAMS R.C., LOZ R., PETZL-ERLER M.L., PARHAM P.;
RL NATURE 357:326-329(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC EMBL; Z15144; G28357; -.
DR DR HSSP; P03989; ILSA.
DR MIM; 142840; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 ALPHA CHAIN CW-8 CW*0803.
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 333 CONNECTING PEPTIDE.
FT DOMAIN 334 366 CYTOPLASMIC TAIL.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.
SQ SEQUENCE 366 AA; 40872 MW; F54756A6 CRC32;
Found using 'seq1' (seq1.key)

...
89 qkykrqatdrvslrnlrgyngseagsh
99 |-----|
108

...
1 match found in sequence:
1C15_HUMAN ; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*1201 ALPHA CHAIN PREC
(from "Swiss-Prot 34")
ID 1C15_HUMAN STANDARD; PRT; 366 AA.
AC P30508;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*1201 ALPHA CHAIN PRECURSOR
DE (HLA-CX52).
GN HLAC.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX MEDLINE: 88330144.
RA TAKATA H., INOKO H., ANDO A., HARANAKA M., WATANABE B., TSUJI K.,
RA IRI H.;
RL IMUNOGENETICS 28:265-270(1988).
RN [2]
RP SEQUENCE FROM N.A.
RA TAKATA H., SONODA A., BECK S., HEYES J.M., BODMER J.G., INOKO H.;
RL SUBMITTED (JUN-1992) TO EMBL/GENBANK/DDJ DATA BANKS.
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC EMBL; M21963; G188541; -.

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DR HSP; P03989; ILSA.
DR MIM; 142840; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366
FT DOMAIN 25 114 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 115 206 ALPHA CHAIN CW*1201.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-1.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-2.
FT TRANSMEM 309 333 EXTRACELLULAR ALPHA-3.
FT DOMAIN 334 366 CONNECTING PEPTIDE.
FT DOMAIN 334 366 CYTOPLASMIC TAIL.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.
SQ SEQUENCE 366 AA; 40851 MW; 0E9BB9A5 CRC32;
Found using 'seq1' (seq1.key)
...

89 qkykrqaqdrvslnrlrgyngseqsht
...
1 match found in sequence:
1C17_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*1401 ALPHA CHAIN PRECU
(from "Swiss-Prot 34")
ID 1C17_HUMAN STANDARD; PRT; 366 AA.
AC P30510;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW*1401 ALPHA CHAIN PRECURSOR
GN HLA-CB-1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89309827.
RA TAKIGUCHI M., NISHIMURA I., HAYASHI H., KARAKI S., KARIYONE A.,
RA KANO K.;
RX MEDLINE; 89309827.
RA J. IMMUNOL. 143:1372-1378(1989).
RL CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M28171; G386905; -.
DR HSP; P03989; ILSA.
DR MIM; 142840; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 366
FT DOMAIN 25 114 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 115 206 ALPHA CHAIN CW*1401.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-1.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-2.
FT TRANSMEM 309 333 EXTRACELLULAR ALPHA-3.
FT DOMAIN 334 366 CONNECTING PEPTIDE.
FT DOMAIN 334 366 CYTOPLASMIC TAIL.
FT DISULFID 125 188 BY SIMILARITY.
FT DISULFID 227 283 BY SIMILARITY.
FT CARBOHYD 110 110 BY SIMILARITY.
SQ SEQUENCE 366 AA; 40855 MW; 05F828B2 CRC32;
Found using 'seq1' (seq1.key)
...

```

```

89 qkykrqaqdrvslnrlrgyngseqsht
...
1 match found in sequence:
1CX_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, C-4 ALPHA CHAIN.
(from "Swiss-Prot 34")
ID 1CX_HUMAN STANDARD; PRT; 342 AA.
AC P10321;
DT 01-MAR-1989 (REL. 10, CREATED)
DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, C-4 ALPHA CHAIN.
GN HLA-C.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 8603791.
RA DAVIDSON W.F., KRESS M., KHOURY G., JAY G.;
RL J. BIOL. CHEM. 260:13414-13423(1985).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M11886; G386777; -.
DR PIR; A24512; HLHUC4.
DR HSP; P03989; ILSA.
DR MIM; 142840; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN.
FT DOMAIN 25 90 EXTRACELLULAR ALPHA-1.
FT DOMAIN 91 182 EXTRACELLULAR ALPHA-2.
FT DOMAIN 183 274 EXTRACELLULAR ALPHA-3.
FT DOMAIN 275 284 CONNECTING PEPTIDE.
FT TRANSMEM 285 309
FT DOMAIN 310 342 CYTOPLASMIC TAIL.
FT CARBOHYD 86 86 BY SIMILARITY.
FT DISULFID 164 203 BY SIMILARITY.
SQ SEQUENCE 342 AA; 38082 MW; CDSF7D52 CRC32;
Found using 'seq1' (seq1.key)
...

65 qkykrqaqdrvslnrlrgyngseqsht
...
1 match found in sequence:
HALL_MOUSE; H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, D-B ALPHA CHAIN PRECURSOR
(from "Swiss-Prot 34")
ID HALL_MOUSE STANDARD; PRT; 362 AA.
AC P01899;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, D-B ALPHA CHAIN PRECURSOR.
GN H2-D.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H;
RX MEDLINE; 88060499.

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RA WATTS S., VOGEL J.M., HARRIMAN W.D., ITOH T., STAUSS H.J.,
RA GOODENOW R.S.;
RL J. IMMUNOL. 139:3878-3885(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD/LT;
RA GIRGIS K.R., CAPRA D.J., STROYNOWSKI I.;
RL SUBMITTED (MAY-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN [3]
RP SEQUENCE OF 105-362 FROM N.A.
RX MEDLINE; 83005712.
RA REYES A.A., SCHOLD M., WALLACE R.B.;
RL IMMUNOGENETICS 16:1-9(1982).
RN [4]
RP SEQUENCE OF 25-122.
RX MEDLINE; 81142266.
RA MALOY W.L., NATHENSON S.G., COLIGAN J.E.;
RL J. BIOL. CHEM. 256:2863-2872(1981).
RN [5]
RP SEQUENCE OF 253-308 AND 332-358.
RX MEDLINE; 83005713.
RA MALOY W.L., COLIGAN J.E.;
RL IMMUNOGENETICS 16:11-22(1982).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 25-296.
RX MEDLINE; 94116065.
RA YOUNG A.C.M., ZHANG W., SACCHETTINI J.C., NATHENSON S.G.;
RL CELL 76:39-50(1994).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M18523; G387452; -.
DR EMBL; L36068; G797272; -.
DR EMBL; K00129; G199341; ALT_INIT.
DR PIR; A02200; HLMSDB.
DR PDB; 1HOC; 30-APR-94.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.
FT SIGNAL 1 24
FT CHAIN 25 362
FT FT
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 309
FT DOMAIN 310 331
FT DOMAIN 332 362
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
FT CARBOHYD 200 200
FT CARBOHYD 280 280
FT STRAND 27 36
FT STRAND 47 51
FT STRAND 56 61
FT TURN 62 63
FT TURN 70 71
FT TURN 75 76
FT TURN 77 79
FT TURN 81 81
FT TURN 82 109
FT TURN 110 110
FT STRAND 118 127
FT TURN 129 130
FT STRAND 133 142
FT TURN 143 144
FT STRAND 145 150
FT TURN 152 153
FT STRAND 157 159
FT TURN 163 163
FT TURN 164 173
FT HELIX 174 175
FT TURN
RA WATTS S., VOGEL J.M., HARRIMAN W.D., ITOH T., STAUSS H.J.,
RA GOODENOW R.S.;
RL J. IMMUNOL. 139:3878-3885(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD/LT;
RA GIRGIS K.R., CAPRA D.J., STROYNOWSKI I.;
RL SUBMITTED (MAY-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN [3]
RP SEQUENCE OF 105-362 FROM N.A.
RX MEDLINE; 83005712.
RA REYES A.A., SCHOLD M., WALLACE R.B.;
RL IMMUNOGENETICS 16:1-9(1982).
RN [4]
RP SEQUENCE OF 25-122.
RX MEDLINE; 81142266.
RA MALOY W.L., NATHENSON S.G., COLIGAN J.E.;
RL J. BIOL. CHEM. 256:2863-2872(1981).
RN [5]
RP SEQUENCE OF 253-308 AND 332-358.
RX MEDLINE; 83005713.
RA MALOY W.L., COLIGAN J.E.;
RL IMMUNOGENETICS 16:11-22(1982).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 25-296.
RX MEDLINE; 94116065.
RA YOUNG A.C.M., ZHANG W., SACCHETTINI J.C., NATHENSON S.G.;
RL CELL 76:39-50(1994).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M18523; G387452; -.
DR EMBL; L36068; G797272; -.
DR EMBL; K00129; G199341; ALT_INIT.
DR PIR; A02200; HLMSDB.
DR PDB; 1HOC; 30-APR-94.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.
FT SIGNAL 1 24
FT CHAIN 25 362
FT FT
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 309
FT DOMAIN 310 331
FT DOMAIN 332 362
FT DISULFID 125 188
FT DISULFID 227 283
FT CARBOHYD 110 110
FT CARBOHYD 200 200
FT CARBOHYD 280 280
FT STRAND 27 36
FT STRAND 47 51
FT STRAND 56 61
FT TURN 62 63
FT TURN 70 71
FT TURN 75 76
FT TURN 77 79
FT TURN 81 81
FT TURN 82 109
FT TURN 110 110
FT STRAND 118 127
FT TURN 129 130
FT STRAND 133 142
FT TURN 143 144
FT STRAND 145 150
FT TURN 152 153
FT STRAND 157 159
FT TURN 163 163
FT TURN 164 173
FT HELIX 174 175
FT TURN
FT HELIX 176 185
FT TURN 186
FT HELIX 187 196
FT TURN 197 198
FT TURN 200 204
FT STRAND 210 210
FT STRAND 213 213
FT TURN 220 221
FT STRAND 225 232
FT STRAND 238 243
FT TURN 244 245
FT STRAND 246 247
FT TURN 250 251
FT STRAND 253 254
FT STRAND 258 259
FT STRAND 265 271
FT TURN 275 276
FT TURN 278 279
FT STRAND 281 286
FT TURN 288 289
SQ SEQUENCE 362 AA; 40836 MW; 6C5B86B5 CRC32;
Found using 'seq1' (seq1.key)
...
89 qkkgqgqfwfrslrnllgynyqsagshsht
99 108
...
-----
1 match found in sequence:
HA14_MOUSE ; H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, D-P ALPHA CHAIN PRECURSOR
(from "Swiss-Prot 34")
ID HA14_MOUSE STANDARD; PRT; 368 AA.
AC P14427;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, D-P ALPHA CHAIN PRECURSOR.
GN H2-D.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86169714.
RA SCHEPART B.S., TAKAHASHI H., COZAD K.M., MURRAY R., OZATO K.,
RA APPELLA E., FRELINGER J.A.;
RL J. IMMUNOL. 136:3489-3495(1986).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M12381; G387454; -.
DR HSSP; P01901; IYAA.
DR PROSITE; PS00290; IG_MHC.
DR MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 21
FT CHAIN 22 368
FT FT
FT DOMAIN 22 111
FT DOMAIN 112 203
FT DOMAIN 204 295
FT DOMAIN 296 300
FT TRANSMEM 304 330
FT DOMAIN 331 368
FT DISULFID 122 185
FT DISULFID 224 280
FT CARBOHYD 107 107
FT CARBOHYD 197 197
FT CARBOHYD 277 277
H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN,
D-P ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
POTENTIAL.

```

SQ SEQUENCE 368 AA; 41342 MW; 7D4C13C1 CRC32;  
Found using 'seq1' (seq1.key)

...

86 qnakdheqsfvrlnllgyynqsgsht  
96 105

...

-----  
1 match found in sequence:  
HLAH\_HUMAN; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, H ALPHA CHAIN PRECURSOR  
(from "Swiss-Prot 34")  
ID HLAH\_HUMAN STANDARD; PRT; 362 AA.  
AC P01893;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)  
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)  
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, H ALPHA CHAIN PRECURSOR  
DE (HLA-AR) (HLA-12.4).  
GN HLAH.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 82151002.  
RA MALISSEN M., MALISSEN B., JORDAN B.R.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 79:893-897(1982).  
CC !- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
THE IMMUNE SYSTEM.  
CC !- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
MICROGLOBULIN).  
CC EMBL: V00526; G386873; ALT\_INIT.  
DR PIR: A02189; HLH12.  
DR HSP: P03989; 1HSA.  
DR MIM: 142925.  
DR PROSITE: PS00290; IG\_MHC.  
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
FT SIGNAL 1 24  
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
ALPHA CHAIN H.  
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.  
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.  
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.  
FT DOMAIN 299 308 CONNECTING PEPTIDE.  
FT TRANSMEM 309 332 CYTOPLASMIC TAIL.  
FT DOMAIN 333 362 BY SIMILARITY.  
FT CARBOHYD 110 110 BY SIMILARITY.  
FT DISULFID 227 283 BY SIMILARITY.  
SQ SEQUENCE 362 AA; 40850 MW; 5E610F63 CRC32;  
Found using 'seq1' (seq1.key)

...

89 qickaqaqternlrlyalryynqsgsht  
99 108

...

--- Search Statistics ---  
Times: CPU Total Elapsed  
00:03:44.14 00:04:09.00  
Number of sequences searched: 241556  
Number of sequence hits: 232  
Number of separate matches: 232  
Number of sequence hits saved: 0

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
 Run on: Thu May 22 08:45:38 1997; MasPar time 1.81 Seconds  
 Tabular output not generated. 70.334 Million cell updates/sec

(TM)

\*\*\*\*\*

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:45:38 1997; MasPar time 1.81 Seconds  
 Tabular output not generated. 70.334 Million cell updates/sec

Title: >US-08-653-294-7  
 Description: (1-6) from US08653294.pep  
 Perfect Score: 49  
 Sequence: 1 YRLAIR 6

Scoring table: PAM 150  
 Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries  
 Maximum DB seq length 60

Database: swiss-prot34  
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
 8:part8 9:part9 10:part10 11:part11

Statistics: Mean 22.440; Variance 22.471; scale 0.999

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query	No.	Score	Match	Length	ID	Description	Pred. No.
-----								

No matches found.

Search completed: Thu May 22 08:45:46 1997  
 Job time : 8 secs.

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\*\*\*\*\*

WATERMAN (TM)

\*\*\*\*\*

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:50:08 1997; MasPar time 2.66 Seconds  
128.376 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-653-294-36  
Description: (1-12) from US08653294.pep  
Perfect Score: 98  
Sequence: 1 YRLAIRRIALRY 12

Scoring table: PAM 150  
Gap 15

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Maximum DB seq length 60

Database: pir50  
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3  
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8  
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 26.905; Variance 45.950; scale 0.586

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description	Pred. No.
--------	-------	-------	-------	--------	----	----	-------------	-----------

No matches found.

Search completed: Thu May 22 08:50:18 1997  
Job time : 10 secs.

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MPERCH (TM)

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MPerch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:49:45 1997; MasPar time 1.88 Seconds  
135.656 Million cell updates/sec

Tabular output not generated.

Title: >US-08-653-294-36  
Description: (1-12) from US08653294.pep  
Perfect Score: 98  
Sequence: 1 YRLAIRRLRY 12

Scoring table: PAM 150  
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries  
Maximum DB seq length 60

Database: swiss-prot34  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 28.088; Variance 37.415; scale 0.751

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query				
No.	Score	Match	Length	ID	Description
					Pred. No.

No matches found.

Search completed: Thu May 22 08:49:51 1997  
Job time : 6 secs.

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MPrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 08:26:14 1997; MasPar time 2.05 Seconds

Tabular output not generated. 61.975 Million cell updates/sec

Title: >US-08-653-294-4  
 Description: (1-6) from US08653294.p  
 Perfect Score: 49  
 Sequence: 1 RIALRY 6

Scoring table: PAM 150  
Gap 15

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: swiss-prot34  
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
 8:part8 9:part9 10:part10 11:part11

Statistics: Mean 22.521; Variance 22.707; scale 0.992

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	49	100.0	359	1	1B01_PANTR CHLA CLASS I HISTOCOMP 5.42e-01	
2	49	100.0	362	1	1B45_HUMAN HLA CLASS I HISTOCOMP 5.42e-01	
3	49	100.0	362	1	1B01_GORGO CLASS I HISTOCOMPATIB 5.42e-01	
4	49	100.0	362	1	1B47_HUMAN HLA CLASS I HISTOCOMP 5.42e-01	
5	49	100.0	362	1	1B52_HUMAN HLA CLASS I HISTOCOMP 5.42e-01	
6	49	100.0	362	1	1B03_GORGO CLASS I HISTOCOMPATIB 5.42e-01	
7	49	100.0	362	1	1B02_GORGO CLASS I HISTOCOMPATIB 5.42e-01	
8	49	100.0	362	1	1B15_HUMAN HLA CLASS I HISTOCOMP 5.42e-01	
9	49	100.0	362	1	1B54_HUMAN HLA CLASS I HISTOCOMP 5.42e-01	
10	49	100.0	362	1	1B62_HUMAN HLA CLASS I HISTOCOMP 5.42e-01	
11	49	100.0	362	1	1B61_HUMAN HLA CLASS I HISTOCOMP 5.42e-01	
12	49	100.0	362	5	HLAH_HUMAN HLA CLASS I HISTOCOMP 5.42e-01	
13	49	100.0	362	1	1B53_HUMAN HLA CLASS I HISTOCOMP 5.42e-01	
14	49	100.0	362	1	1B60_HUMAN HLA CLASS I HISTOCOMP 5.42e-01	
15	49	100.0	365	1	1A04_GORGO CLASS I HISTOCOMPATIB 5.42e-01	
16	49	100.0	365	1	1A23_HUMAN HLA CLASS I HISTOCOMP 5.42e-01	
17	49	100.0	365	1	1A32_HUMAN HLA CLASS I HISTOCOMP 5.42e-01	
18	49	100.0	365	1	1A24_HUMAN HLA CLASS I HISTOCOMP 5.42e-01	
19	49	100.0	365	1	1A25_HUMAN HLA CLASS I HISTOCOMP 5.42e-01	
20	46	93.9	409	1	AA2A_CAVPO ADENOSINE A2A RECEPTO 2.89e+00	
21	46	93.9	410	1	AA2A_RAT ADENOSINE A2A RECEPTO 2.89e+00	
22	46	93.9	412	1	AA2A_HUMAN ADENOSINE A2A RECEPTO 2.89e+00	

23	46	93.9	412	1	AA2A_CANFA ADENOSINE A2A RECEPTO 2.89e+00
24	46	93.9	1420	1	APOA_MACMU APOLIPOPROTEIN(A) (EC 2.89e+00
25	45	91.8	383	6	MEYA_PSEAE MULTIDRUG RESISTANCE 4.96e+00
26	45	91.8	462	2	COXA_YEAST CYTOCHROME C OXIDASE 4.96e+00
27	45	91.8	880	8	RNA-DIRECTED RNA POLY 4.96e+00
28	45	91.8	959	6	MSH1_YEAST NUTS PROTEIN HOMOLOG 4.96e+00
29	45	91.8	1726	8	RPB1_YEAST DNA-DIRECTED RNA POLY 4.96e+00
30	45	91.8	1752	8	RPB1_SCHPO DNA-DIRECTED RNA POLY 4.96e+00
31	45	91.8	2225	8	PYR1_HUMAN CAD PROTEIN (CONTAINS 4.96e+00
32	45	91.8	2225	8	PYR1_MESAU CAD PROTEIN (CONTAINS 4.96e+00
33	44	89.8	85	10	V192_BPT7 GENE 19.2 PROTEIN. 8.43e+00
34	44	89.8	332	1	AA2B_RAT ADENOSINE A2B RECEPTO 8.43e+00
35	44	89.8	638	1	60 KD INNER-MEMBRANE 8.43e+00
36	44	89.8	953	2	COBP_RAT COATOMER BETA SUBUNIT 8.43e+00
37	43	87.8	646	6	LEPA_MYCLE GTP-BINDING PROTEIN L 1.42e+01
38	43	87.8	767	5	HREB_ECOLI ATP-DEPENDENT HELICAS 1.42e+01
39	43	87.8	817	8	RRPO_CRV PROBABLE RNA-DIRECTED 1.42e+01
40	43	87.8	817	8	RRPO_CNV PROBABLE RNA-DIRECTED 1.42e+01
41	43	87.8	817	8	RRPO_TBSVC PROBABLE RNA-DIRECTED 1.42e+01
42	43	87.8	968	4	HEPA_ECOLI PROBABLE ATP-DEPENDEN 1.42e+01
43	43	87.8	1859	8	RPB1_CAEEL DNA-DIRECTED RNA POLY 1.42e+01
44	42	85.7	436	10	VU10_HSV6U U10 PROTEIN. 2.36e+01
45	42	85.7	1165	3	CYA6_CANFA ADENYLATE CYCLASE, TY 2.36e+01

#### ALIGNMENTS

RESULT 1  
 ID 1B01\_PANTR STANDARD; PRT; 359 AA.  
 AC P13750;  
 DT 01-JAN-1990 (REL. 13, CREATED)  
 DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)  
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)  
 DE CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR  
 DE (FRAGMENT).  
 OS PAN TROGLODYTES (CHIMPANZEE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 89030641.  
 RA MAYER W.E.; JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,  
 RA KLEIN J.;  
 RL EMBO J. 7:2765-2774(1988).  
 RN [2]  
 RP REVISIONS.  
 RA MAYER W.;  
 RL SUBMITTED (FEB-1989) TO EMBL/GENBANK/DBJ DATA BANKS.  
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 THE IMMUNE SYSTEM.  
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 MICROGLOBULIN).  
 CC EMBL; X13115; G755776; -.  
 DR FIR; S03537; S03537.  
 DR HSSP; P03989; 1HSA.  
 DR PROSITE; PS00290; IG\_MHC.  
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
 FT NON\_TER 1  
 FT SIGNAL <1 20  
 FT CHAIN 21 359  
 FT  
 FT DOMAIN 11 110  
 FT DOMAIN 21 202  
 FT DOMAIN 203 294  
 FT DOMAIN 295 305  
 FT DOMAIN 306 329  
 FT DOMAIN 330 359  
 FT DOMAIN 121 184  
 FT DISULFID 223 279  
 FT DISULFID 106 106  
 FT CARBOHYD 359 AA; 40173 MW; 53955FFC9 CRC32;  
 SQ SEQUENCE  
 Query Match 100.0%; Score 49; DB 1; Length 359;

Best Local Similarity 100.0%; Pred. No. 5.42e-01;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 rialry 104  
| | | | |  
QY 1 RIALRY 6

RESULT 2  
ID 1849\_HUMAN STANDARD; PRT; 362 AA.  
AC P18464;  
DT 01-NOV-1990 (REL. 16, CREATED)  
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B\*51(B-5) B\*5101 ALPHA CHAIN  
DE PRECURSOR.  
GN HLAB.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 90207291.  
RA ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 89080265.  
RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,  
RA TAKIGUCHI M.;  
RL J. IMMUNOL. 142:306-311(1989).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 89233295.  
RA POHLA H., KOON W., TABACZESKI P., DOERNER C., WEISS E.H.;  
RL IMMUNOGENETICS 29:297-307(1989).  
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
THE IMMUNE SYSTEM.  
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
MICROGLOBULIN).  
DR EMBL; M22319; G307223; -.  
DR EMBL; M22792; G553533; ALT\_SEQ.  
DR EMBL; M22786; G553533; JOINED.  
DR EMBL; M22787; G553533; JOINED.  
DR EMBL; M22788; G553533; JOINED.  
DR EMBL; M22789; G553533; JOINED.  
DR EMBL; M22790; G553533; JOINED.  
DR EMBL; M22791; G553533; JOINED.  
DR EMBL; L41087; G735902; -.  
DR EMBL; L41086; G735902; JOINED.  
DR PIR; A30345; A30345.  
DR PIR; A30548; A30548.  
DR HSP; P03989; ILSA.  
DR MIM; 142830; -.  
DR PROSITE; PS00290; IG\_MHC.  
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
FT SIGNAL 1 24  
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
ALPHA CHAIN B\*51(B-5) B\*5101.  
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.  
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.  
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.  
FT DOMAIN 299 308 CONNECTING PEPTIDE.  
FT TRANSMEM 309 332 CYTOPLASMIC TAIL.  
FT DOMAIN 333 362 BY SIMILARITY.  
FT DISULFID 110 110 BY SIMILARITY.  
FT CARBOHYD 125 188 BY SIMILARITY.  
FT DISULFID 227 283 BY SIMILARITY.  
SQ SEQUENCE 362 AA; 40566 MW; 4D846F30 CRC32;

Query Match 100.0%; Score 49; DB 1; Length 362;  
Best Local Similarity 100.0%; Pred. No. 5.42e-01;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108  
| | | | |  
QY 1 RIALRY 6

RESULT 3  
ID 1B01\_GORGO STANDARD; PRT; 362 AA.  
AC P30379;  
DT 01-APR-1993 (REL. 25, CREATED)  
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)  
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)  
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECURSOR.  
OS GORILLA GORILLA GORILLA (LOWLAND GORILLA).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 92078860.  
RA LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;  
RL J. EXP. MED. 174:1491-1509(1991).  
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
THE IMMUNE SYSTEM.  
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
MICROGLOBULIN).  
DR EMBL; X60255; G22866; -.  
DR PIR; JH0539; JH0539.  
DR HSP; P03989; ILSA.  
DR PROSITE; PS00290; IG\_MHC.  
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
FT SIGNAL 1 24  
FT CHAIN 25 362 CLASS I HISTOCOMPATIBILITY ANTIGEN,  
GOGO-B0101 ALPHA CHAIN.  
FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.  
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.  
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.  
FT DOMAIN 299 308 CONNECTING PEPTIDE.  
FT TRANSMEM 309 332 CYTOPLASMIC TAIL.  
FT DOMAIN 333 362 BY SIMILARITY.  
FT DISULFID 125 188 BY SIMILARITY.  
FT DISULFID 227 283 BY SIMILARITY.  
FT CARBOHYD 110 110 BY SIMILARITY.  
SQ SEQUENCE 362 AA; 40170 MW; 2E33E2B8 CRC32;

Query Match 100.0%; Score 49; DB 1; Length 362;  
Best Local Similarity 100.0%; Pred. No. 5.42e-01;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108  
| | | | |  
QY 1 RIALRY 6

RESULT 4  
ID 1B47\_HUMAN STANDARD; PRT; 362 AA.  
AC P30487;  
DT 01-APR-1993 (REL. 25, CREATED)  
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B\*49(B-21) B\*4901 ALPHA CHAIN  
DE PRECURSOR.  
GN HLAB.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 89235215.  
RA PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;  
RL J. IMMUNOL. 142:3937-3950(1989).  
RN [2]  
RP REVISIONS TO 78.  
RX MEDLINE; 93056529.



RA HILDEBRAND W.H., MADRIGAL J.A., BELICH M.P., ZEMMOUR J., WARD F.E.,  
 RL J. IMMUNOL. 149:3563-3568(1992).  
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 DR EMBL; M24037; G407191; -.  
 DR HSSP; P03989; IHSA.  
 DR MIM; 142830; -.  
 DR PROSITE; PS00290; IG\_MHC.  
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 24  
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 FT ALPHA CHAIN B-49(B-21) B\*4901.  
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.  
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.  
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.  
 FT DOMAIN 299 309 CONNECTING PEPTIDE.  
 FT TRANSMEM 310 333  
 FT DOMAIN 334 362 CYTOPLASMIC TAIL.  
 FT CARBOHYD 110 110 BY SIMILARITY.  
 FT DISULFID 125 188 BY SIMILARITY.  
 FT DISULFID 227 283 BY SIMILARITY.  
 SQ SEQUENCE 362 AA; 40581 MW; E996F82F CRC32;  
 Query Match 100.0%; Score 49; DB 1; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 5.42e-01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 103 rialry 108  
 QY 1 RIALRY 6  
 RESULT 5  
 ID 1B52\_HUMAN STANDARD; PRT; 362 AA.  
 AC P30489;  
 DT 01-APR-1993 (REL. 25, CREATED)  
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)  
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)  
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B\*5104 ALPHA CHAIN  
 DE PRECURSOR.  
 GN HLAB.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 92269955.  
 RA BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,  
 RA WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;  
 RL NATURE 357:326-329(1992).  
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 DR EMBL; Z15143; G28235; -.  
 DR HSSP; P03989; IHSA.  
 DR MIM; 142830; -.  
 DR PROSITE; PS00290; IG\_MHC.  
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 24  
 FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 FT ALPHA CHAIN B-51(B-5) B\*5104.  
 FT DOMAIN 25 114 EXTRACELLULAR ALPHA-1.  
 FT DOMAIN 115 206 EXTRACELLULAR ALPHA-2.  
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.  
 FT DOMAIN 299 308 CONNECTING PEPTIDE.  
 FT TRANSMEM 309 332  
 FT DOMAIN 333 362 CYTOPLASMIC TAIL.  
 FT CARBOHYD 110 110 BY SIMILARITY.  
 FT DISULFID 125 188 BY SIMILARITY.

FT DISULFID 227 283 BY SIMILARITY.  
 SQ SEQUENCE 362 AA; 40560 MW; F22F08AB CRC32;  
 Query Match 100.0%; Score 49; DB 1; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 5.42e-01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 103 rialry 108  
 QY 1 RIALRY 6  
 RESULT 6  
 ID 1B03\_GORGO STANDARD; PRT; 362 AA.  
 AC P30381;  
 DT 01-APR-1993 (REL. 25, CREATED)  
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)  
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)  
 DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0103 ALPHA CHAIN PRECURSOR.  
 DE GORILLA GORILLA (LOWLAND GORILLA).  
 OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 92078860.  
 RA LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;  
 RL J. EXP. MED. 174:1491-1509(1991).  
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 DR EMBL; X60254; G22870; -.  
 DR PIR; JH0541; JH0541.  
 DR HSSP; P03989; IHSA.  
 DR PROSITE; PS00290; IG\_MHC.  
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 24  
 FT CHAIN 25 362 BY SIMILARITY.  
 FT DOMAIN 25 114 CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 FT DOMAIN 115 206 GOGO-B0103 ALPHA CHAIN.  
 FT DOMAIN 207 298 EXTRACELLULAR ALPHA-1.  
 FT DOMAIN 299 308 EXTRACELLULAR ALPHA-2.  
 FT TRANSMEM 309 332 EXTRACELLULAR ALPHA-3.  
 FT DOMAIN 333 362 CONNECTING PEPTIDE.  
 FT DISULFID 125 188 CYTOPLASMIC TAIL.  
 FT DISULFID 227 283 BY SIMILARITY.  
 FT CARBOHYD 110 110 BY SIMILARITY.  
 SQ SEQUENCE 362 AA; 40248 MW; FEA6A941 CRC32;  
 Query Match 100.0%; Score 49; DB 1; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 5.42e-01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 103 rialry 108  
 QY 1 RIALRY 6  
 RESULT 7  
 ID 1B02\_GORGO STANDARD; PRT; 362 AA.  
 AC P30380;  
 DT 01-APR-1993 (REL. 25, CREATED)  
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)  
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)  
 DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECURSOR.  
 DE GORILLA GORILLA (LOWLAND GORILLA).  
 OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 92078860.  
 RA LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;

RL J. EXP. MED. 174:1491-1509(1991).  
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 DR EMBL; X60693; G22868; -.  
 DR PIR; JH0540; JH0540.  
 DR HSSP; P03989; 1HSA.  
 DR PROSITE; PS00290; IG\_MHC.  
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 24  
 FT CHAIN 25 362  
 FT DOMAIN 25 114  
 FT DOMAIN 115 206  
 FT DOMAIN 207 298  
 FT DOMAIN 299 308  
 FT TRANSMEM 309 332  
 FT DOMAIN 333 362  
 FT CARBOHYD 110 110  
 FT DISULFID 125 188  
 FT DISULFID 227 283  
 FT CARBOHYD 110 110  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.  
 SQ SEQUENCE 362 AA; 40204 MW; 3CFI19AD CRC32;  
 Query Match 100.0%; Score 49; DB 1; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 5.42e-01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 103 rialry 108  
 QY 1 RIALRY 6  
 RESULT 8  
 ID 1B15\_HUMAN STANDARD; PRT; 362 AA.  
 AC P10317;  
 DT 01-MAR-1989 (REL. 10, CREATED)  
 DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)  
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)  
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B\*2702 ALPHA CHAIN  
 DE PRECURSOR (B-27K) (B27.2).  
 GN HLAB.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 86220133.  
 RA SEEMANN G.H.A.; REIN R.S.; BROWN C.S.; PLOEGH H.L.;  
 RL EMBO J. 5:547-552(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA FARHAM P.; ARNETT K.L.; ADAMS E.J.;  
 RL SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RN [3]  
 RP SEQUENCE OF 86-107 AND 171-181.  
 RX MEDLINE; 86042671.  
 RA VEGA M.A.; EZQUERRA A.; ROJO S.; APARICIO P.; BRAGADO R.;  
 RA LOPEZ DE CASTRO J.A.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 82:7394-7398(1985).  
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 CC EMBL; X03684; G871296; -.  
 DR EMBL; X03667; G871296; JOINED.  
 DR EMBL; L38504; G896271; -.  
 DR PIR; B25092; HLHUBK.  
 DR HSSP; P03989; 1HSA.  
 DR MIM; 142830;  
 DR PROSITE; PS00290; IG\_MHC.  
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 24

FT CHAIN 25 362  
 FT DOMAIN 25 114  
 FT DOMAIN 115 206  
 FT DOMAIN 207 298  
 FT DOMAIN 299 308  
 FT TRANSMEM 309 332  
 FT DOMAIN 333 362  
 FT CARBOHYD 110 110  
 FT DISULFID 125 188  
 FT DISULFID 227 283  
 SQ SEQUENCE 362 AA; 40397 MW; 9798F0BB CRC32;  
 Query Match 100.0%; Score 49; DB 1; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 5.42e-01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 103 rialry 108  
 QY 1 RIALRY 6  
 RESULT 9  
 ID 1B54\_HUMAN STANDARD; PRT; 362 AA.  
 AC P30491;  
 DT 01-APR-1993 (REL. 25, CREATED)  
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)  
 DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)  
 DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 B\*5301 ALPHA CHAIN  
 DE PRECURSOR.  
 GN HLAB.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 91033941.  
 RA HAYASHI H.; Ooba T.; NAKAYAMA S.; SEKIMATA M.; KANO K.;  
 RA TAKIGUCHI M.;  
 RL IMMUNOGENETICS 32:195-199(1990).  
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 DR EMBL; M58336; G187757; -.  
 DR PIR; A45834; A45834.  
 DR HSSP; P03989; 1HSA.  
 DR MIM; 142830; -.  
 DR PROSITE; PS00290; IG\_MHC.  
 KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 24  
 FT CHAIN 25 362  
 FT DOMAIN 25 114  
 FT DOMAIN 115 206  
 FT DOMAIN 207 298  
 FT DOMAIN 299 308  
 FT TRANSMEM 309 332  
 FT DOMAIN 333 362  
 FT CARBOHYD 110 110  
 FT DISULFID 125 188  
 FT DISULFID 227 283  
 SQ SEQUENCE 362 AA; 40495 MW; 2BDC746E CRC32;  
 Query Match 100.0%; Score 49; DB 1; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 5.42e-01;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 103 rialry 108  
 QY 1 RIALRY 6

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RESULT 10
ID 1B62_HUMAN STANDARD; PRT; 362 AA.
AC P10319;
DT 01-MAR-1989 (REL. 10, CREATED)
DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-58(B-17) B*5801 ALPHA
DE CHAIN PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN). CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 86008247.
RA WAYS J.P., COPPIN H.L., PARHAM P.;
RL J. BIOL. CHEM. 260:11924-11933(1985).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M11799; G386885; -.
DR PIR; A23895; HLH08.
DR MIN; 142830; -.
DR HSSP; P03989; IHSA.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT SEQUENCE 362 AA; 40337 MW; 355E7534 CRC32;
Query Match 100.0%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.42e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108
Qy 1 RIALRY 6

RESULT 11
ID 1B61_HUMAN STANDARD; PRT; 362 AA.
AC P30497;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B*57(B-17) B*5702 ALPHA CHAIN
DE PRECURSOR (BW57.2).
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93056508.
RA MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
RA LITTLE A.M., ZEMOUR J., ENNIS P.D., WARD F.E., PETEL-ERLER M.L.,
RA MARTELL R.W., DU TOIT E.D., PARHAM P.;
RL J. IMMUNOL. 149:3411-3415(1992).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).

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DR EMBL; X61707; G32187; -.
DR PIR; S16774; S16774.
DR HSSP; P03989; IHSA.
DR MIN; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
FT SEQUENCE 362 AA; 40342 MW; 628C2156 CRC32;
Query Match 100.0%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.42e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108
Qy 1 RIALRY 6

RESULT 12
ID HLAH_HUMAN STANDARD; PRT; 362 AA.
AC P01893;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, H ALPHA CHAIN PRECURSOR
DE (HLA-AR) (HLA-12.4).
GN HLAH.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 82151002.
RA MALISEN M., MALISEN B., JORDAN B.R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 79:893-897(1982).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; V00526; G386873; ALT_INIT.
DR PIR; A02189; HLH012.
DR HSSP; P03989; IHSA.
DR MIN; 142925; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 227 283
FT SEQUENCE 362 AA; 40850 MW; 5E610F63 CRC32;
Query Match 100.0%; Score 49; DB 5; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.42e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 103 r1alry 108
QY 1 RIALRY 6

RESULT 13
ID 1B53_HUMAN STANDARD; PRT; 362 AA.
AC P30490;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN
DE PRECURSOR.
GN HLAB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX MEDLINE: 85080265.
RA HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
RA TAKIGUCHI M.;
RL J. IMMUNOL. 142:306-311(1989).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M22799; G553538; ALT_SEQ.
DR EMBL; M22793; G553538; JOINED.
DR EMBL; M22794; G553538; JOINED.
DR EMBL; M22795; G553538; JOINED.
DR EMBL; M22796; G553538; JOINED.
DR EMBL; M22797; G553538; JOINED.
DR EMBL; M22798; G553538; JOINED.
DR PIR; B30345; B30345.
DR PIR; B30548; B30548.
DR HSP; P03989; ILSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40521 MW; 3B436FE8 CRC32;

Query Match 100.0%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.42e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 r1alry 108
QY 1 RIALRY 6

RESULT 14
ID 1B60_HUMAN STANDARD; PRT; 362 AA.
AC P18465;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5701 ALPHA
DE CHAIN PRECURSOR (BW57.1).
GN HLAB.
OS HOMO SAPIENS (HUMAN).

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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE; 90207291.
RA ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2833-2837(1990).
RN [2]
RX SEQUENCE FROM N.A.
RX MEDLINE; 91067476.
RA ISAMAT M., GIRDLESTONE J., MILSTEIN C.;
RL NUCLEIC ACIDS RES. 18:6702-6702(1990).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; M32318; G307222; -.
DR EMBL; X55711; G32181; -.
DR PIR; S12622; S12622.
DR PIR; D35997; D35997.
DR HSP; P03989; ILSA.
DR MIM; 142830; -.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114
FT DOMAIN 115 206
FT DOMAIN 207 298
FT DOMAIN 299 308
FT TRANSMEM 309 332
FT DOMAIN 333 362
FT CARBOHYD 110 110
FT DISULFID 125 188
FT DISULFID 227 283
SQ SEQUENCE 362 AA; 40224 MW; D91DF8DD CRC32;

Query Match 100.0%; Score 49; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.42e-01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 r1alry 108
QY 1 RIALRY 6

RESULT 15
ID 1A04_GORGO STANDARD; PRT; 365 AA.
AC P30378;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-A0501 ALPHA CHAIN PRECURSOR.
DE GORILLA GORILLA GORILLA (LOWLAND GORILLA).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE; 9207860.
RA LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
RL J. EXP. MED. 174:1491-1509(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
DR EMBL; X60256; G22860; -.
DR PIR; JH0537; JH0537.
DR HSP; P01892; IHHG.
DR PROSITE; PS00290; IG_MHC.
KW MHC I; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 365
FT CLASS I HISTOCOMPATIBILITY ANTIGEN,

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FT DOMAIN 25 114 GOGO-A0501 ALPHA CHAIN.  
FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.  
FT DOMAIN 207 288 EXTRACELLULAR ALPHA-2.  
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.  
FT TRANSMEM 309 332 CONNECTING PEPTIDE.  
FT DOMAIN 333 365 CYTOPLASMIC TAIL.  
FT DISULFID 125 188 BY SIMILARITY.  
FT DISULFID 227 283 BY SIMILARITY.  
FT CARBOHYD 110 110 BY SIMILARITY.  
SQ SEQUENCE 365 AA; 40895 MW; 520225DF CRC32;

Query Match 100.0%; Score 49; DB 1; Length 365;  
Best Local Similarity 100.0%; Pred. No. 5.42e-01;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 rialry 108  
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|  
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|  
QY 1 RIALRY 6

Search completed: Thu May 22 08:26:26 1997  
Job time : 12 secs.

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